Abundance estimation and Conservation Biology

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Abundance is the state variable of interest in most population–level ecological research and in most programs involving management and conservation of animal populations. Abundance is the single parameter of interest in capture–recapture models for closed populations (e.g., Darroch, 1958; Otis et al., 1978; Chao, 2001). The initial capture–recapture models developed for partially (Darroch, 1959) and completely (Jolly, 1965; Seber, 1965) open populations represented efforts to relax the restrictive assumption of population closure for the purpose of estimating abundance. Subsequent emphases in capture–recapture work were on survival rate estimation in the 1970's and 1980's (e.g., Burnham et al., 1987; Lebreton et al., 1992), and on movement estimation in the 1990's (Brownie et al., 1993; Schwarz et al., 1993). However, from the mid–1990's until the present time, capture–recapture investigators have expressed a renewed interest in abundance and related parameters (Pradel, 1996; Schwarz & Arnason, 1996; Schwarz, 2001). The focus of this session was abundance, and presentations covered topics ranging from estimation of abundance and rate of change in abundance, to inferences about the demographic processes underlying changes in abundance, to occupancy as a surrogate of abundance.

The plenary paper by Link & Barker (2004) is provocative and very interesting, and it contains a number of important messages and suggestions. Link & Barker (2004) emphasize that the increasing complexity of capture–recapture models has resulted in large numbers of parameters and that a challenge to ecologists is to extract ecological signals from this complexity. They offer hierarchical models as a natural approach to inference in which traditional parameters are viewed as realizations of stochastic processes. These processes are governed by hyperparameters, and the inferential approach focuses on these hyperparameters. Link & Barker (2004) also suggest that our attention should be focused on relationships between demographic processes such as survival and recruitment, the two quantities responsible for changes in abundance, rather than simply on the magnitudes of these quantities. They describe a type of Jolly–Seber capture–recapture model that permits inference about the underlying relationship between per capita recruitment rates and survival rates (Link & Barker, this volume). Implementation used Bayesian Markov Chain Monte Carlo methods and appeared to work well, yielding inferences about the relationship between recruitment and survival that were robust to selection of prior distribution. We believe that readers will find their arguments compelling, and we expect to see increased use of hierarchical modeling approaches in capture–recapture and related fields.

Otto (presentation without paper) also recommended use of hierarchical models in analysis of multiple data sources dealing with population dynamics of North American mallards. He integrated survival inferences from ringing data, abundance information from aerial survey data, and recruitment information based on age ratios from a harvest survey. He used a Leslie matrix population projection model as an integrating framework and obtained estimates of breeding population size using all data.

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Otto's approach also permitted inference about biases in estimated quantities. As with the work of Link & Barker (2004), we find Otto's recommendation to use hierarchical models to integrate data from multiple sources to be very compelling.

Alisauskas et al. (2004) report results of an analysis of capture–recapture data for a Saskatchewan population of white–winged scoters. They used the approach of Pradel (1996) to estimate population growth rate (λ) directly. Estimates for 1975–1985 were quite low, but estimates for the recent period, 2000–2003, increased to values > 1. Parameter estimates for seniority, survival and per capita recruitment (Pradel, 1996) led to the inference that increased recruitment was largely responsible for the improvements in population status and growth. However, various data sources also indicated that this increase in recruitment was likely a result of increased immigration rather than improved reproduction on the area. This latter inference is important from a conservation perspective in indicating the importance of birds in other locations to growth and health of the study population.

Lukacs and Burnham presented material to be published elsewhere that dealt with the use of genetic markers in capture–recapture studies. The data sources for such studies are samples of hair or feces, which are then analyzed using molecular genetic techniques in order to determine individual genotypes with respect to a usually small number of loci. Two types of classification error can arise in such analyses. First, if only a small number of loci is examined, then there may be nonnegligible probabilities that multiple individual animals will have the same genotypes. The second type of error arises during the polymerase chain reaction (PCR) process and can result from failure of alleles to amplify (allelic dropout) or from PCR inhibitors in hair and feces that produce the appearance of false alleles or misprinting (Creel et al., 2003). Lukacs and Burnham developed models that formally incorporate possible misclassification of samples resulting from these errors. These models permit estimation of parameters such as abundance and survival in a manner that properly incorporates this uncertainty of individual identity. We anticipate that noninvasive sampling based on molecular genetic analyses of hair or feces will become extremely important for some species, and that the models of Lukacs and Burnham will become very popular for such analyses.

MacKenzie & Nichols (2004) discuss the use of occupancy (proportion of patches or habitat area that is occupied) as a surrogate for abundance. In cases of territorial species and where birds occur at low densities, the number of occupied patches may provide a reasonable estimate of abundance. In other cases, occupancy can be viewed as providing information about one tail of the abundance distribution, $P(N = 0)$. The motivation for considering occupancy as a surrogate for abundance is that occupancy is based on so–called presence–absence surveys that are frequently less expensive of time and effort than methods that estimate abundance directly. We describe one set of models that can be used to estimate occupancy for a single season and another that can be used to estimate parameters such as local probabilities of extinction and colonization that are associated with occupancy dynamics. We outline a possible hybrid approach that combines occupancy data with data on marked individuals in order to better explore the mechanisms underlying occupancy dynamics.

These five presentations made for an interesting session containing useful information and recommendations for future work. A number of themes connecting these presentations could be emphasized. For example, two of the presentations considered alternatives to standard capture–recapture sampling that can be used to draw inferences about abundance, or a portion of the abundance distribution, with field methods that should be less expensive than usual capture–recapture approaches of handling animals. We believe that the most important theme of the session was the emphasis on the processes responsible for changes in abundance. In particular, we are excited by the potential for using hierarchical models as a means of investigating relationships among vital rates and as a means of combining multiple sources of data relevant to system dynamics. Indeed, we expect the importance of this session theme to be reflected in the content and presentations of the next EURING meeting.

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