Statistical Bioinformatics: For Biomedical and Life Science Researchers

Jae K. Lee
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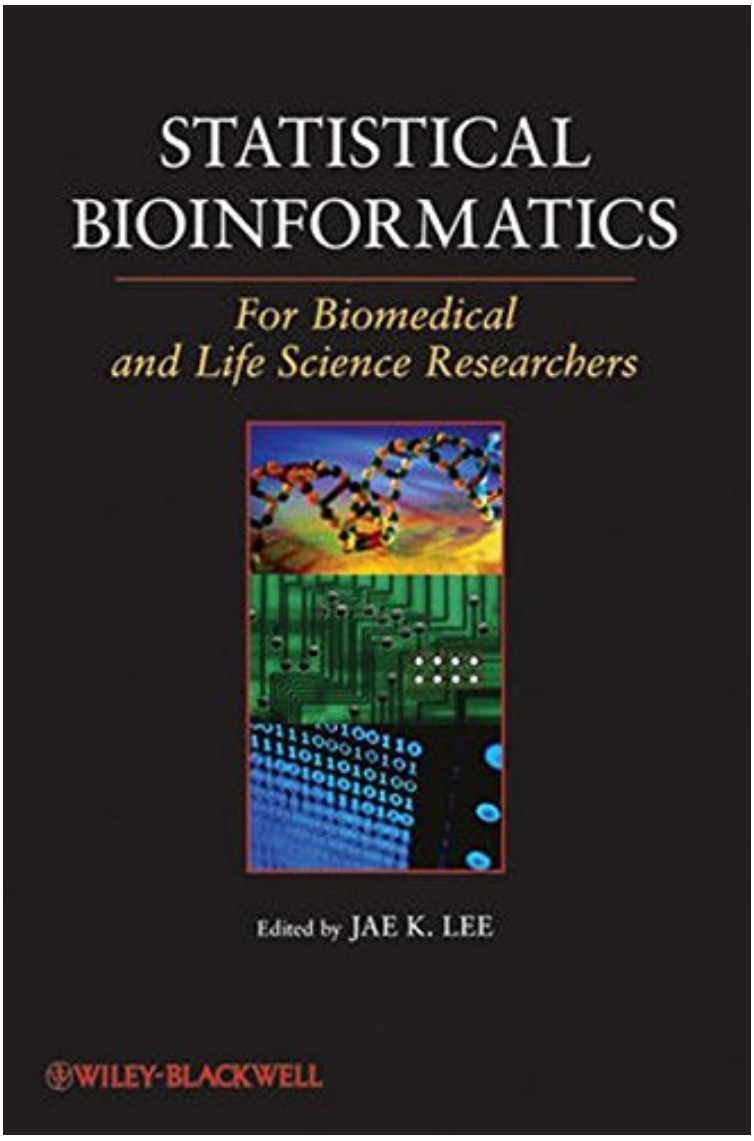

#2893541 in Books 2014-06-23Original language:EnglishPDF # 1 9.26 x .82 x 6.12l, 1.20 #File Name: 0471692727384 pages | File size: 71.Mb

Jae K. Lee : Statistical Bioinformatics: For Biomedical and Life Science Researchers before purchasing it in order to gage whether or not it would be worth my time, and all praised Statistical Bioinformatics: For Biomedical and Life Science Researchers:

7 of 7 people found the following review helpful. A DisappointmentBy statprof3We evaluated this book as a textbook for a graduate level statistics class. It surveys a large number of concepts in techniques, including the requisite chapter

on concepts in probability and distributions--each chapter is written by a different author. Other topics include quality control, supervised classification, unsupervised analysis, experimental designs, network analysis, and techniques for GWAS studies. Overall, the depth is extremely shallow for most topics and includes just a few equations or concepts. Although it does include snippets of R code, the included code is mostly one-liners without much in the way of explanation or exposition. Also mostly absent are worked examples with real biological data, which would have been welcome. There are much better textbooks out there both for practical techniques using R (the O'reilly books the R Cookbook and R in a nutshell come to mind) and for biostatistics (too many to mention).Conclusion: Might be suitable for an introductory undergraduate course at a community college, but not for serious practitioners.

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.

From the Back CoverA practical introduction to the underlying statistical concepts and techniques for successful use of bioinformatics tools Effective use of the tools and methods of bioinformatics requires a careful understanding of not only the relevant biology and computational problems, but also critical statistical principles. Statistical Bioinformatics provides an essential understanding of the novel statistical concepts necessary for the analysis of genomic and proteomic data using various bioinformatics and computational techniques. Dr. Jae Lee and the authors present both basic and advanced topics, focusing on those that are relevant to the efficient and rigorous analysis of large data sets in biology. The book starts with an introduction to probability and statistics for genome-wide data, and moves into topics such as clustering, classification, multidimensional visualization, experimental design, statistical resampling, and statistical network analysis. Chapters begin with a description of a statistical concept and practical examples from biomedical research, followed by more detailed presentation, discussion of limitations, and problems. 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.About the AuthorJae K. Lee, Ph.D., is a professor of biostatistics and epidemiology in the Department of Health Evaluation Sciences at the University of Virginia School of Medicine, where he designed and teaches a course on Statistical Bioinformatics in Medicine. He earned his doctorate in statistical genetics from the University of Wisconsin, Madison. He was previously a research scientist in the Laboratory of Molecular Pharmacology, National Cancer Institute. Among his current research interests is the integration of statistical and genomic information for the analysis of microarray data.