BOOK REVIEWS

EDITOR: THOMAS M. LOUGHIN

Useless Arithmetic: Why Environmental Scientists Can't Predict the Future	Textbook of Clinical Trials, 2nd edition(D. Machin, S. Day, and S. Green)Rick Chappell
(O. H. Pilkey and L. Pilkey-Jarvis) A. John Bailer	Statistical Development of Quality in Medicine
Sampling Strategies for Natural Resources and the En-	(P. Winkel and N. F. Zhang) Stefan Steiner
vironment(T. G. Gregoire and H. T. Valentine)Lucio Barabesi	Analyzing Receiver Operating Characteristic Curves with SAS
Model-Based Geostatistics	(M. Gonen) Liansheng lang
(P. J. Diggle and P. J. Ribeiro) Sudipto Banerjee	Applied Asymptotics: Case Studies in Small Sample Statistics
Reconstructing Evolution: New Mathematical and Computational Advances Computational Advances (O. Gascuel and M. Steel) Emmanuel Paradis	(A. R. Brazzale, A. C. Davison, and N. Reid) Lourens Waldorp
Bayesian Inference for Gene Expression and	Brief Reports by the Editor
Proteomics(KA. Do, P. Müller, and M. Vannucci)J. Sunil Rao	Analysis of Correlated Data with SAS and R, 3rd edition (M. M. Shoukri and M. A. Chaudhary)
Data Depth: Robust Multivariate Analysis, Computa- tional Geometry and Applications (R. Liu, R. Serfling, and D. L. Souvaine) Mia Hubert	Elementary Bayesian Statistics (L. A. Moyé)
Data Clustering: Theory Algorithms and Applications (G. Gan, M. A. Chaoqun, and J. Wu) Gilles Celeux	Information Criteria and Statistical Modeling (S. Konishi and G. Kitagawa)
Reliability and Risk: A Bayesian Perspective (N. D. Singpurwalla) Louise M. Ryan	Modelling for Field Biologists and Other Interesting People (H. Kokko)

PILKEY, O. H. and PILKEY-JARVIS, L. Useless Arithmetic: Why Environmental Scientists Can't Predict the Future. Columbia University Press, New York, 2007. xv + 230 pp. US\$29.95. ISBN 978-0-231-13212-1 (cloth).

Useless Arithmetic describes a number of mathematical models for physical systems that have been misused or naively applied to the detriment of societal decisions that were supported by the application of these models. This very accessible book begins with an illustration of how fisheries modeling efforts did not prevent the collapse of the cod populations in the Grand Banks. This first chapter sets the tone for the remainder of the book. Models used to predict the cod stock are blamed, in part, for the catastrophic failure of this population. Critiques of these models include being overly simplistic, failing to address uncertainty in the model predictions, and making assumptions to bridge data gaps. These critiques are all familiar to a statistical reader. The second chapter introduces the authors' vocabulary for describing models and examples of failures of models including predictions of the age of the earth and prediction of AIDS cases in Africa. Modelers might find the definitions incomplete, and statisticians would long for a greater discussion of uncertainty and variability here. Chapter 3 provides history of the Yucca Mountain nuclear waste storage facility along with a discussion of modeling questions such as the infiltration of water into the waste storage facilities. The authors express concern about unreasonable, refutable assumptions that are used to extrapolate the performance of a storage system 100,000 years into the future.

The first author is a coastal geologist and the second author is a geologist. Their concern about misapplication of models in their field of expertise surfaces clearly in Chapters 4-6. These chapters deal with climate change and rising sea levels (Chapter 4), shoreline retreat and erosion (Chapter 5), and beach preservation and design (Chapter 6). The widespread use of a particular shoreline retreat model is the focus of Chapter 5. The authors pull no punches in describing the "uncritical use of an outdated model" and stating the "failure of the engineering and science communities to incorporate a world of new observations . . . borders on the scandalous" (p. 107). Predicting beach "life" based on average conditions falls prey to the extremes of weather that are a reality not incorporated in many of these models. One concern noted in Chapters 5 and 6 and in a number of other chapters is that of "ordering complexity" in the sense that ". . . even if you know how each of the factors works and interacts with other factors . . . you still can't predict the future because you don't know the order in which the factors will occur" (p. 107).

Open pit mining and the modeling of its impact take center stage in Chapter 7. In these applications, the quality of water in open pit mines is characterized. Here, the authors fear that "impossible models for complex processes that we clearly can never predict are piled on top of other impossible models of other complex processes" (p. 156).

The modeling of invasive species is reviewed and lauded in Chapter 8. The book closes with a recap of this tour of modeling failures in physical systems and recommendations for modeling practice. Included in this chapter is a ranking of worst (beach nourishment life spans) to best (invasive species) models (Table 9.1) and harsh words for engineers-"problem is that engineers often don't recognize the difference between the behavior of natural processes and the behavior of steel and concrete" (p. 187). Federal officials do not fare better-"agency incompetence and intransigence ... add another element to the spreading use of models" (p. 188). The authors assert: "applied mathematical modeling has become a science that has advanced without the usual broad-based, vigorous debate, criticism and constant attempts at falsification that characterize good science" (p. 190). Modelers who subject their work to rigorous review and validation efforts will find this declaration surprising and not well supported in their experience.

Statisticians reading this book may find themselves looking for more formal discussion of model predictions incorporating uncertainty and variability. Statisticians working in a collaborative context typically develop models in partnership with content specialists, and the concern for model validity is central. In addition, statisticians tend to be very sensitive to the scope of a model and extrapolation. Thus, statisticians reading this book may find the cautionary tales interesting, the political impact on model outputs disturbing, and the omission of more statistical, stochastic elements frustrating. George Box's often-quoted wisdom—All models are wrong but some are useful—bears repeating in light of this book.

> A. JOHN BAILER Department of Mathematics and Statistics Miami University Oxford, Ohio, U.S.A.

GREGOIRE, T. G. and VALENTINE, H. T. Sampling Strategies for Natural Resources and the Environment. Chapman & Hall/CRC, Boca Raton, Florida, 2007. 496 pp. US\$80.96/£35.99. ISBN 9781584883708.

In recent decades, scientific interest in environmental problems has been increasing. Since extensive collection of environmental data may often be expensive or practically prohibitive, quantitative analyses must be based on a limited sampling effort. Consequently, the choice of a suitable sampling strategy plays a central role in many scientific studies in ecology, forestry, and environmental sciences. This wellwritten book addresses the need for an up-to-date survey of the topic. The text provides a general formulation for the classical sampling designs and areal sampling designs (tailored for environmental settings), by using an innovative approach based on the concept of discrete and continuous populations. Indeed, areal sampling designs—such as plot sampling or lineintersect sampling—are implemented by selecting a point in a region, i.e., by sampling a population defined in a *continuum*. This approach makes it possible to embed areal sampling theory into the general framework of Monte Carlo integration.

