- Harrell, F. E., Jr. 2001. Regression modeling strategies. Springer, New York, New York, USA.
- Hilborn, R., and M. Mangel. 1997. The ecological detective: confronting models with data. Princeton University Press, Princeton, New Jersey, USA.
- Hurlbert, S. 1984. Pseudoreplication and the design of ecological field experiments. Ecological Monographs 54: 187–211.
- Ionides, E. L., C. Bretó, and A. A. King. 2006. Inference for nonlinear dynamical systems. Proceedings of the National Academy of Sciences (USA) 103:18438–18443.
- Jackson, D. L. 2003. Revisiting sample size and number of parameter estimates: some support for the N : q hypothesis. Structural Equation Modeling 10:128–141.
- Kerman, J. 2007. Umacs: universal Markov chain sampler. R package version 0.924. (http://cran.r-project.org/web/ packages/Umacs/)
- Lele, S. R., B. Dennis, and F. Lutscher. 2007. Data cloning: easy maximum likelihood estimation for complex ecological models using Bayesian Markov chain Monte Carlo methods. Ecology Letters 10:551–563.

- Martin, A. D., K. M. Quinn, and J. H. Park. 2008. MCMCpack: Markov chain Monte Carlo (MCMC) package. R package version 0.9-4. (http://mcmcpack.wustl.edu)
- McCarthy, M. 2007. Bayesian methods for ecology. Cambridge University Press, Cambridge, UK.
- Oksanen, L. 2001. Logic of experiments in ecology: is pseudoreplication a pseudoissue? Oikos 94:27–38.
- Okuyama, T., and B. M. Bolker. 2005. Combining genetic and ecological data to estimate sea turtle origins. Ecological Applications 15:315–325.
- Spiegelhalter, D. J., N. Best, B. P. Carlin, and A. Van der Linde. 2002. Bayesian measures of model complexity and fit. Journal of the Royal Statistical Society B 64:583–640.
- Ver Hoef, J. M., and K. Frost. 2003. A Bayesian hierarchical model for monitoring harbor seal changes in Prince William Sound, Alaska. Environmental and Ecological Statistics 10: 201–209.
- Whittingham, M. J., P. A. Stephens, R. B. Bradbury, and R. P. Freckleton. 2006. Why do we still use stepwise modelling in ecology and behaviour? Journal of Animal Ecology 2675: 1182–1189.
- Woodworth, G. G. 2004. Biostatistics: a Bayesian introduction. Wiley, Hoboken, New Jersey, USA.

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Preaching to the unconverted

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Rapid advances in computing in the past 20 years have lead to an explosion in the development and adoption of new statistical modeling tools (Gelman and Hill 2006, Clark 2007, Bolker 2008, Cressie et al. 2009). These innovations have occurred in parallel with a tremendous increase in the availability of ecological data. The latter has been fueled both by new tools that have facilitated data collection and management efforts (e.g., remote sensing, database management software, and so on) and by increased ease of data sharing through computers and the World Wide Web. The impending implementation of the National Ecological Observatory Network (NEON) will further boost data availability. These rapid advances in the ability of ecologists to collect data have not been matched by application of modern statistical tools. Given the critical questions ecology is facing (e.g., climate change, species extinctions, spread of invasives, irreversible losses of ecosystem services) and the benefits that can be gained

from connecting existing data to models in a sophisticated inferential framework (Clark et al. 2001, Pielke and Connant 2003), it is important to understand why this mismatch exists. Such an understanding would point to the issues that must be addressed if ecologists are to make useful inferences from these new data and tools and contribute in substantial ways to management and decision making.

