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A review of Applied Hierarchical Modeling in Ecology: Volume 2 by Kéry and Royle

This book, a secondary volume to that published in Kéry and Royle (2016), aims to both consolidate the monographs on hierarchical modelling in ecology presented in the first volume, with additional extended and advanced topics, and act as a stand-alone text on these advanced topics. This overarching topic is one of significant interest across a wide range of applied questions in ecology and encompasses many large subfields, such as occupancy modelling, distance sampling and survival analysis, and it is a daunting task in which the authors succeed. The authors highlight seven unifying concepts of the two books, which emphasises their overall aims in providing overarching frameworks and "cookbooks", to allow users to conduct simulation, error analysis and prediction in an accessible manner.

This volume consists of two major parts, broken down into five and seven chapters respectively. These topics follow on from where volume 1 left off, with some topics being extensions to those previously covered and others being stand-alone. The first of these parts covers dynamic or open-population-model versions of those covered in the first volume, with the addition of models for survival. The second part falls under the heading 'Advanced models', and covers topics of basic spatial models, integrated models, and distance sampling along transects. Again, these are likely to have been chosen from the point of view of practitioners, although they are extensive in their breadth.

The first part introduces some of the important concepts of the volume and discuss differences in absolute and relative abundance models. The authors then concentrate on survival models, which generally makes the assumption that individuals are marked, in contrast to the majority of topics in the two volumes, before moving onto models for single and multispecies distributions. The second section approaches advanced models, including multistate occupancy models, false positive errors, multispecies occupancy, spatial kriging and similar methods, integrated models and hierarchical distance sampling. Each of the chapters is bookended by an introduction to the topic and a 'Summary and outlook' section, which is a welcome look at further advancements and developments that are feasible or required in each topic.

The text provides a plethora of real data examples covering a wide variety of topics that will be invaluable to many users. This cements the volume as a very practical guide that will act as a central location for ecologists aiming to conduct these analyses, or quantitative ecology students looking for a reference

for their courses. This is supplemented throughout the volume, as examples of code written in R and/or BUGS are provided, with specific choice of JAGS for much of the Bayesian inference. The authors justify this in the preface with the fact that 'R and BUGS are the de facto industry standard in ecology', and this is indeed currently true. The choice to use R and BUGS/JAGS is also taken as they are the basis of many of the authors' own publications. Whilst these software are fundamental in the history of Bayesian inference software, they do have limitations (for example, the authors highlight JAGS cannot account for spatial autocorrelation), and ecologists are increasingly moving towards other software, such as Stan or NIMBLE to conduct inference. Whilst there would not be space in a single volume to provide code for all of these packages, I would question the long-term nature of the application of BUGS as model complexity and the required inference flexibility increases. This inevitably needs to be weighed up against making a volume that is of immediate use to the intended audience and I therefore respect that the authors had to make a decision one way or the other. The authors highlight that a NIMBLE version of all the code from the first book has now been produced by another author and is available on Github and similar toolkits may become available in due course.

An additional small problem is that the first volume provides a basic introduction to the BUGS language, so as a stand-alone volume, this would require users to already have a reasonable understanding of coding in BUGS, or an alternative resource to fall back on. Given that the topics in this volume are more advanced, it is probably not unrealistic to assume users will have that basic understanding, or if not will refer to the first volume where required.

The combined volumes come with an associated R package AHMbook, available through CRAN and with additional resources on the package author's Github page, which contains all of the datasets introduced in the book, simulation functions and additional utility functions. This alone is a huge contribution to the field and will allow more advanced modellers and statisticians to gain use from the publication.

The difficulty in this type of text is that each chapter could, and in many cases does, warrant (a) whole textbook(s) dedicated to the topic and there are many links and similarities between topics in different sections. It is, however, inevitable that there is not sufficient space to provide all the detail and links between sections. What the authors are successful at doing here is providing an important central resource for ecologists and applied statisticians looking for an introduction to these topics, that will enable them to apply the methods to data and extract relevant inference. The advanced section of this volume also paves the way for an understanding of more complex and developing topics in this incredibly varied field.

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