The book provides various innovative topics not covered by existing texts that deal with environmental designs, such as Schreuder et al. (1993) or Thompson (1992). Despite the fresh global approach to the presentation of sampling strategies, areal sampling designs commonly used in forestry are extensively surveyed. Moreover, special attention is devoted to the topic of edge effect correction, whose recent developments are comprehensively analyzed. In addition, a thorough discussion of randomized branch sampling and sampling with partial replacement is considered.

The book may be ideally divided into three main parts. The first part—comprising the chapters from 1 to 6—introduces the basic concepts of design-based inference by paralleling the theory for the cases of finite and continuous populations. More precisely, Chapters 1 and 2 tackle issues concerning the fundamentals, while Chapters 3 and 4 provide the results for equal and unequal probability sampling. Finally, Chapter 5 contains the details for stratified sampling, while Chapter 6 deals with the use of auxiliary information.

In the second part of the book—from chapter 7 to 10—the most important areal sampling designs are explored. Sampling designs based on fixed-area plots are considered in Chapter 7, while Bitterlich sampling (equivalently known as variable radius plot sampling) is presented in Chapter 8. Line intersect sampling is extensively analyzed in Chapter 9. Finally, in Chapter 10 the emphasis is devoted to the reformulation of these areal sampling designs in the Monte Carlo integration framework. Chapter 10 also gives an exhaustive presentation of edge correction methods.

The third part—from chapter 11 to 14—introduces some specialized sampling strategies. Chapter 11 provides a *miscellanea* of sampling designs mainly adopted in forestry, such as horizontal line sampling, point and transect relascope sampling, and 3P sampling. Chapter 11 also covers two further strategies that are used in environmental studies, ranked set sampling, and adaptive cluster sampling. Two-stage sampling designs and cluster designs are described in Chapter 12. Finally, Chapter 13 introduces a comprehensive treatment of randomized branch sampling, while Chapter 14 discusses sampling with partial replacement.

The style of presentation is terse and the notation is rigorous without being cumbersome. The mathematical arguments are developed by avoiding unnecessary technical details, although the more demanding reader may find accurate proofs of the main statements in the chapter appendices. Moreover, the large number of examples and graphical displays helps the reader in understanding the ideas. I consider this book excellent and I would highly recommend it both to scientists interested in sampling strategies and to applied researchers who can find in this text the necessary guidelines for the correct field implementation of sampling designs. The book is also well structured as a course guide, both at the undergraduate and postgraduate levels.

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LUCIO BARABESI Dipartimento di Metodi Quantitativi Università di Siena Siena, Italy

DIGGLE, P. J. and RIBEIRO, P. J. Model-Based Geostatistics. Springer, New York, 2007. xiii + 228 pp. US $979.95 \in 69.50$. ISBN 978-0-387-32907-9.

With the emergence of highly efficient Geographical Information Systems (GIS), developments in statistical models for spatially referenced data continue to thrive. This book focuses upon geostatistics, or point-referenced spatial statistics, dealing with the modeling and analysis of spatially continuous phenomena based upon data collected over a finite set of points. Such data arise in diverse disciplines including geological and environmental sciences, ecological systems, public health, and so on.

The book's primary objective is to present statistical methods for geostatistical data in an expository and exampleoriented manner rather than emphasizing mathematical rigor. In keeping with this spirit, the books splendid in its treatment of the motivating examples, its lucid explanation of the computational issues, and its illustrations with data sets. Most of the datasets used in the book are a part of geoR, a package written by the authors that can be installed and implemented from within the R statistical computing environment (r-project.org). After a friendly introduction to the package and its utilities, subsequent discussions of models throughout the book are accompanied by clear explanations of how they can be estimated using the geoR package. This considerably increases the book's accessibility to practicing spatial statisticians and data analysts.

The text also offers an excellent overview of model-based geostatistics. It elucidates the fundamental issues underlying modeling of geostatistical data by adopting a gentler illustrative approach that allows the reader to better grasp what components a geostatistical model should have and how they should be interpreted. It is worth pointing out that although the book's emphasis is not on theoretical rigor, the authors provide excellent concise discussions of the relevant theory underlying geostatistical processes that should be accessible to those having some exposure to mathematical statistics. This is an attractive feature for students and researchers who are new to the subject and want to understand the essentials.

In terms of coverage of the models, the authors have opted to concentrate on the basics rather than overwhelm the reader with loads of different models for different spatial settings. In fact, the text has largely focused upon models that can be estimated using geoR. This might have limited the scope for discussion of more challenging geostatistical settings, but helps serve the objectives quite well. Indeed, rather than presenting complex models that will require specialized algorithms for estimation, the text emphasizes a thorough and illustrative understanding of the key underlying concepts of spatial processes. Still, a few key issues such as multivariate geostatistical models, spatiotemporal models, missing data and spatial misalignment problems, and "low-rank kriging" for large datasets should have received more space than they were accorded, given their prominence in geostatistical analysis. Also, the overemphasis on geoR and geoRglm also had the undesirable effect of excluding many other packages in R for geostatistical analysis such as fields, akima and MBA, gstat, and spBayes.

The text covers both classical and Bayesian inference along with spatial design issues, again with plenty of illustrations and data analysis. Certain sections of the text, such as "What does kriging do to the data," are especially attractive, offering a thorough illustrative understanding of spatial prediction. The chapter on Bayesian inference is also well laid out. Having treated classical estimation and prediction differently, the authors use the Bayesian paradigm to bring these inferential issues under one roof. The hierarchical spatial models are developed on the lines of the conjugate Bayesian linear model specification. Estimation techniques such as direct sampling from the posterior and Markov chain Monte Carlo methods are discussed for Gaussian and non-Gaussian models. Although written clearly, students without any exposure to Bayesian statistics may find this section somewhat daunting. Another criticism is the somewhat surprising omission of the BUGS language and its interfaces with R in the text.

In conclusion, this text offers an excellent introduction to geostatistical modeling and data analysis for spatial analysts and researchers. Given its highly accessible approach, the text will be useful not only to statisticians but also to geologists and environmental scientists who deal with point-referenced data. The text can also serve as a very useful resource for teaching an M.S. or a Ph.D. level course in spatial statistics (in conjunction with some additional computational resources). Compared to the texts by Cressie (1993) and Stein (1999) that may be deemed too general or theoretical or those by Banerjee, Carlin, and Gelfand (2004), Schabenberger and Gotway (2004), and Le and Zidek (2006) that may be considered too complex in terms of modeling, this book's organized and focused presentation of the fundamental issues should serve as a more suitable text for a first course in geostatistical modeling.

