

NEW BOOKS

Biostatistics- A Methodology for the Health Sciences. By Gerald van Belle, Lloyd D. Fisher, Patrick J. Heagerty, and Thomas Lumley, Wiley-Interscience, 2004, x+871 pp., \$110.00

This is the second edition of a volume in the Wiley Series in Probability and Statistics, first published in 1993. This edition adds a chapter on randomized trials and one on longitudinal data analysis. Substantial changes have been made in discussing robust statistics, model building, survival analysis, and discrimination. Some material has been shifted to the book's web-page. The purpose of the book continues to be to teach readers how to apply statistical methods to the biomedical sciences; it is written so that those with no prior training in statistics and a mathematical knowledge through algebra can follow the text. Chapter headings: 1. Introduction to biostatistics; 2. Biostatistical design of medical studies; 3. Descriptive statistics; 4. Statistical inference: population and samples; 5. One- and two-sample inference; 6. Counting data; 7. Categorical data: contingency tables; 8. Nonparametric, distribution-free, and permutation models: robust procedures; 9. Association and prediction: linear models with one predictor variable; 10. Analysis of variance; 11. Association and prediction: multiple regression analysis and linear models with multiple predictor variables; 12. Multiple comparisons; 13. Discrimination and classification; 14. Principal component analysis and factor analysis; 15. Rates and proportions; 16. Analysis of the time to an event: survival analysis; 17. Sample sizes for observational studies; 18. Longitudinal data analysis; 19. Randomized clinical trials; 20. Personal postscript.

Bioinformatics and Computational Biology Solutions Using R and Bioconductor. Edited by Robert Gentleman, Vincent J. Carey, Wolfgang Huber, Rafael A. Irizarry, and Sandrine Dudoit, Springer, 2005, xix+471 pp., \$89.95

This book covers a broad area and ranges across most of the key capabilities of the Bioconductor project, which is an open source and open development software project for the analysis and comprehension of genomic data. It is rooted in the open source statistical computing environment *R*. Tables, figures, and other outputs are dynamically generated directly from the experimental data. Through the companion website, www.bioconductor.org/mogr, readers have full access to the source code and necessary supporting libraries. The book is divided into 25 chapters, by different authors, grouped into five parts: I. Preprocessing data from genomic experiments; II. Meta-data: biological annotation and visualization; III. Statistical analysis for genomic experiments; IV. Graphs and networks; V. Case studies.