Encouraging the adoption of modern statistical methods such as hierarchical Bayesian (HB) models requires that we consider three distinct questions: (1) What are the benefits of using these methods relative to existing, widely used approaches? (2) What are the barriers to their adoption? (3) What approaches would be most effective in promoting their use? The first question has to do with motivation, that is, why does one build a complex statistical model? Like Cressie et al. (2009) we argue that while the goal of a model may be estimation, prediction, forecasting, explanation, or simplification, the purpose of modeling is the synthesis of information. However, HB methods are not the only tools available for synthesis (Hobbs and Hilborn 2006). So the question needs to be refined to address the specific benefits to be derived from HB models relative

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to more traditional statistical approaches vis-a-vis specific user goals. The second question deals primarily with education, which we believe to be the main barrier to the widespread adoption of these methods. Lastly, answers to the third question build on the answers of questions 1 and 2 to propose a series of actions that would lead to a wider use of HB methods in ecology.

1. What are the benefits to be derived from HB models relative to other statistical tools?.-Statistical modeling in general and HB modeling in particular, are powerful means to synthesize diverse sources of information. With respect to other statistical means of synthesis, hierarchical models have the advantage of allowing us to coherently model processes at multiple levels. Consider, for example, how we might answer the question of the extent to which 10 species growth rates differ and whether differences between tree species in growth rates are correlated to some species trait, ST. One option might be to first fit separate models using growth data for each individual species together with important covariates (e.g., individual level measurements), and then use the results to fit a regression of the mean growth of each species versus their mean ST values. Another option might be to fit all the data at once and include the ST repeated for all individuals in the plot. Although each of these approaches might work adequately, consider now that you have 100 species with unequal sample sizes. With hierarchical models we could include predictors at both the species and individual levels and allow for partial pooling to improve inferences on rarer species in a way that does not ignore the initial uncertainty in the species growth estimates when estimating the effect of ST across species.

Although the above statistical model could be fit using non-Bayesian hierarchical models, HB becomes a superior choice as we try to incorporate more of our understanding of a process into a model. Returning to the example above, consider the case in which there is spatial autocorrelation between individuals sampled in the same area and we realized that growth was measured with error. Both are real concerns that we might typically ignore or deal with in some ad hoc way; however in a HB framework these sources of error could easily be included an estimated as long as we had an adequate data set.

In addition to their value for synthesis, and of far more pragmatic significance, is the value of HB as a tool for inference, particularly through the process of model checking. The majority of ecologists seek to use data to infer which processes are key in structuring populations, communities and ecosystems. Inference is at the heart of our discipline and therefore attaining the statistical literacy necessary to use HB models can be extremely rewarding, since such models allow us to incorporate the complex variance structures inherent in most biological systems. By working with simulated data derived from HB models, rather than simple point estimates (with associated confidence intervals), we can capture inferential uncertainty and propagate it into predictions in a straightforward manner (Gelman and Hill 2006). The ability to not only make predictions from models but also to quantify the uncertainty in our predictions, is imperative for providing sound scientific advice for management and policy decision makers.

For biologists interested solely in basic, rather than applied questions, prediction serves as an important tool for inference. If we approach a problem with an open mind and the understanding that models are always an approximation of reality, then comparison of the actual data to replicate observations drawn from the posterior predictive distribution (i.e., simulated observations based on our model) becomes a learning exercise rather than an effort to formalize what we already know or believe. Although Cressie et al. (2009) argue that model checking is necessary, but tedious, we see it not only as the key to inference but also as one of the strongest selling points of HB models. Prediction using traditional statistical tools is limited, allowing only for a very limited representation of the true complexity of ecological data. In this context, model checking is an opportunity to truly understand what the models are saying, learn which parts of reality are not captured adequately and suggest future steps. In particular, if simulated data sets do not match the original data sets adequately it leads directly to further model development, reexamination of our interpretation of prior studies, or alterations in experimental design for collection of additional data (Fig. 1).