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SUDIPTO BANERJEE Division of Biostatistics, School of Public Health University of Minnesota Minneapolis, Minnesota, U.S.A.

GASCUEL, O. and STEEL, M. (eds). Reconstructing Evolution: New Mathematical and Computational Advances. Oxford University Press, Oxford, U.K., 2007. xxix + 318 pp. US\$80.00/£39.50. ISBN 978-0-19-920822-7.

The study of biological evolution is a rich source of statistical, mathematical, and computational problems. The last two decades have seen a gradual change from a situation where a mix of paleontology and genetics was the ideal approach to evolution, to a more exclusive position of molecular phylogenetics with its heavy mathematics and statistics to fill this role. A symptom of this changing paradigm is the rapid accumulation of molecular data: the number of DNA sequences in publicly accessible databases has reached 100 billion bases in August 2005, and has continued to increase at a fast rate since then. The simultaneous increase in computer performance has led mathematicians and computer scientists to develop methods and tools to digest these enormous databases in order to address evolutionary issues. Gascuel and Steel invited leaders in these issues to a meeting in Paris in June 2005. The present book is the result of written contributions from this meeting. The introduction by the Editors states an ambitious goal: to present recent models to reconstruct evolution, "their biological relevance, their mathematical basis, their properties, and the algorithms for applying them to data."

The book includes five parts each consisting of two chapters written by 26 contributors. All chapters are of high quality but they deliver very differently. They provide a review of selected recent advances in 10 specialized topics. Four chapters are overviews of essential research in the field. Chapter 1 is a broad review of an important and vast topic: the coalescent and its applications to the analysis of past population dynamics. The literature reviewed is wide and important topics are touched; some crucial conceptual connections are also made. Chapter 3 is a dive into the Markovian models used to analyze the evolution of DNA or protein sequence data; it includes a discussion of some concepts and two applications illustrating how patterns of natural selection can be so revealed. Chapter 4 is an essentially mathematical review on the presence of invariants in phylogenetic analyses, and their potential applications such as the identifiability of some DNA substitution models. Chapter 5 is an extensive review of the models of macroevolutionary diversification, a topic of increasing importance among evolutionists as they allow us to analyze the patterns of speciation and extinction through time or in relation to biotic or abiotic factors, and thus to infer the causes of biological diversity on the earth.

The six other chapters are closer to a summary of the contributors' own research. Chapter 2 reviews the issue of analyzing DNA sequences sampled sequentially through time, a very important but underappreciated subject. Chapter 6 is a highly mathematical treatment of the problem of phylogenetic diversity, a critical problem in ecology and conservation biology, but no application is presented. Chapter 7 is a short review of selected contributions on the issue of building so-called phylogenetic "supertrees" by combining several, often heterogeneous, data sets. Chapter 8 is another strongly mathematical view on the formalization of some basic questions in phylogenetics such as identifying trees with the help of homoplasy-free characters. Chapter 9 is a richly illustrated summary of current advances on networks, a promising topic for future research in phylogenetics. Finally, Chapter 10 is an exciting review of some aspects of constructing hybridization or recombination networks.

Overall, the book is clearly written, the editing style is homogeneous among the different chapters, and typographic errors are very few. As indicated by the subtitle of the book, most chapters are very mathematically oriented. However, inferential and statistical issues are clearly apparent in some of them (Chapters 1, 2, 3, 5). These problems of inference are actually underlying all the contributions, even in a very remote or implicit fashion. The main weakness of the book is its fragmentation: the topics covered are so specialized that they are treated with little connection in spite of the clear unity of the book displayed by its title.

This book is clearly not recommended for biologists seeking ways to analyze their data. Neither is it suitable for an introduction to courses on phylogenetics. I would recommend this book to phylogenetists who wish to have an overview on the topics covered herein. Biometricians or statisticians curious about evolutionary problems may find some inspiration in these pages as well.

> EMMANUEL PARADIS Institut de Recherche pour le Développement UR 175 CAVIAR Montpellier, France

DO, K.-A., MÜLLER, P., and VANNUCCI, M. **Bayesian Inference for Gene Expression and Proteomics.** Cambridge University Press, Cambridge, U.K., 2006. 456 pp. US\$80.00/£45.00. ISBN 978-0-521-86092-5.

One has to look no further than any issue of a mainstream statistics journal or the plethora of new journals in bioinformatics, or the number of sessions related to bioinformatics at any national statistics meeting, to realize that the field of high throughput genomic and proteomic data analysis is "hot." Accompanying this trend has been the emergence of a number of books related to statistical analysis of such data. This particular text is an especially useful publication in that it is entirely devoted to Bayesian methods in genomics and proteomics. One of the obvious reasons for this concentration of methodologies is that the Bayesian paradigm provides a very rich framework for accounting for the propagation of uncertainties from multiple layers of sources that are quite typical of these kinds of data. As a result, a text that brings together Bayesian approaches for a spectrum of high throughput data problems is a very useful contribution to the scientific community. The contributors comprise leading groups from around the world and as such, the quality of the entries is generally very high. Most chapters are also illustrated with case studies that are explored in some depth and as a result, give the reader a better context of how one might relate findings to the underlying biology.

There are broadly four major areas covered in the text: gene expression analysis, proteomic analysis, motif discovery, and the derivation of gene regulatory networks. Given how the field has emerged, it is not surprising that the text is heavily weighted toward gene expression analysis techniques. This emphasis will no doubt shift somewhat as more and more statisticians are confronted with working with the other types of data.

To briefly summarize, Chapters 2-10, 13, and 22 concentrate on various aspects of Bayesian approaches to gene expression analysis ranging from low-level inferences like estimation of expression indices, to higher level inferences that include the identification of differentially expressing genes, clustering of gene expression profiles, building high-dimensional classification models, and sample size analysis. Not separating out some of these chapters would have made the flow a little more logical, however. Chapters 12, 14, and 15 focus on the analysis of proteomic mass spectroscopy data. Chapters 16 and 17 deal with motif discovery and Chapters 18-21 deal with building transcriptional regulatory networks. There are a few chapters that seem to stand more on their own but are no less important. One deals with expression quantitative trait loci (eQTL) analysis where expression phenotypes are linked to genetic markers in the search for a genetic basis for variation in gene expression, and a very useful introductory chapter that helps to bring the reader up-to-speed on jargon and technology issues for the kinds of data to be discussed in the text.

