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# Conclusions

Now that you are through, it is perhaps worth looking back and seeing where you have come. I hope that you have achieved four things. First, you have achieved some practical understanding for how Bayesian inference with vague priors works and why Bayesian inference is simply so *useful* (Link and Barker, 2010). Second, you have gained plenty of practice with WinBUGS, the most widely used general-purpose Bayesian software. Third, I imagine that many of you have obtained a much deeper understanding for what you have been doing for years: fitting linear, generalized linear, and mixed models. In addition to the insights provided by the simulation of data sets, it is the natural way of model specification in the BUGS language that makes WinBUGS uniquely suitable to really understand these models. So, funny perhaps for a book about applied Bayesian modeling, I think that one of its greatest benefits for you may be something more general: an improved understanding for linear models and their extensions.

Finally, and fourth, I hope you have gained a taste for modern statistical modeling. In statistics classes at university, many ecologists have only seen a sad caricature of statistics. We were taught to think in terms of a decision tree for black-box procedures. The tree started with a question like "Are the data normally distributed?" and its terminal branches prescribed a t-test or a Kruskal–Wallis test or an analysis of covariance with homogeneous slopes (or else we were in deep trouble …). And then, a $p$-value popped up somewhere, and if it was <0.05, life was good. This is a terrible way of doing statistics, boring and devoid of any creative energy. It also does great injustice to the inspiring activity of trying to make sense of incomplete and imperfect observations made in a noisy world. Perhaps it should come as no surprise that many "sensible" people hate and distrust statistics.

To me, collaborating with some statistician colleagues, and especially starting to use WinBUGS, has been an eye-opener. I have come to see data analysis as equivalent with the creation of a statistical model that attempts to emulate the main features of the stochastic process that

could conceivably have generated our data. We then study features of our statistical model representation of that part of the world we are interested in, such as body mass of peregrines, snout-vent length of snakes, population size of lizards, or the distribution of a plant. By doing so, we hope to learn something about that world, something that may be hidden underneath the tangle of detail, distortion, and noise that is a hallmark of most data sets.

Many modern statisticians build their models in an organic way, without ever thinking about that old decision tree that many of us ecologists have come to learn by heart. They choose their ingredients from a vast array and assemble their models in a modular way: take a little of this distribution and add a little of that feature to the linear predictor. This is a much more creative and inspiring act than simply working our way along the branches of that old tree. And one that likely leads to much improved inference and mechanistic insight, since the model can be adapted to the particular situation at hand rather than the converse, with us having to shoehorn reality into the conceptual box provided by our statistics program. Thus, modern statistical analysis means to build one's own custom models.

Unfortunately, I doubt whether most ecologists will ever be sufficiently numerate to fit their custom models by maximum likelihood, at least, if they have to specify themselves the likelihood of their model in an explicit way. This is where WinBUGS comes in. It is the only software I know that allows the average, somewhat numerate ecologist to conduct his or her own creative statistical modeling. Therefore, again, I believe that WinBUGS has the potential to free the statistical modeler in us. Even without the benefits of the Bayesian paradigm of statistical inference, this would be enough for me to recommend WinBUGS to any ambitious quantitative ecologist.

Where will you go from here? I hope that my book enables you to better tackle more advanced books on ecological modeling, such as by Royle and Dorazio (2008), King et al. (2009), or Link and Barker (2010). Much of this advanced modeling is based on the powerful notion of *hierarchical models* (HMs; e.g., Royle and Dorazio, 2006, 2008). HMs describe observed data as the result of a series of linked stochastic processes, whose outcomes may be observed or unobserved, i.e., latent. HMs are very powerful to understand and predict complex ecological systems. They can be fitted also using frequentist methods (e.g., Lee et al., 2006; Ponciano et al., 2009), but their implementation in WinBUGS is much more straightforward and arguably easier to understand for an ecologist. The reason for this is that in the BUGS language, a complex model is naturally broken apart into hierarchically linked submodels. Indeed, in this book, we have seen many instances of HMs: all the models containing random effects and more particularly the site-occupancy and binomial mixture

models for inference about metapopulation distribution and abundance (Chapters 20 and 21). In these final chapters, we have just about reached the level of modeling where the book by Royle and Dorazio (2008) starts.

Another direction that you may want to explore is nonlinear models and especially nonlinear mixed models (Pinheiro and Bates, 2000). In this book, we have exclusively adopted linear statistical models, but there is no reason to restrict the deterministic part of our system description to be additive. Nonlinear models may be more realistic representations of a study system and may yield better predictions, especially outside of the observed range of covariates.

Finally, I have no doubts that many Bayesians would accuse me of being Bayesian only in a purely opportunistic way. In this book, we have used the Bayesian computing machinery as a handy way of fitting sometimes complex models without ever really taking advantage of that true hallmark of Bayesian inference: the ability to formally combine the information contained in the data with all available knowledge about the study system. That is, we don't really use informative priors. This is true, and I believe that much can be gained by not feigning ignorance about the system analyzed in the way that inference by maximum likelihood or Bayesian analysis with vague priors does. Indeed, especially with the small data sets that are so typical for ecology, much may be gained in terms of precision of the estimates and parameter estimability when informative priors are used. It seems likely that in the future, we will increasingly see Bayesian analyses with informative priors.

Perhaps WinBUGS may not allow you to go all the way there. WinBUGS may be too slow for your data set, you may never get convergence, be caught in a trap, or just lose the patience when WinBUGS behaves just like a 15-year old. Also, new programs are likely to be developed and improved in the future, such as OpenBugs (*http://mathstat.helsinki.fi/ openbugs/*), *AD Model Builder (http://admb-foundation.org/), JAGS (http:// www-fis.iarc.fr/~martyn/software/jags/), PyMC (http://code.google.com/p/pymc/ ), among others, and they may eventually be even more accessible to ecologists than WinBUGS is now and offer greater computing power. Or, you may learn how to code your own Markov chain Monte Carlo samplers and perhaps use a general programming language such as Fortran or C++, which may speed up your Bayesian computations by orders of magnitude relative to what you can achieve in WinBUGS. But even then, I believe that for many of you, WinBUGS will have achieved one important thing: it will have changed forever the way in which you think about, and conduct, statistical modeling.*