Reviews of Books and Teaching Materials

Handbook of Univariate and Multivariate Data Analysis and Interpretation with SPSS.

Robert HO. Boca Raton, FL: Chapman & Hall/CRC, 2006, 406 pp., $89.95 (H), ISBN: 1-58488-602-1.

This hardback covers most statistical methods provided by SPSS Base software in an easily understood manner, due in part to its liberal use of SPSS output and screenshots. The stated aim of the book is to "provide clear guidelines to both the execution of specific statistical tests and the interpretation of the findings." Despite the handbook title, the book is not terse but quite readable and accessible.

Indicative of its title, the book does assume readers have some experience with SPSS as well as an understanding of statistical methods. Stylistically, it is very similar to another SPSS-oriented book that I really like (and have used in the classroom), Elliott and Woodward (2007). However, *Handbook of Univariate and Multivariate Data Analysis and Interpretation with SPSS* is more advanced with respect to the statistical topics discussed and the execution of those methods in SPSS (both point-and-click and syntax-based). The latter is one of the greatest strengths of the book, because its provides a simple path to SPSS maturity by teaching the more powerful syntax method alongside the beginner-oriented point-and-click approach.

The basic template for each chapter follows this format: (1) Aim, (2) Checklist of Requirements, (3) Assumptions, and (4) Examples. However, most chapters consist primarily of examples. Chapter topics include frequencies and cross-tabulations; dependent- and independent-sample t-tests; one-way analysis of variance (ANOVA) with posthoc tests; factorial ANOVA; general linear models (GLM); correlation; simple and multiple linear regression (MLR); factor analysis; instrument reliability; structural equation modeling (SEM); and nonparametric tests. As indicated by the topics listed, the book is relatively heavy on univariate (and multi*variable* methods), but light on multi*variate* methods. Topics *not* covered include loglinear models, generalized linear models, discriminant analysis, and multivariate analysis of variance.

The SEM chapter deserves comment, because it is the longest by far. Compared to other chapters, the author spends more time explaining the methodology, and specifically addresses other topics such as model fit and assessment that do not receive much attention in other chapters where the topics are very relevant (e.g., GLM and MLR). The extra attention paid to SEM is probably a reflection of Ho's background in quantitative psychology. Unfortunately, SPSS Base software does not have the capability to do SEM, so the author uses the SPSS-affiliated software AMOS 5.0, for which a free student version can be downloaded. However, that software is at least two versions behind the latest release of AMOS.

Overall, the positives of this book greatly outweigh the negatives. The inclusion of SPSS syntax is a strong selling point, as well as the focus on interpretation of SPSS output. It is an excellent choice for graduate students and researchers outside the statistics community who use SPSS, and is probably best-suited for those in the social sciences due to the topics covered.

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REFERENCES

Elliott, A. C., and Woodward, W. A. (2007), *Statistical Analysis: Quick Reference Handbook*, Thousand Oaks, CA: Sage.

Introduction to Bayesian Statistics (2nd ed.).

William M. BOLSTAD. Hoboken, NJ: Wiley, 2007, xxiv+437 pp., $117.00 (H), ISBN: 978-0-470-14115-1.

Widespread application of Bayesian inference has been hindered by intensive computation. However, the recent advancement of computational techniques has made Bayesian inference very popular among scientists from all disciplines. Therefore, it may be desirable to introduce the concept of Bayesian inference at the undergraduate level, and this book intends to serve this purpose by introducing the concept of integrating prior knowledge in an inference procedure.

This book is composed of 16 chapters, of which Chapters 1–3, 5, and 7 present the ground work for people who have not been exposed to basic statistical ideas. Bayesian inference for discrete random variables is discussed in Chapter 6 whereas Bayesian inference for a population proportion based on binomial samples is introduced in Chapter 8. Chapter 9 contains Bayesian inference on a population mean based on normal samples. There is a good discussion on the choice of prior, so that the practitioner can use his/her own judgment when choosing a prior. This second edition has two new chapters. One on Bayesian inference on the Poisson parameter and another on Bayesian inference for the standard deviation of a normal population. Much attention has been paid to Bayesian inference under various choices of priors.

There are two important aspects of the book. First, it contains a good comparison between frequentist and Bayesian approaches, which makes complete sense to readers who are familiar with the frequentist approach. Second, the book introduces the idea of robust Bayesian inference and, consequently, mixture priors for Bayesian inference.

Different concepts are well illustrated in a lucid manner with real-life examples, figures, and graphs. Each chapter has ended with a summary of main points of that chapter, which I think is very useful to the reader. Also, the appendix of necessary calculus formulas should be helpful to many. One minor comment is that the exercises at the end of each chapter could be made more interesting and lively.

The given macros in R and in Minitab are useful, and the R functions, which were used in the text are available from *www.wiley.com* and are downloadable to Unix and Windows systems.

In summary, this book will play a key role in introducing Bayesian thinking at the college level and can serve as a helpful reference to the people who intend to use Bayesian methodology in their own work.

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Introduction to Bioinformatics.

Anna TRAMONTANO. Boca Raton, FL: Chapman & Hall/CRC, 2007, 174 pp., $59.95 (P), ISBN: 1-58488-569-6.

Bioinformatics, a field of problem solvers, is an interdisciplinary study born out of the necessity to both store and analyze colossal sums of biological data. Tramontano succinctly and tactfully describes bioinformaticians as those who are "expert users of the available tools as well as developers of new and more powerful methods." As the recipient of both a B.S. and an M.S. degree in bioinformatics, I am often charged with the difficult task of providing a quick, clear description of the entire discipline. Upon suppressing the urge to delve into a multitude of bioinformatics-related tangents and digressions, invariably leaving my curious colleague with much regret for offering such an open-ended question, I resort to discussing a three-legged stool model of bioinformatics. Such a model can be used for nearly any integration of technologies or disciplines. I prefer to characterize the three "legs" supporting the bioinformatics stool to be: biology, computer science and information technology, and quantitative sciences. This particular view about the number of "legs" and their exact composition will certainly vary through personal opinion and experience, but is nevertheless an easily understood, somewhat visual model. A most exciting side-effect of said stool is that, under Tramontano's definition of a bioinformaticist, anyone with experience in one or more "legs" of the stool could potentially add their expertise and contribute to this emerging discipline, and yes, even be labeled a bioinformaticist!

With its hand in such far-reaching disciplines as mathematics, statistics, information technology, computer science, and, of course, biology, the field of bioinformatics may appear somewhat daunting. Indeed, the word bioinformatics is in itself as unapproachable as any word with three consecutive vowels

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