This text is potentially useful to not only people working in similar capacities as the contributors, but also to the broader quantitative scientific community-many of whom are struggling with the issues explored in the text on a daily basis. From a practical standpoint however, I do feel that the chapters would have benefited from more comparisons to other "standard" approaches so that the gains of the new methods could be made clear. Another practical limitation of the text is that only a few of the chapters discuss software implementations of the methodologies. Details on available software can often be found in other sources, but still such details help to stimulate the reader who wants to try out these modeling strategies on their own data. Another useful addition might have been some sort of an appendix that lists all of the datasets that were analyzed in the chapters and that are freely available.

Overall, I find this text an excellent contribution to the literature on statistical methods for high throughput genomic and proteomic data analysis. The chapters are well written, the case studies are informative, and the range of topics covered is quite broad and generally logically grouped. I would highly recommend this text to both those people already working in the area and those wanting to break in. It is not only suitable for researchers developing their own methodologies but also for applied quantitative scientists looking for the most cutting-edge tools to analyze their high throughput datasets.

> J. SUNIL RAO Biostatistics and Genetic Epidemiology Case Western Reserve University Cleveland, Ohio, U.S.A.

LIU, R., SERFLING, R., and SOUVAINE, D. L., **Data Depth: Robust Multivariate Analysis, Computational Geometry and Applications**. DIMACS Series in Discrete Mathematics and Theoretical Computer Science, Vol. 72, American Mathematical Society, Providence Rhode Island, 2006. xiii + 246 pp. US \$89.00. ISBN 0-8218-3596-3.

This book collects 15 papers from the DIMACS workshop on "Data Depth: Robust Multivariate Analysis, Computational Geometry and Applications," held at Rutgers University in May 2003.

The notion of data depth provides concepts of ordering and ranking of multivariate data points. Quantities derived from data depth include depth contours, scale curves, depth-based order statistics, depth-weighted location and scatter matrices, and many more. Varying applications have been developed so far, including nonparametric statistical quality control, aviation safety data analysis, and gene clustering.

Although the methods usually possess good theoretical properties, such as resistance to outliers, their application is often restricted by their high computational complexity. There is thus a substantial need for (approximate) algorithms that, in the ideal case, inherit the theoretical properties of the estimators, while being fast even at datasets with a large number of observations and/or dimensions. As most notions of data depth have a nice geometrical interpretation, this offers challenging problems in the area of computational geometry. Therefore, the workshop aimed at bringing together scientists from statistics and computational geometry.

The proceeding papers collected in this book very well reflect the different aspects of data depth. Some papers focus on new definitions and provide theoretical results, while others put more emphasis on computational improvements. All authors are renowned scientists from both communities.

For readers not yet familiar with the available depth functions and algorithms, the overview papers by Robert Serfling (Depth Functions in Nonparametric Multivariate Inference) and Greg Aloupis (Geometric Measures of Data Depth) are very valuable. The former paper is the first paper in the book and concisely explains the role of depth functions in nonparametric statistics, as well as the connection with ranks, order statistics, quantiles, and outlyingness. The latter paper enumerates the available algorithms for the computation of the depth of a multivariate point as well as the deepest point.

The review paper by Serfling is followed by eight statistical papers. The first one introduces rank tests for multivariate scale differences and applies them to compare the stability of several airlines. The second paper is more theoretical and provides asymptotic results for scale curves. The third paper reviews the properties of the zonoid depth and gives an application to classification. This is also the topic of the next paper in which parametric, semiparametric, and nonparametric (based on the L1 depth) discriminant rules for separating two populations are compared. Yet another classification procedure is considered in the following paper. Here, regression depth is related to support vector machines with linear kernels, and to notions of overlap and complete separation in logistic regression. Next, spherical data depth is introduced, together with its properties and those of the corresponding multivariate median. The last two statistical papers are concerned with functional data. First, a classification of curves is presented based on concepts of depth for functions. It is shown that the classifiers have good robustness properties. This is also the topic of the next paper in which robust estimates of the center of a functional distribution are obtained by means of an impartial trimmed mean approach.

The following six papers focus more on computational aspects of depth functions and deepest points. After the review paper by Aloupis, new algorithms for the computation of the halfspace depth are presented in two papers. The first proposes a simulated annealing algorithm, while the second is a primal-dual algorithm that updates lower and upper bounds of the depth. A modified definition of simplicial depth with better finite-sample properties is proposed in the next paper, followed by a contribution on fast algorithms for convex hull peeling, and generalizations of it. The final paper copes with new fast algorithms for bivariate depth and depth contours by making use of modern graphics architectures.

This book clearly satisfies the goals of the editors: it contains state-of-the-art contributions on data depth that may be of interest to statisticians, mathematicians, computer scientists, and computational geometers. Connections between the different research fields are well exposed. This will certainly stimulate further interdisciplinary research.

> MIA HUBERT Department of Mathematics Katholieke Universiteit Leuven Leuven, Belgium

GAN, G., CHAOQUN, M. A., and WU, J. Data Clustering: Theory Algorithms and Applications. ASA-SIAM Series on Statistics and Applied Probability. SIAM, Philadelphia, and ASA, Alexandria, Virginia, 2007. xxii + 466 pp. US\$114.00 (ASA/SIAM Member Price \$79.80). ISBN 978-0-898716-23-8.

This book gives a tour of cluster analysis methods and algorithms. The authors present a considerable number of techniques and programs for clustering using a direct, fairly terse approach to the subject. Many of the described techniques have been proposed recently in conference proceedings. The authors provide an algorithmic point of view, and many algorithms are presented in pseudo code.

The first part of the book (six chapters) describes basic concepts (type of data, coding, data transformation and visualization, distances, and so forth). This part is rather complete, but provides little advice for choosing appropriate ways to describe data.

The second part, which is the core of the book (11 chapters), is devoted to clustering algorithms. Classical clustering methods are presented, along with more recent approaches such as subspace clustering for high-dimensional databases. The authors put some emphasis on fuzzy clustering and optimization techniques. The organization of this important part of the book is good. I was just a little bit surprised to see the chapter on fuzzy clustering presented before the chapter on center-based clustering algorithms. (Consequently, the fuzzy k-means algorithm is presented before the k-means algorithm.)

A third part begins with a short chapter on clustering gene expression data, which contains the one and only numerical illustration of the book, and ends with two chapters giving some material on clustering programming in MATLAB and C++. The book is completed with appendices, an extensive bibliography, and subject and author indexes. Other than an almost systematic correspondence problem between the author names and the page numbers in the author index, it is rather difficult to detect errors in the whole book.

