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Hierarchical models and the analysis of bird survey information

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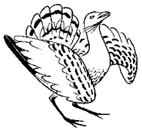

Management of birds often requires analysis of collections of estimates. We describe a hierarchical modeling approach to the analysis of these data, in which parameters associated with the individual species estimates are treated as random variables, and probability statements are made about the species parameters conditioned on the data. A Markov-Chain Monte Carlo (MCMC) procedure is used to fit the hierarchical model. This approach is computer intensive, and is based upon simulation. MCMC allows for estimation both of parameters and of derived statistics. To illustrate the application of this method, we use the case in which we are interested in attributes of a collection of estimates of population change. Using data for 28 species of grassland-breeding birds from the North American Breeding Bird Survey, we estimate the number of species with increasing populations, provide precision-adjusted rankings of species trends, and describe a measure of population stability as the probability that the trend for a species is within a certain interval. Hierarchical models can be applied to a variety of bird survey applications, and we are investigating their use in estimation of population change from survey data.

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1. Introduction

In studies of the population ecology of birds, collections of species are often the subject of analyses. In North America, population change and abundance of groups of species that share a common characteristic such as migration status (*e.g.* Neotropical migrants) or breeding habitats (*e.g.* grassland birds) have been the subject of much public interest due to perceived declines (*e.g.* Peterjohn & Sauer 1999, Robbins *et al*. 1989). Furthermore, conservation initiatives focus on taxa such as waterfowl (*e.g.* the North American Waterfowl Management Plan), shorebirds, or colonial waterbirds that share a common life history characteristic. Managers are interested in summarizing information for these taxa, and may use the collective response of all species as a response measure for management.

A common summary of group population change, or an interval-specific trend, is often of primary interest to managers. The average population trend, number of "declining" species, number of species with significant trend estimates, ranks of species by population trend, and lists of species with extreme changes are often presented for groups (Link & Sauer 1995). Managers also seek to identify species whose populations are unstable or changing. In this paper, we discuss some of the difficulties associated with summary of attributes of groups of species. Our focus is on summary of collections of estimates of population trend, but the hierarchical model approach we describe can be used for many attributes. A more complete discussion of the models and methods used in this paper is available in Sauer and Link (2002).

1.1 Are Summaries Meaningful?

The fundamental notion associated with summary of group attributes is that the collection of species is meaningful, in that some common characteristic of the species permits summary of population attributes among species. Often, conceptual and practical difficulties exist with any summary. Practical concerns include the problem that quality of information may vary greatly among species; simple averages and summaries of estimates can be misleading. Conceptual difficulties are based on the notion that all species are different, and that all groupings rely on the characteristic of interest to be a common influence for all groups. For example, several North American grassland-breeding birds also winter in South America, while others winter in North America. Any grouping is likely to compartmentalize only a portion of the variation associated with the attribute of interest (Mannan *et al*. 1984). It is also likely that taxonomic similarity is partially confounded with other possible groups, and hence any similarities may reflect common ancestry (Pagel & Harvey 1991).

1.2. Difficulties Associated with Imprecise Information.

Collections of estimates of population trend tend to differ in both estimated magnitude and precision of individual estimates. An imprecise trend estimate may be quite large while still having a confidence interval large enough to include zero, indicating that the trend is not significantly different from zero. Magnitude alone is therefore not sufficient to establish the importance of a trend estimate. However, ‘statistical significance’ is also a flawed criterion, because a very small rate of change may be identified as ‘statistically significant’ but be of no practical significance. Separating notions of statistical significance from magnitude of trend has been a conceptual difficulty for exercises in species prioritization. In any collection of trend estimates, some are very imprecise, some are very precise, and all summaries of results are influenced by these differences in estimated precision. The consequences are:

1. Simple averages of trend estimates are generally not good descriptors of the collection.
2. Ranked lists of trends do not reflect the real ranking of trends.
3. Number of species with positive trend estimates is not a good estimate of the number of species with positive trends.

1.3. Analysis of Collections of Estimates

For single species analyses, we generally consider the data Y_s to be governed by a fixed, unknown parameter θ_s. Statistics are based on distribution of data, given the unknown parameter, $f(Y_s|\theta_s)$. For multiple species, it is reasonable to view parameters as random variables sampled from some distribution. These multi-level models in which data and parameters are both random variables are called hierarchical Models. In these models data are observed, but their distributions are described conditionally on realized values of parameters that are also random variables. This necessitates that one or more additional levels of distributional assumptions should be included in the analysis.

Hierarchical models are often analyzed using Bayesian methods. Bayes approaches are model-based, and are used to make probability statements about θ_s (Gilks *et al*. 1996). In a Bayes analysis, we define the standard sampling distribution of the data given the unknown parameter, or $f(Y_s|\theta_s)$, but also define the distribution of the parameters in a prior, or $\pi(\theta_s|\Psi)$, where Ψ is a represents hyperparameters that govern the distribution of the parameters. Bayesian inference about the θ_s is based on the posterior distribution $f(\theta_s|Y_s)$. Unfortunately, derivation of the posterior distribution is often difficult mathematically, limiting the use of Bayes analyses for complicated models. Definitions of the prior also can be controversial, because the prior makes assumptions about the distribution of parameters.

