

# Preface

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You are looking at a gentle introduction for ecologists to Bayesian population analysis using the BUGS software. We emphasize learning by doing and leisurely walk you through a wide range of statistical methods for a broad array of model classes that are relevant for population ecologists. We focus on hierarchical models for estimation and modeling of quantities such as population size or survival probability, while accounting for imperfect detection probability. The reading is intended to be light and engaging, while at the same time, we hope that the content is represented accurately.

This book has been written by ecologists for ecologists. For this project, two experienced population ecologists have teamed up in a complementary way. Marc has been working chiefly in projects involving the estimation and modeling of population size and occurrence and the simplest description of population dynamics, population trends. The work of Michael has focused on teasing apart the demographic rates that underlie the observed dynamics (i.e. trends) of a population. In this way, we neatly combine our strengths and experience. We have published papers that use WinBUGS to fit almost all model classes described in this book and have experience in their frequentist analysis as well.

Both in content and in style, this book is a sequel to a similar book written by Marc (Kéry, 2010). In content, the latter is more introductory and directed to the general ecologist or indeed to anybody interested in regression modeling in WinBUGS. In Kéry (2010), most of the typical ecological statistics examples, such as estimation of population size and demographic rates, that is, our Chapters 6–11, are lacking conspicuously. In addition, in Chapters 12 and 13, we now extend the binomial mixture and the site-occupancy model to multiple “seasons” and the single-state site-occupancy model to multiple states. These important generalizations are lacking in Kéry (2010). We make occasional reference to Kéry (2010), but our current book is independent from the earlier one. Nevertheless, should you find some material in here difficult to follow, we suggest to use Kéry (2010) for learning about ecological modeling in WinBUGS at a more introductory level.

In style, the key concepts of Kéry (2010) have been retained for this book:

1. We provide a large number of richly commented worked examples to illustrate a wide range of statistical models that are relevant to

- the research of a population ecologist and to the analyses of wildlife or fisheries managers or analysts in more applied branches of ecology.
2. We have written the book using WinBUGS, but most of the code should run fine with OpenBUGS and JAGS as well.
  3. All WinBUGS analyses are run from within software R; hence, this is also an R book.
  4. We provide a complete documentation of *all* R and WinBUGS code required to conduct *all* our analyses and show *all* the necessary steps from having the data in some sort of text file to interpreting and processing the output from WinBUGS in R. Thus, you are almost *guaranteed* to be able to replicate our analyses for your own data sets.
  5. We make extensive use of the simulation of data sets and their analysis. We believe that simulating data sets can be crucial to your understanding of the models. However, we also provide 1–2 analyses of real-life data in each chapter.
  6. We have a clear and consistent layout for all computer code.
  7. We aim at a light and engaging language.
  8. Each chapter has a set of exercises with solutions for all of them provided on the book website ([www.vogelwarte.ch/bpa](http://www.vogelwarte.ch/bpa)).

In scope and in style, our book intends to build a bridge between introductory texts by McCarthy (2007) or Kéry (2010) and three more advanced texts on the analysis of populations, metapopulations, and communities, which have recently been published and which all use WinBUGS as their primary software: Royle and Dorazio (2008), King et al. (2010), and Link and Barker (2010). If your primary research topic is population ecology as covered in our book, you should consider buying some or all of these books as well.

Our book is based on a one-week course for graduate students and post-doctoral researchers that we teach at universities and research institutes. For this course, we require participants to have some basic knowledge of program R or other programming languages as well as of basic statistical methods such as regression and ANOVA. It helps a lot if they have also had some exposure to generalized linear models (GLMs) and random-effects models and know what the design matrix of a linear model is. These requirements fairly accurately describe the intended audience of our book. We believe that our book is well suited for a one-semester course in modern population analysis for subjects such as quantitative conservation biology, resource management, fisheries, wildlife management, or general population ecology. In addition, our book is perfect for self-study, owing to its gentle style and because the complete code is shown and is amply documented. Our book website contains a text file with all R-WinBUGS code, data sets, solutions to all exercises, our utility functions,

additional bonus material, a list of Errata plus some other information, such as about upcoming workshops.

Recently, the active software development of the BUGS project has moved over from WinBUGS to OpenBUGS (Lunn et al., 2009 see [www.openbugs.info](http://www.openbugs.info)). As of early 2011, the syntax of the two BUGS sisters has remained virtually identical. We have written and tested our code in WinBUGS 1.4. (and with R 2.12.), but we have checked a sample in OpenBUGS also and most ran fine. The latest release of OpenBUGS contains a series of ecological examples that are all of relevance for the readers of this book. The JAGS software (see [www-fis.iarc.fr/~martyn/software/jags](http://www-fis.iarc.fr/~martyn/software/jags)) is another MCMC engine that uses the BUGS language, as do WinBUGS and OpenBUGS. Hence, most code in our book should run in JAGS as well. In contrast to Win- and OpenBUGS, JAGS also runs on Macs.

Here are a few tips on how to use this book. We strongly suggest you first read Chapters 1–4 because they contain important introductory material that you will need to know in later chapters. Only then should you pick chapters according to your interests. Evidently, before starting to work through this book, you need to have installed the necessary software: R, with some packages (especially R2WinBUGS, but also lme4) and WinBUGS, with both the upgrade patch and the immortality key decoded, or else have OpenBUGS or JAGS functional. When using WinBUGS from R, you need to always first load the R2WinBUGS package (Sturtz et al., 2005). We do not usually say this, but simply assume that you issue the command `library(R2WinBUGS)` at the start of every R session. In addition, you need to tell R where the WinBUGS executable is residing on your computer. For that, we define an object that contains this address (`bugs.dir <- "c:/Program Files/WinBUGS14/"`; this is the default) and refer to it when calling WinBUGS with function `bugs()`. If WinBUGS is placed in another folder on your computer, the path information needs to be modified accordingly. Such information can also be written into the text file `Rsite.profile`, which sits in the R folder etc and contains global R settings (see Kéry, 2010, p. 32). Several models in the book take a long time to fit, hence, we give approximate bugs run times (BRT) for each. We use the R function `sink()` to write into the R working directory (which you can set yourself using `setwd()`), a text file containing the model description in the BUGS language. We find it useful to have all our code in a single document. You have to be totally clear about which part of the code is in the BUGS language and which is in the R language. This may be a little confusing at first, especially, because the two languages are quite similar (R is a dialect of S, and BUGS is strongly inspired by S). See the WinBUGS tips in Appendix 1 for more explanation. Finally, an important tip for when you cannot follow an analysis in this book is to execute code line by code line (if possible) and inspect all objects generated until you understand what they represent and how they fit together.

We truly hope that you find our book useful, whether you do population analysis for your research or for more applied goals, such as management or conservation biology. We even hope that you actually *enjoy* reading and working through it for its content, its style, and its presentation. In reality, we have written a book that we would have liked to have when we started our statistical population modeling in WinBUGS some years ago. If you have comments or find errors, please drop us an email at [marc.kery@vogelwarte.ch](mailto:marc.kery@vogelwarte.ch) or [michael.schaub@vogelwarte.ch](mailto:michael.schaub@vogelwarte.ch). We hope that WinBUGS frees the creative population modeler in you, as it has done for us.

*Marc and Michael,  
April 2011*