I have some difficulty understanding the aim pursued in this book. It is good to have gathered in a single volume numerous clustering algorithms arising from different communities. In particular, the authors describe succinctly many algorithms proposed in Data Mining and Knowledge Discovery conferences. But while the clustering algorithms are well described in Part 2, their rationale is rarely given or suggested. Moreover, the possible advantages and drawbacks of the algorithms are not discussed, and no numerical comparisons are provided. Thus, some important chapters are somewhat disappointing. For instance, the chapter on hierarchical methods is frustrating: the standard theoretical properties of the methods are not given and their practical behavior is not discussed. From that point of view, Chapter 17 on the difficult question of the evaluation of clustering techniques is also disappointing since the authors do not seriously analyze the presented criteria. In the same spirit, the discussion on assessing the number of components in a mixture appears rather superficial in Chapter 14 on model-based clustering. (See McLachlan and Peel [2000, Chapter 6], for a complete and clear presentation of this important question.)

I do not think that the authors succeed to illustrate the advantages and shortcomings of different clustering algorithms they presented as they claimed in the Preface. And, I do not believe that this book can be recommended as a textbook for an introductory course in cluster analysis in replacement of the excellent books that the authors cite in their Section 1.5.2, because the authors failed too often to comment on the rationale underlying all the described clustering techniques.

Moreover, despite the considerable number of presented algorithms, some important and recent topics of cluster analysis are absent: spectral clustering (see von Luxburg [2007] for an excellent tutorial), which is one of the most promising techniques of graph-based clustering, bi-clustering (see for instance van Mechelen, Bock, and De Boeck [2004]), and simultaneous clustering of the rows and columns of an array (see for instance Govaert and Nadif [2005]), which are useful techniques for gene clustering.

Also, the latent class model (see, for instance, Everitt [1974]), which is the reference mixture model for clustering categorical data, does not appear in the chapter on modelbased clustering methods in which are described two algorithms for categorical data not really related to the mixture model.

In spite of those criticisms, I think that this book can certainly be quite useful for researchers and users who have some practice in statistical data analysis. The authors have completed a considerable piece of work in compiling all these algorithms (more than 50 algorithms are detailed). And some chapters are really quite informative and original. I think, in particular, that Chapter 9 on center-based clustering algorithms gives a rich and clear description of many useful algorithms; Chapter 10, concerning evolutionary optimization algorithms, is quite interesting; and Chapter 15 on subspaces clustering is simply impressive.

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GILLES CELEUX Institut National de Recherche en Informatique et Automatique Orsay, France

SINGPURWALLA, N. D. Reliability and Risk: A Bayesian Perspective. John Wiley and Sons, Hoboken, New Jersey, 2006. 396 pp. US\$130.00/€97.50. ISBN 978-0-470-85502-7.

What is the chance that a nuclear power plant experiences a catastrophic failure in the next 50 years? How likely is it that a patient taking a prescribed cholesterol-lowering medicine will experience a life-threatening side effect as a result? These are the kinds of questions posed in the introduction of Nozer Singpurwalla's new book, "Reliability and Risk: A Bayesian Perspective." As Director of the Institute for Reliability and Risk Analysis in the Department of Statistics at the George Washington University, Professor Singpurwalla is well placed to address these provocative, important, and timely questions. The book provides some interesting background reading on the history of risk analysis, probability theory, and the quantification of uncertainty. The author argues that risk

analysis will only become more important in our increasingly consumer-oriented and litigious society that relies on complex infrastructure for functionality and survival. He contrasts the perspectives of the physics/engineering and biomedical fields toward risk analysis, arguing for the value of a blended approach. Indeed, providing a framework for such a blending is the main purpose of the book. At one level, engineers and biostatisticians can be argued as simply addressing similar issues using different terminology (e.g., reliability versus survival analysis). More fundamentally, however, there are important differences. The training received by engineers and physicists tends to make them comfortable using subjective judgment (assumptions) to build models to characterize uncertain situations. Indeed, their modus operandi involves the construction of models that reflect underlying mechanisms and causal relationships. In contrast, biostatisticians generally attempt to be very factual and objective, as a rule preferring more empirical approaches that minimize overly strong modeling assumptions and emphasizing the stochastic aspects of the model. These ideas resonate with a recent report from the National Academy of Sciences, Models in Environmental Regulatory Decision Making, which attempts to elucidate a common framework for constructing and evaluating models used to support environmental decision making. Interestingly, even the word "model" can have dramatically different meanings to an environmental engineer who might, for example, use a complex set of differential equations to represent the spread of a contaminant through soil, compared to an epidemiologist who might use classical statistical theory to estimate a dose-response relationship. Professor Singpurwalla argues that the engineers have much to learn from the statisticians in terms of quantifying stochastic variability, while the statisticians have much to learn from the engineers in terms of building models that reflect scientific theory. He then devotes much of his book to laying out a rich tapestry of methods that draw on the best of both these worlds. The book is heavily Bayesian in orientation, a perspective that resonates well with the broader context, namely building models that reflect expert opinion (in this case, scientific theory). Considerable attention is given, for example, to the construction and solicitation of prior distributions. A convincing argument is also made for the importance of thinking beyond the traditional frequentist view to probability: it simply does not make sense, for example, to think about hypothetical repetitions of the lifetime of a nuclear reactor—actions are needed to protect against the possibility of a catastrophic accident in the one realization that we have to live with! Not surprisingly, given the emphasis on models derived from mechanism-based scientific theory, much of the material presented in the book's technical chapters is parametric in nature (the author refers to "chance distributions"). Multistate models also play a big role. There is a chapter, however, on nonparametric Bayes. The Dirichlet distribution plays a big role here, and there are interesting discussions about the link between some of the described approaches and classical semi- and nonparametric survival analysis (e.g., Kaplan-Meier curves; Nelson-Aalen estimators; and so on).

All in all, this is a very interesting, provocative, and worthwhile book. It is not perfect, of course. For example, some of the definitions of causality and spurious correlation given in Section 4.8 seem nonstandard and I am not sure I agree with them. There are a few typos sprinkled throughout. The lack of detail was frustrating in a few places: I was disappointed, for example, by the very limited discussion of the Dempster– Shafer probability framework. I also wish that there were more detailed and concrete examples provided. What I like most about this book, however, is the way it blends interesting technical material with foundational discussion about the nature of uncertainty. This is not a cookbook and would make great material for a graduate seminar or discussion group.

> LOUISE M. RYAN Department of Biostatistics Harvard University Boston, Massachusetts, U.S.A.