2. Implementing Hierarchical Models

In earlier publications, we used empirical Bayes methods to implement a hierarchical model for species group attributes (Link & Sauer 1995). In empirical Bayes, hyperparameters are estimated using information from the data. We applied a simple model to the case of estimation of a prior mean trend for the group, and then we estimated posterior means of the species trend parameters. These ‘shrunken’ estimates are a weighted average of the prior mean (the estimate of the group mean trend parameter) and the estimated trend. The resulting estimate for each species is intermediate between the original estimated trend and the prior mean, with the actual value dependant on the relative precision of the original trend. We used this model to re-order trends (Link & Sauer 1996), and to estimate the number of increasing species using a bootstrapping procedure (Link & Sauer 1995). However this approach is limited, because quite simple models must be used.

Here, we implement a complete analysis using Markov Chain Monte Carlo (MCMC) methods, a very flexible procedure for fitting hierarchical models. MCMC is a simulation-based approach to estimation, in which:

1. A model is defined in terms of distributions of parameters and hyperparameters.
2. The distribution information for each variable is written as ‘full conditionals,’ distributions with all other parameters being fixed.
3. An iterative sampling is conducted using these full conditionals.

This iterative procedure produces results that converge on posterior distributions for the parameters. See Spiegelhalter *et al.* (1995) or Sauer and Link (2002) for more details of the estimation procedure.

3. Our Model

We assume that a series of *n* trend estimates $\hat{\beta}_s$, $s=1, 2,\ldots, n$, exist, and that these estimates are normal random variables with parameters β_s and σ^2_s. The estimated variance $\hat{\sigma}^2_s$ is distributed as a chi-square. The parameter β_s is distributed as a normal distribution with hyperparameters μ and

τ^2. The hyperparameters are also assumed to follow distributions, with μ distributed normally (mean 0, variance=100 000), and τ^2 and σ^2_s are assumed to follow gamma distributions.

To fit this model, we used Program BUGS (Spiegelhalter *et al*. 1995). In this program, a simulation is conducted as described above. After a large number of iterations, the results converge on posterior distributions. After this convergence occurs, the simulation is continued and each iteration provides a set of replicate results based on sampling from the distributions. Consequently, means and variances from the simulation results can be used as estimates of parameters and hyperparameters and their variances.

3.1 Estimates Produced by our Analysis

The estimates associated with parameter β_s represent the posterior mean trend estimates for individual species. These can be thought of as precision-adjusted estimates that are 'shrunken' toward the overall prior mean estimate (μ). These numbers are similar to the re-ordered trend estimates described by Link & Sauer (1995), but the MCMC approach better accommodates imprecision in the estimates of precision than did the empirical Bayes approach. The number of species with positive trend estimates (N_{Inc}) are estimated directly from the MCMC results, simply by counting the number of positive posterior mean trend estimates from each MCMC replicate and using these as replicates to obtain a mean and variance.

3.2 Defining Population Stability

Another attribute that can be derived from the MCMC analysis is a notion of stable populations. Population stability has proven difficult to define using estimated population trends because of the difficulties associated with use of magnitude of trends, because large estimated trends may simply be poorly estimated. However, use of the posterior mean trends from the MCMC accommodates the relative imprecision in the context of the collection of estimates, and can be used to define a stable population. We define stability in terms of a maximum acceptable deviation of trend from 0, denoted as δ. The probability that population is stable can be defined as $\Pr(\beta_s \in (-\delta,\delta)|Y)$, that is, the probability that the posterior mean is in the interval, conditional on the observed data Y. Given δ and a probability *p*, we can estimate the probability that β_s is not in $(-\delta,\delta)$ exceeds *p*, or $\Pr(\beta_s \in (-\delta,\delta)|Y) \leq 1-p$. This quantity can be evaluated directly from the MCMC replicates, simply by determining whether each replicate of β_s is in the interval $(-\delta,\delta)$. The proportion of replicates that fall outside the interval is an estimate of *p*.

3.3. MCMC Analysis

The North American Breeding Bird Survey (BBS) provides population change data for 28 species of grassland-breeding birds for the survey interval 1966-2000. The BBS is a roadside survey, conducted along secondary roads in the United States and Canada. The 24.5-mile routes are surveyed once each year, in June, and are composed of 50 stops, at which 3-minute point counts are conducted. Total counts of individuals of each species summed over the route comprise the yearly index to abundance. Estimating trends (% change /

year) over the survey interval using the Route-regression trend estimates (Link & Sauer 1994) provides estimates that differ greatly in precision and magnitude among species, although many species are declining. 61% of species have significant negative trends, and only 18% of species have trend estimates >0.

From the North American Breeding Bird Survey, we conducted the MCMC analysis on the 28 grassland bird species for which trends could be estimated over the interval 1966-2000. We calculated the posterior mean estimates β_s, estimated the number of species with positive trend estimates, and calculated the probability that each species is stable for δ=2%/year.