That model development typically follows model checking illustrates that actual modeling of complex data sets is typically an iterative process. Multiple simpler models are fitted before attempts at the full hierarchical model that we may have had in mind all along or that may have evolved as we critically evaluate the process we are trying to model and better understand the data. Published studies typically emphasized final models but understanding the iterative process of model checking and model development is a key to demystifying modeling to an audience of beginners, who are often supplied only with unfamiliar technical descriptions of models in the methods and little discussion of model fit or misfit. Although standard statistical models caution against extensive model checking because it can lead to overfitting (data dredging), in a simulation framework checks are means of understanding the limits of the models' applicability in realistic replications rather than a reason for accepting or rejecting a model.

From a conceptual perspective, HB models offer a consistent framework that allows the user to apply a large, flexible number of models with complex variance structures (e.g., repeated-measures models, time series analysis, simultaneous consideration of observation and process error, and so on). This is important not only because we can tackle more complex problems but also because it offers a way to educate students and practitioners in a more self-consistent and coherent

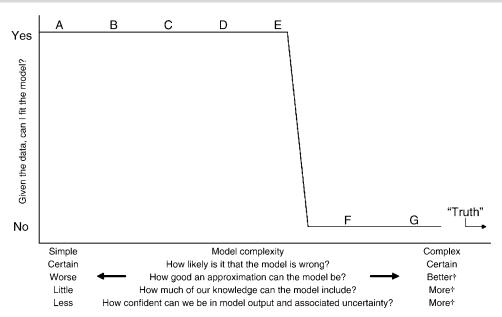


FIG. 1. The model fitting process often consists of fitting progressively more complex models (e.g., A, then B) and/or trying and failing at fitting more complex models (e.g., G, then F) and working backward until one finds a more simplified model that can be fit with the data available (e.g., E). The exact location of the cutoff between E and F will depend on the nature of the data at hand. Knowing which part of reality to allow back into the model by relaxing assumptions or partitioning uncertainty is dependent both on an understanding of the ecological question, the data, and one's statistical literacy. As model complexity increases, one can more closely approximate reality, include more substantial outside (prior) knowledge/intuition, and gain more confidence in the model output and associated uncertainty; however, added complexity only helps if ecological understanding is properly translated into the model structure (the daggers in the figure indicate this caveat).

In the example, Cressie et al. (2009) address a number of models of differing complexity. Model A might correspond to a simple linear regression of numbers vs. time. Such unrealistically simplified models could potentially lead to estimates with tight confidence intervals and low P values, but unreliable inference. Model B might correspond to a generalized linear model with Poisson distributed errors, whereas model C might correspond to the simplest model considered by Cressie et al. (2009), a generalized linear mixed model with multiple explanatory variables. In this context, model C has the advantage that it is no longer assumed that all sites are the same, something we know is false. Partitioning uncertainty into all its potential components and adding site-specific parameters may lead to a model F that cannot be fit with the data at hand, while adding in the assumption that site parameters are related and come from a distribution may result in model D.

approach to statistical analysis that gets away from what has termed a "field-key" approach to statistics, where students collect statistical tools and techniques but fail to see any connections among them at a deep level (Clark 2005, Hobbs and Hilborn 2006).

2. What are the main barriers to the adoption of HB methods?.-Using HB methods is not easy. There are considerable conceptual and computational barriers to overcome. Conceptually, students must move from a descriptive, test-based statistical framework to an inferential, estimation-based, complex one. Learning to use HB methods requires a larger initial investment to gain a holistic understanding of statistical inference, as opposed to the short term solutions of finding a test for the question at hand or restricting oneself to questions that can be answered with the tests we already know. HB methods may not always be the best tool for answering a particular question, and often simpler methods may be adequate. Nonetheless, learning HB opens up the possibility of addressing a range of previously intractable questions that more accurately encompass the complexity of biological systems. As ecologists accrue larger datasets, much of it based on remotely gathered data with multiple sources of error, the potential benefits of adopting more complex models increase, moving the curve in Fig. 1 further to the right. Often, students will not see the need for the initial investment in learning HB methods because they lack an understanding of its potential benefits and they perceive modeling as a skill rather than as a tool that anyone can pick up. Thus, ignorance begets indifference, or worst, fear. If they see a paper in say, Ecological Applications exhorting the benefits of HB models, they are likely to turn the page and dismiss it as just another modeling paper or simply over their heads. Even if a student or practitioner is interested, the barriers may seem insurmountable without at least some knowledge of either programming or advanced statistical methods.