MACHIN, D., DAY, S., and GREEN, S. Textbook of Clinical Trials, 2nd edition. John Wiley and Sons, Chichester, U.K., 2006 US400.00/€315.00. ISBN 978-0-470-01014-3.

David Machin, Simon Day, and Sylvan Green have done the clinical research community a great service by first writing and then updating (in 2006) their Textbook of Clinical Trials. A notable distinction of the first edition, as its preface pointed out, is that it was more a catalog than a standard textbook. This quality is maintained and expanded upon in the second edition; after a 35-page introduction, the book is divided into 13 (increased from seven in the first edition) sections such as "Cancer" and "Psychiatry," most of which are composed of multiple chapters ("Breast Cancer," "Childhood Cancer," and so on). Each chapter gives an overview of methodologic but generally nonquantitative considerations in the conduct of clinical trials for diseases in its medical specialty. The chapters do not build on each other except that the introductory section is a useful prelude to them all. As a result, each can be read in isolation by a researcher who wishes to improve his knowledge of clinical research in a particular field; as another result, there is considerable overlap. Those who want an orderly exposition should be warned that, for example, they will be rereading definitions of Phase I - Phase IV trials on p. 422 after having seen them in the introduction and elsewhere prior to this.

The index is complete and enhances the book's advantages. "Intention to treat" has seven (up from four) entries—in the introduction and examples from psychiatry, contraception, and infertility. A reader can find the definition of a crossover trial in the introduction accompanied by a sample schematic diagram and examples from 12 (up from five) medical disciplines; equivalence trials appear in seven (up from three) chapters in addition to the introduction. (My parenthetic statistics are meant to show those readers who own and enjoy the first edition the return on shelling out US\$400 for the second.)

This book will give a good basic education with only minor lacunae to those who learn best by example. But only the most dedicated would read all 730 pages from "The Development of Clinical Trials" through "Clinical Trials in Rare Diseases," a pair of well-written summaries by Simon Day. To do so, despite the uniform excellence of those entries that I examined, would be too much like reading the encyclopedia. A reader wanting more comprehensive coverage may find it elsewhere for a very few specialties (e.g., Green et al., 2002 for cancer), but not for most. The book is ideal for those beginning to do clinical research who want a field-specific primer. Where else could they easily find a survey of issues and important trials in reproductive health, dentistry, or psychiatry? Note that many disciplines that do not have their own chapter, such as biological agents, vaccines, and radiotherapy, are still very well represented. I can only hope for more of a good thing in a future third edition as clinical trials continue to expand into new areas.

My usual suggestion to students with basic backgrounds in statistics and medicine who want to learn the elements of clinical trials has been to buy the Friedman et al. (1998) introduction (I disclaim that one author is my chairman) and to read as many articles in medical journals and Controlled Clinical Trials: the Journal of the Society for Clinical Trials as possible. From this perspective, Machin et al.'s overview of the clinical trials field is more useful as an adjunct to a traditional textbook on clinical trials than as a stand-alone primer or reference. But, just as I first learned about clinical trials from the lamentably out of print compendium edited by Buyse et al. (1984), I can see Machin et al. giving a good education-although its price may limit it to libraries. A student may pick her approach. I conclude by echoing a review of the earlier edition that "This is an unconventional textbook ... very useful as an introduction to clinical research, or for those planning specific studies within therapeutic or disease areas" (Søreide, 2005).

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RICK CHAPPELL Departments of Statistics and of Biostatistics & Medical Informatics University of Wisconsin Medical School Madison, Wisconsin, U.S.A.

WINKEL, P. and ZHANG, N. F. Statistical Development of Quality in Medicine. John Wiley and Sons, Chichester, U.K., 2007. 280 pp. US $90.00 \neq 67.50$. ISBN 978-0-470-02777-6.

As stated by the authors, the purpose of the book is "to present statistical techniques of major relevance for quality development in medicine," and the intended audience is "people who are directly or indirectly involved in the quality assurance of clinical work, i.e., physicians, nurses, administrators, and students..."

While somewhat unsure about the title, I translated quality development to mean quality improvement. From the Wiley website we learn that Per Winkel is a senior researcher at the Copenhagen Trial Unit, Centre for Clinical Intervention Research at the University Hospital of Copenhagen, and Nien Fan Zhang is Manager of Metrology Statistics and Computation Group, Statistical Engineering Division, US National Institute of Standards and Technology. As both authors have many years of experience in their fields they are highly qualified to write a book of this sort.

The two main topics covered in the book are control charts (in a medical context), and the use of risk adjustment to adapt both control charts and other comparisons of performance to situations where patient case mix should be taken into account. There is also a short chapter on learning curves and one on quality assessment that deals mostly with management issues.

The book does a credible job of introducing the ideas and uses of control charting. I worry, however, about defining random variation (as opposed to assignable causes of variation) as "unavoidable causes, which one cannot identify." Using this definition, once a process is in a state of statistical control (i.e., there are no signals on the control chart) there is nothing we can do to make it better even if it does not exhibit acceptable performance.

A strength of the book is the comprehensive discussion of a variety of uses and methods of risk adjustment. Risk adjustment is clearly a very important topic in assessing and improving quality in a medical context since usually patients are very heterogeneous. While some of this material, such as hierarchical models, is complicated, it is important. Another strength of the book are the real-life clinical examples used throughout. This helps a great deal to show how the presented methodology can be useful in practice.

The main drawback of the book, to my mind, is that improving quality in medicine should involve much more than just control charts and risk adjustment. Control charts are designed to monitor a process and signal if the process has changed. This is useful, but is too passive to be a good general strategy for improvement (Steiner, 2006). Control charts are only one tool and should be employed, as appropriate, within a more global improvement algorithm such as Six Sigma. There have been a number of good recent books, such as de Mast et al. (2006), that illustrate the use of Six Sigma in medical contexts.

Overall the book has a very clean attractive appearance and is well researched. There are a few typos, grammatical errors and awkward sentences, but this does not detract substantially from the presentation. For instance, for the plot in Figure 1, the limits are said to be at plus/minus three standard deviations from the mean, but are shown at plus/minus two standard deviations. Also, using three levels of subsections (e.g., 5.4.4.1) helps to break up the text, but is excessive, especially when there are sub-subsections (e.g., 5.4.3) consisting of a single sentence. Finally, unfortunately, I could not access the problems and solutions page for the book from the Wiley website.

Overall, I recommend this book to people involved in clinical work who wish to learn about control charts and risk adjustment, but there are more comprehensive treatments of quality improvement in medicine.

