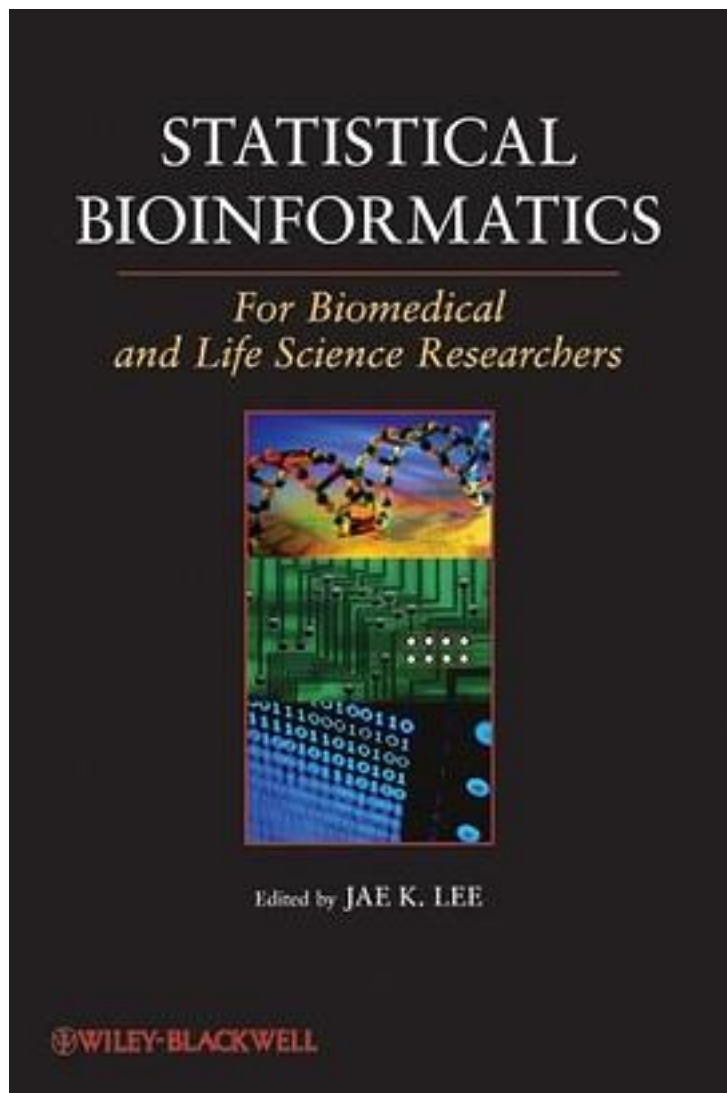


Statistical Bioinformatics



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This book provides an essential understanding of statistical concepts necessary for the analysis of genomic and proteomic data using computational techniques. The author presents both basic and advanced topics, focusing on those that are relevant to the computational analysis of large data sets in biology. Chapters begin with a description of a statistical concept and a current example from biomedical research, followed by more detailed presentation, discussion of limitations, and problems. The book starts with an introduction to probability and statistics for genome-wide data, and moves into topics such as clustering, classification, multi-dimensional visualization, experimental design, statistical resampling, and statistical network analysis. Clearly explains the use of bioinformatics tools in life sciences research without requiring an advanced background in math/statistics Enables biomedical and life sciences researchers to successfully evaluate the validity of their results and make inferences Enables statistical and quantitative researchers to rapidly learn novel statistical concepts and techniques appropriate for large biological data analysis Carefully revisits frequently used statistical approaches and highlights their limitations in large biological data analysis Offers programming examples and datasets Includes chapter problem sets, a glossary, a list of statistical notations, and appendices with references to background mathematical and technical material Features supplementary materials, including datasets, links, and a statistical package available online Statistical Bioinformatics is an ideal textbook for students in medicine, life sciences, and bioengineering, aimed at researchers who utilize computational tools for the analysis of genomic, proteomic, and many other emerging high-throughput molecular data. It may also serve as a rapid introduction to the bioinformatics science for statistical and computational students and audiences who have not experienced such analysis tasks before.

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评论

covers various topics from microarray analysis to model validations

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