Indeed, such knowledge is a prerequisite for learning HB methods. One way to acquire these skills is through formal graduate-level courses. Curricula that connect models and quantitative thinking to important questions in ecology have proven to both ignite students' interest in modeling and to convey the relevance and usefulness of models. However, many ecology and evolution programs still rely on statistics departments to train their students and only a few offer advanced statistical methods courses within their department. Farming out ecology students to be trained in statistics departments is far from ideal because courses are likely to be developed to address the needs of statistics students rather than those of other areas of science. If students fail to see the relevance of the methods to their own discipline, motivation will decline.

Although there are a number of open, short-term courses available (Duke University summer course in ecological forecasting, one-day workshop in Bayesian methods at the Ecological Society of America annual meetings), these offerings are limited, unpredictable, and costly. Moreover, short courses education in HB models often requires not only some programming skills but a complete conceptual overhaul of the students' existing conceptual statistical framework. Although short courses may offer an entry into HB models, the tension between a focus on tools (e.g., WinBUGS) and concepts is very real when time is limited.

A second way to learn HB is through self-teaching. Although a few books have appeared in the last couple of years that make self-teaching possible (Woodworth 2004, Gelman and Hill 2006, Clark 2007, McCarthy 2007), it is still a daunting task to learn these methods on your own without a support network. Fortunately, cyber-communities are becoming an increasingly important form of scientific exchange, and considerable progress can be made in this way (e.g., contributions and exchanges around the development and use of R and WinBUGS Statistical freeware). Auto-didactic approaches are powerful means to learn but they often leave behind major lacunas in knowledge because they tend to focus on the mechanics of carrying out complex statistical analysis with little attention paid to the foundations of underlying statistical inference (e.g., Taper and Lele 2004).

Another barrier to the adoption of HB is the lack of consensus in many of the details of implementation. HB methods are relatively new and there seems to be a lack of consensus on what are the best non-informative priors to use, how best to assess convergence, the utility of deviance information criterion (DIC), etc. This is a major barrier to biologists who are trying to learn and implement these methods, since there is often no clear path to follow. Many ecologists will choose those methods that they know well despite their shortcomings.

3. What approaches would be most effective in promoting their use?.—Although there are a small number of graduate ecology programs that train some students in modern statistics including HB methods, an impediment to widespread training teaching in these methods is the availability of ecology faculty with statistical background sufficient to offer such courses. Faculty members need efficient and relevant ways to get training in modern statistical modeling and the neces-

sary tools and materials to teach them effectively. Given the time demands placed on faculty, self-education approaches may be unrealistic. One potential solution is to offer one-semester sabbatical leaves that interested faculty could use to attend existing courses at universities where such courses are offered. Better yet, these leaves could be structured around the development of intensive courses that brought together a small group of expert teachers and student-faculty. The advantages of this approach are threefold. First, the burden of teaching could be shared among a small group of experts. Second, the students would be exposed to a variety of viewpoints. Third, participating faculty would gain not only technical and conceptual skills but also a support network to carry the newly acquired skills back to their home institutions. This approach would probably work best with faculty who are already teaching statistics or use modeling in their research, or with postdoctoral researchers who have the time and motivation to learn and use the methods. Costs could be shared by interested institutions and funding agencies.