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STEFAN STEINER Dept. of Statistics and Actuarial Science University of Waterloo Waterloo, Ontario, Canada

GÖNEN, M. Analyzing Receiver Operating Characteristic Curves with SAS. SAS Press, Cary, North Carolina, 2007. 152 pp. US\$ 31.95. ISBN 978-1-59994-298-8.

The book provides a brief overview of existing methods for analyzing receiver operating characteristic (ROC) curves. Its main goal is to introduce SAS codes for implementing these methods. The book does not include theoretical details and it is accessible to a wide audience including statisticians in industry, advanced students with interests in ROC curves, and physicians without much statistical background.

This book is practical and seems to be complementary to the existing two books by Zhou, McClish, are obuchowski (2002) and Pepe (2003) which cover the subject in more depth. Although many ROC methods have been introduced lately, SAS codes to implement these methods are not readily available. The book is well written and nicely laid out. The book starts with SAS codes to estimate and plot single ROC curve. It then introduces codes to compare two ROC curves and to adjust for covariates in ROC analysis. From my viewpoint, this part of the book is of great interest to the targeted audience. Therefore, it would have been better to see more recent developments in the area of covariate adjustment and related SAS codes. In fact, some of recent ROC regression methods can be easily implemented using PROC GLM procedure. I like the chapter on ROC curves with censored data. This is a relatively new area and it helps readers get familiar with related methods and their practical implementation using SAS.

All the **SAS** codes and sample data sets are available online, so readers will not have difficulty implementing the methods in this book. This book would be useful for those who are interested in the practical use of ROC curves.

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LIANSHENG TANG Department of Statistics George Mason University Fairfax, Virginia, U.S.A. BRAZZALE, A. R., DAVISON, A. C., and REID, N. Applied Asymptotics: Case Studies in Small Sample Statistics. Cambridge University Press, Cambridge, U.K., 2007. viii + 248 pp. US\$65.00/£45.00. ISBN 978-0-521-84703-2.

This is an excellent book for applied statisticians. It presents applications of higher order asymptotic theory in likelihood in many different contexts. The book is generally well written and can be used by applied researchers to extend the presented case studies to include their own research interests.

Higher order asymptotic theory makes it possible to obtain very accurate distributional results in statistics. It is an important topic that has remained somewhat in the background in applied statistics and other sciences. The reason is, as the authors mention, that the theory can appear difficult and may not have a large impact in practice. This is unfortunate because many of the standard techniques for hypothesis testing can be greatly improved by using these results. The two coauthors, but especially Reid, are well known for their work in asymptotic theory. By writing this book, I think the authors have succeeded in making higher order theory more accessible and they will succeed in getting more scientists involved in this theory. The book can also be used as material for a course on higher order theory. There are sufficient problems of different levels of difficulty at the end of the book.

The book begins in Chapter 2 with a brief explanation of the results from higher order theory that will be applied to data in different contexts. The concepts involved are well explained in this conceptual introduction. This chapter is easy to read and quite convincing. At the end of this chapter, however, there are several technical definitions that remain rather vague to applied researchers, like that of the canonical parameter that uses ancillary statistics. It is understandable that the authors chose to defer discussion of these technical details until Chapter 8, where more details of asymptotic approximations are explained. But I think the authors could have spent a few more words on the conceptual understanding on some of these definitions.

The next four chapters, 3–7, contain applications of higher order asymptotics to different types of data. The authors have selected the examples well and have presented them very clearly. I enjoyed going through them. Chapter 3 involves small data sets that illustrate the principles well. This chapter is very good to get a first understanding of the possibilities and potential of higher order asymptotics. Chapters 4 and 5 demonstrate many different possible applications of the theory for discrete and continuous data, respectively. Together with more in-depth illustrations in Chapter 6, these chapters make it possible for the reader to find a familiar application and then try to extend it to her own situation. Because the book includes R code for several packages, it is easy to verify the results presented in the book. It is also very easy to extend the obtained results to your own research and apply the R code to your own data. Chapter 7 emphasizes more methods than the previous chapters. The examples presented in this chapter show in great detail how some problems, like dependent data, can be handled using higher order theory.

Chapters 8 and 9 are much more technical. Chapter 8 is a theoretical discussion of asymptotic approximations in likelihood theory and Chapter 9 is on computer implementation. Even though the material is quite technical I think that many applied researchers will find it accessible. Chapter 8 follows generally the books by Barndorff-Nielsen and Cox (1989, 1994), but is, of course, much less extensive. The authors do provide more details here and there than Barndorff-Nielsen and Cox. However, I think that Chapter 8 could be better. For example, Chapter 9 on higher order theory by Young and Smith (2005) is much more accessible than Chapter 8 by Brazzale, Davison, and Reid. Young and Smith integrated topics like Edgeworth expansion into the text, whereas Brazzale, Davison, and Reid deferred these kinds of topics to the appendix.

In summary, I highly recommend the book to researchers looking for ways to improve accuracy in statistical testing. The book is well written, the examples are clear, and because all examples can be verified by the reader through the provided packages and code in R, the analyses can be explored in great detail. I particularly like the fact that at the end of each chapter there are bibliographic notes, which refer to the literature and describe a bit of the history of the subject. Especially the notes of Chapter 8 are enlightening.

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LOURENS WALDORP Department of Psychological Methods University of Amsterdam Amsterdam, The Netherlands

BRIEF REPORTS BY THE EDITOR

SHOUKRI, M. M. and CHAUDHARY, M. A. Analysis of Correlated Data with SAS and R, 3rd edition. Chapman and Hall/CRC, Boca Raton, FL, 2007. xv + 295 pp. US\$89.95/£47.99. ISBN 9781584886198.

Previous editions of this book were published under the name, *Statistical Methods for Health Sciences* (Shoukri and Edge, 1996; Shoukri and Pause, 1999). The new title reflects the real concentration of the book. It tersely describes standard methods of analysis for relationships between variables—linear, logistic, and Poisson regression, and contingency table and survival analysis—then focuses on special cases of clustered and longitudinal data. Basic forms of each model and analysis are presented, using a combination of prose and formulas. Examples are studied, and basic, no-frills SAS and R code are given for most examples. The level of the book is appropriate for quantitative undergraduates or practitioners: there are no derivations, but also no shortage of formulas. There are occasional inaccuracies (such as defining the linear predictor as a "link function") and confusing descriptions (such as the use of " χ^{2} " to represent both the Pearson test statistic and its asymptotic distribution, or setting population quantities equal to sample quantities). And only basic analyses of each type are presented, limiting the usefulness of the book to simple problems. There are better references for each of the book's subjects, but the convenience of having the subjects addressed in one volume may make the book worthwhile. On the whole, this is a serviceable book that fills a niche, but there is ample room for improvement.

