

a course, this book seems to me to be a very useful course text for an audience of students in the health sciences.

RABE-HESKETH, S. and SKRONDAL, A. **Multilevel and Longitudinal Modeling Using Stata, 2nd edition**. Stata Press, College Station, Texas, 2008. xxxiii + 562 pp. \$59.00. ISBN 9781597180405.

The first edition of this book was reviewed in *Biometrics* **62**, p. 951. The reviewer summarized that “Established users of *Stata* who already possess knowledge of random effects and longitudinal models will be well served by this book,” while noting that “the presentation is inextricably tied to the software,” rendering it not very useful to non-*Stata* users. This is a considerably expanded version, nearly double the size of the original. Much of the added material serves to delineate more clearly between statistics and software.

The book now begins with a new chapter reviewing linear regression, including applications in *Stata*. New introductory material has been added to the inaugural chapter on basic random-effects models, making the book more accessible to readers who are inexperienced in the use of these models. Another new chapter has been created based upon expanded material from sections on longitudinal, panel, and growth data. This serves also to allow the development of simple random-intercept and random-coefficient models to transpire more concisely. A third new chapter on discrete-time survival data has been added. Finally, throughout the book

separate sections and subsections entitled “Estimation with *Stata*” help to separate the discussion of the models from the discussion of the fitting of the models using *Stata*. This improves the readability of the book and opens it up to a potentially broader audience.

GOLLERY, M. **Handbook of Hidden Markov Models in Bioinformatics**. Chapman & Hall/CRC Press, Boca Raton, Florida, 2008. xx + 156 pp. \$59.95/£31.99. ISBN 9781584886846.

This is not a book about hidden Markov models (HMMs), per se. Rather, it is more of a book on how to use software packages based on HMMs for the purpose of doing bioinformatics analyses and database searches. Clearly, the book’s audience is those who want to use the tools rather than those who want to develop them. One can read the book cover to cover and still not really know what HMMs are or how they work beyond a very superficial level. Indeed, a colleague of mine who does research on HMMs, Rachel Altman, read the book and agreed with this assessment. She further commented, “In my opinion, the researchers in this field are using the term HMM because (i) there are some hidden states and (ii) there is a Markovian component to their models. However, I personally would not classify their models as HMMs” (in the same sense as is used in current methodological research).