In institutions that lack faculty trained in modern statistical methods, ecology departments could also work with faculty in the statistics department to develop advanced courses or at least to discuss statistical issues and problems as they arise. The advantage of this approach is that students would be exposed to both the rigor of statistics and disciplinary applications. The shortcomings are generating faculty interest and the considerable investments required to develop a course with multiple instructors from different disciplines and departments. Existing or new collaborations between statisticians and ecologists within the same institution could be leveraged to this end. Educators in ecology and other fields that depend on statistics departments for introductory courses could also initiate a dialog with their statistical colleagues about restructuring "service" courses to cover basic concepts that are at the heart of modern statistical methods such as distributional theory. University administrators could also be approached to offer faculty incentives for the development of courses that cross disciplinary boundaries.

Students can also act as catalysts in the adoption of modern statistics in ecology. Although we caution against the perils of unabashedly using graduate students as a means to improve existing programs, both students and faculty have much to gain from judicious small-scale efforts. Graduate students are often looking for teaching opportunities that give them some experience in curriculum development and allow flexible didactic approaches. At the same time, faculty members are also searching for means to increase students' engagement. One way to address the goals of these two groups is to allow graduate students to structure parts of existing course or to have them offer workshops that provide an introduction to the tools and techniques that will facilitate self-teaching for other students. For instance, a short course in R, or structuring labs in

existing statistics courses in R software rather than a commercial package, will provide students with some familiarity with programming and open the door to a large cyber community with which they can engage. This approach would require some thought on the part of the faculty and students but could potentially be very powerful because students readily accept new knowledge and methods from their peers.

Cyber courses can also be a means to bring statistical literacy to ecologists. This approach could make a number of existing graduate courses in modern statistical methods accessible to ecologists. These courses include among others Ecological Models and Data at the University of Florida, Ecological Theory and Data at Duke University, Modeling for Conservation of Populations at the University of Washington, and Systems Ecology at Colorado State University. With relatively minor investments, these courses could be broadcasted to other graduate program in the United States and abroad. Although interactions between students and teaching faculty would be limited, this approach would provide students with a foundation to pursue further education in statistics either through selfteaching or collaboration with statistics faculty at their home institutions. To encourage use and discussion, the cyber courses could be structured around studentfaculty groups at the receiving institutions.

Ultimately the widespread adoption of modern statistical methods will require a mix of approaches. What makes sense for individual institutions will depend on the availability of faculty and on motivations to develop offerings in this area. Funding agencies can help by providing incentives to institutions and individual faculty. To the degree that faculty and students are interested and willing, statistical literacy can be developed.

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LITERATURE CITED

- Bolker, B. M. 2008. Ecological models and data in R. Princeton University Press, Princeton, New Jersey, USA.
- Clark, J. S. 2005. Why environmental scientists are becoming Bayesians. Ecology Letters 8:2–14.
- Clark, J. S. 2007. Models for ecological data: an introduction. Princeton University Press, Princeton, New Jersey, USA.
- Clark, J. S., et al. 2001. Ecological forecasts: an emerging imperative. Science 293:657–660.
- Cressie, N., C. A. Calder, J. S. Clark, J. M. Ver Hoef, and C. K. Wikle. 2009. Accounting for undertainty in ecological analysis: the strengths and limitations of hierarchical statistical analysis. Ecological Applications 19:553–570.
- Gelman, A., and J. Hill. 2006. Data analysis using regression and multilevel/hierarchical models. Cambridge University Press, New York, New York, USA.
- Hobbs, N. T., and R. Hilborn. 2006. Alternatives to statistical hypothesis testing in ecology: a guide to self teaching. Ecology 16:5–19.
- McCarthy, M. A. 2007. Bayesian methods for ecology. Cambridge University Press, Cambridge, UK.
- Pielke, R. A., and R. T. Connant. 2003. Best practices in predictions for decision-making: lessons from the atmospheric and earth sciences. Ecology 84:1351–1358.
- Taper, M. L., and S. R. Lele. 2004. The nature of scientific evidence: statistical, philosophical, and empirical considerations. University of Chicago Press, Chicago, Illinois, USA.
- Woodworth, G. G. 2004. Biostatistics: a Bayesian introduction. Wiley, Hoboken, New Jersey, USA.