MOYÉ, L. A. Elementary Bayesian Statistics. Chapman and Hall/CRC, Boca Raton, FL, 2008. xxi + 377 pp. \$79.95/£42.99. ISBN 9781584887249.

I am a strong believer in the need for members of the statistics profession to publish works on modern statistical methods that are accessible to the non-statisticians with whom we work. Such works help to ease the permeation of modern methods into the disciplines of our colleagues where they are most needed. Moyé's book is a member of this class of works. The stated target audience is "someone in healthcare, without a strong calculus background," and Moyé's dual training in statistics and medicine enables him to write prose effectively for his audience.

He takes a different approach to content from many other general books on Bayesian methods that I have seen. There is much less focus on different kinds of models or large, computationally intensive examples than seems to be the norm. Instead, the chapters attempt to explain in clear terms what the Bayesian paradigm is, how it is useful, what a prior is and how to select one, and what sorts of problems are especially amenable to Bayesian solutions. There is, on the other hand, almost a total lack of discussion of how to *do* Bayesian statistical analysis. For example, I found no mention of MCMC or related computational subjects, and the concept of a credible interval does not appear in the book. Clearly, the book is intended to be an exposition on Bayesian statistics, rather than a how-to manual.

As such, it has a number of drawbacks that keep it from fully achieving its intended purpose. The least of these is the sorts of examples that are used in the book. True, they tend to be based on real studies and problems in medicine, but the actual questions that are posed are akin to those in many pedestrian intro-to-stat books. I found myself thinking, "Why would I want to know that?" for example, when reading about finding the probability that 200 people must be screened in order to find 4 cases of tuberculosis. Maybe there is a good reason for it, but the motivation is lacking. More serious is the imprecise writing and inconsistent notation that plagues a disappointingly large fraction of these examples. Instances include (1) stating "if the patient dies of an arrhythmia, then $\Theta = 1$ " and "X = 1 mean[s] that the patient has died" and then in the next sentence writing " $P(X=1|\Theta=1)=.70$ "; and (2) reference to a posterior for a parameter θ that is defined as a probability is made conditionally on " $\bar{x} = 0.10$ " when the only data available are that 10 out of 80 patients were hospitalized. In addition to such misstatements, there are numerous typos that at times detract from the clarity of presentation. These are things that a statistically experienced reader can correct

mentally, but that the novice may become hopelessly hung up on. The good news is that I think that most of the book's problems are accidental and easily fixed. Until this book undergoes rigorous editing, however, I hesitate to recommend it.

KONISHI, S. and KITAGAWA, G. Information Criteria and Statistical Modeling. Springer, New York, 2008. xii + 273 pp. \$79.95/€69.50. ISBN 9780387718866.

The authors' stated goals for this book are (1) "to provide comprehensive explanations of the concepts and derivations of the AIC, BIC, and related criteria," and (2) "to provide a theoretical basis for the analysis and extension of information criteria via a statistical functional approach." Their book achieves these goals quite admirably. The book falls distinctly into three parts. The first, which is four chapters long, supplies a readable, concise explanation of how and why AIC works as a model-selection criterion. The mathematical level is modest; a first-year graduate sequence in basic probability and statistics is more than enough to prepare a reader for the authors' clear derivations of the statistical properties of AIC. This portion of the book is concluded by a series of mathematical and numerical examples exhibiting prototypical use of AIC. Because AIC and other information criteria are limited to use with maximum likelihood estimation, the second part of the book develops a generalized information criterion (GIC) that has its basis in statistical functionals, of which MLEs are a special case. This part of the book is considerably more technical than the first. Although the overall level of mathematics is not much higher than in the first part, there is much more of it. This part, too, contains a chapter of examples, demonstrating how to derive the GIC for a variety of estimation problems. The last part of the book is a brisk tour through bootstrap and Bayesian information criteria and other model-selection criteria.

This book is quite different from the oft-cited Burnham and Anderson (2002). Burnham and Anderson explain how to use AIC and related criteria, and offer extensive wisdom and advice regarding the practice of model selection, and subsequent interpretation and inference. They explain some of the theory that underlies information criteria, but their book is intended to be readable to a non-mathematical audience. In contrast Konishi and Kitagawa are much more focused on the mathematical properties of information criteria. There is really very little in the book that a data analyst could use.

Considering the intended scope of the book, I was fully satisfied with it. The authors are obviously well-qualified to write on the subject. The derivations show all important steps, so that a well-prepared reader can fill in the gaps relatively easily. The examples, while limited in depth, give the reader a clear impression of how to repeat the derivations for cases not covered. Its likely readership is limited to those wanting to develop and research information criteria, but the book will serve those readers well.

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Burnham, K. P. and Anderson, D. R. (2002). Model Selection and Multimodel Inference: A Practical Information-Theoretic Approach, 2nd ed. New York: Springer. KOKKO, H. Modelling for Field Biologists and Other Interesting People. Cambridge University Press, Cambridge, U.K., 2007. xii + 230 pp. \$59.00/£27.00 (Paperback) \$128.00/£65.00 (Hardback). ISBN 9780521538565 (Paperback), 9780521831321 (Hardback).

The title of this book says a lot about its contents. First, it covers the subject of mathematical and statistical modeling from a low-math perspective. Second, the examples used are taken from field biology, especially the author's area of specialization, sexual selection. Finally, the spirit of the book is light and often humorous ("chatty," to use the author's own description). The book is intended to be an introduction to a variety of topics, rather than a complete how-to manual. Chapters skim the surface of such topics as population genetics, optimization, game theory, and simulation. Subtitles to each chapter are reminiscent of those in books in the Winnie-the-Pooh series. Meanwhile, chapter contents provide practical, level-headed descriptions and justifications of various models, developed and illustrated extensively through the use of one or more examples. There are a few equations (this *is* about modeling, after all) and occasional reference to concepts from calculus. Small bits of Matlab code are given to demonstrate how to accomplish some of the tasks involved in modeling, but this aspect of the book is not its main focus.

I found the spirit of this book to be wonderful. Kokko informs and amuses simultaneously, consistently staying on the proper side of the fine line between "entertaining" and "silly." At the same time, the coverage of mathematical and statistical topics does not sacrifice fact for simplicity. Some familiarity with evolutional ecology is assumed, but not so much that marginally informed statistician like me will be excluded from the book. I was genuinely impressed with Kokko's ability to provide such an accessible bridge between subjects. I can wholeheartedly recommend this book, not only to members of the stated target population, but also to more mathematical types who may want a light and easy glimpse into how some of our tools are used "in real life," perhaps to stimulate further thinking in their own areas.