Species rankings are summarized in Fig. 1, in which the trends are ranked by size of posterior mean and the estimated trends are displayed for each posterior mean estimate. The posterior mean estimates show less variation, especially for the species with extreme estimates of increases and declines. This is evident from observation of individual species estimates. For example, the estimated trend for Henslow's Sparrow *Ammodramus henslowii* was -7.46%/*yr*, n=155, but the posterior mean trend was -3.91%/*yr*. For Baird's Sparrow *A. bairdii* the estimated trend was -2.88, n=124, but the posterior mean was -2.35. The populations of four species were estimated to be unstable, using the 2% criterion and a critical value of P<0.10: Eastern Meadowlark *Sturnella magna*, posterior mean trend -2.87, P<0.001; Grasshopper Sparrow *A. savannarum*, -3.71, P<0.001; Henslow's Sparrow and Sprague's Pipit *Anthus spragueii*, -4.73, P=0.055. The N of species with positive trend estimates was 5.16 species (*SE*: 1.216), while the naive estimate (*i.e.* based on the estimated trends) was 5. Although similar, the MCMC estimate has a precision estimate associated with it. In this case, the similarity indicates that most species in the group were quite precisely estimated.

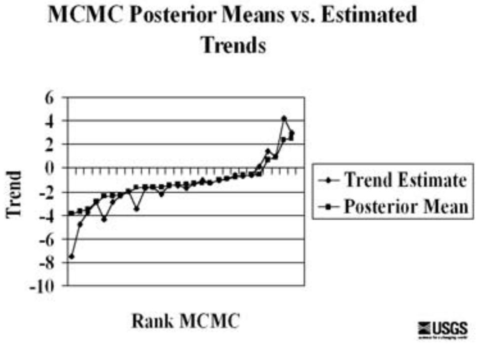

Fig. 1. Posterior mean trends, ranked by magnitude, displayed with estimated trends.

4. Benefits of Hierarchical Models

The hierarchical models described here provide an appropriate conceptual framework for dealing with collections of estimates. The hierarchical structure provides a framework for estimating attributes associated with the parameters, and the MCMC provides a convenient tool for estimation. The derived attributes such as population stability and number of increasing species can be conveniently estimated during the MCMC simulations. Although some of these attributes can also be defined using empirical Bayes methods, the MCMC approach is superior in that it provides much greater flexibility in defining models and implementing the estimation. In the case described here, the MCMC had an additional component that accommodated uncertainty in estimation of the variance of the estimated trends, and our earlier empirical Bayes procedures could not accommodate this source of variation.

The population stability metric is a useful attribute, in that it resolves the consistent difficulty associated with defining population stability based on magnitude of estimated trends. Because estimated trends differ greatly in precision, the magnitude of the trend does not convey the significance of the trend. Use of the posterior mean estimates does accommodate the relative precision of the estimates and is an appropriate measure of actual magnitude of trend.

We note that there are many other applications for hierarchical models in estimation of population attributes. We are developing methods for estimation of population change using hierarchical models that will accommodate regional variation in precision of time series (Link & Sauer 2002). Finally, we note that although hierarchical models are computer intensive, they are now relatively easy to implement in programs such as BUGS.

References

Gilks, W. R., Richardson, S. & D. J. Spiegelhalter. 1996. Markov Chain Monte Carlo in Practice. – Chapman and Hall, New York, USA.

Link, W. A. & J. R. Sauer. 1995. Estimation of empirical mixing distributions in summary analyses. – Biometrics 51: 810-821.

Link, W. A. & J. R. Sauer. 1996. Extremes in ecology: avoiding the misleading effects of sampling variation in summary analyses. – Ecology 77: 1633-1640.

Link, W. A. & J. R. Sauer. 1998. Estimating population change from count data: application to the North American Breeding Bird Survey. – Ecol. Appl. 8: 258-268.

Link, W. A. & J. R. Sauer. 2002. A hierarchial model of population change with application to Cerulean Warblers. – Ecology 83: 2832-2840.

Mannan, R. W., Morrison, M. L. & E. C. Meslow. 1984. Comment: the use of guilds in forest bird management. – Wildlife Soc. Bull. 12: 426-430.

Pagel, P. H. & M. D. Harvey. 1991. The comparative method in evolutionary biology. – Oxford University Press, New York, USA.

Peterjohn, B. G. & J. R. Sauer. 1999. Population status of North American grassland birds from the North American Breeding Bird Survey, 1966 - 1996. – Stud. in Avian Biol. 19: 27-44.

Robbins, C. S., Sauer, J. R., Greenberg, R. S. & S. Droege. 1989. Population declines in North American birds that migrate to the Neotropics. – Proc. Nati. Acad. Sci., USA 86: 7658-7662.

Sauer, J. R. & W. A. Link. (2002) Hierarchical modeling of population stability and species group attributes using Markov Chain Monte Carlo methods. – Ecology 83: 1743-1751.

Spiegelhalter, D. J., Thomas, A., Best, N. G. & W. R. Gilks. 1995. BUGS: Bayesian inference using Gibbs sampling, Version 0.50. MRC Biostatistics Unit, Cambridge, U.K.