

Statistical Bioinformatics with R

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Designed for a one or two semester bioinformatics course at the senior undergraduate or graduate level, this book takes a broad view of bioinformatics—not just gene expression and not just sequence analysis. A careful balance of statistical theory in the context of bioinformatics applications, including the development of advanced methodology such as Bayesian and Markov models provides students with the underlying foundation needed to conduct bioinformatics. A wide variety of applications in different biomedical and genomic areas, including the identification of differentially expressed genes, sequence analysis, location of recombinant breakpoints, complex designs, and gene clustering, are included.

Statisticians interested in bioinformatics and applied science researchers interested in finding solutions to high-dimensional problems in their fields will find this an essential reference. The inclusion of R code is unique and a real advantage to graduate students and beginning researchers.

Prerequisite knowledge includes one semester of calculus and an introduction to statistics course.

Features:

- integrates biological, statistical, and computational concepts at an accessible level
- inclusion of R code on the website
- provides the extensive coverage of MCMC methods, likelihood methods, design of experiments, and Bayesian Methods used in bioinformatics
- covers new concepts in biological sciences such as proteomics
- modern coverage of current tools—covers details of techniques and methods to use the online tools available, such as SAM, ORIOGEN, BAMARRAY, etc., for genomic data analysis.



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