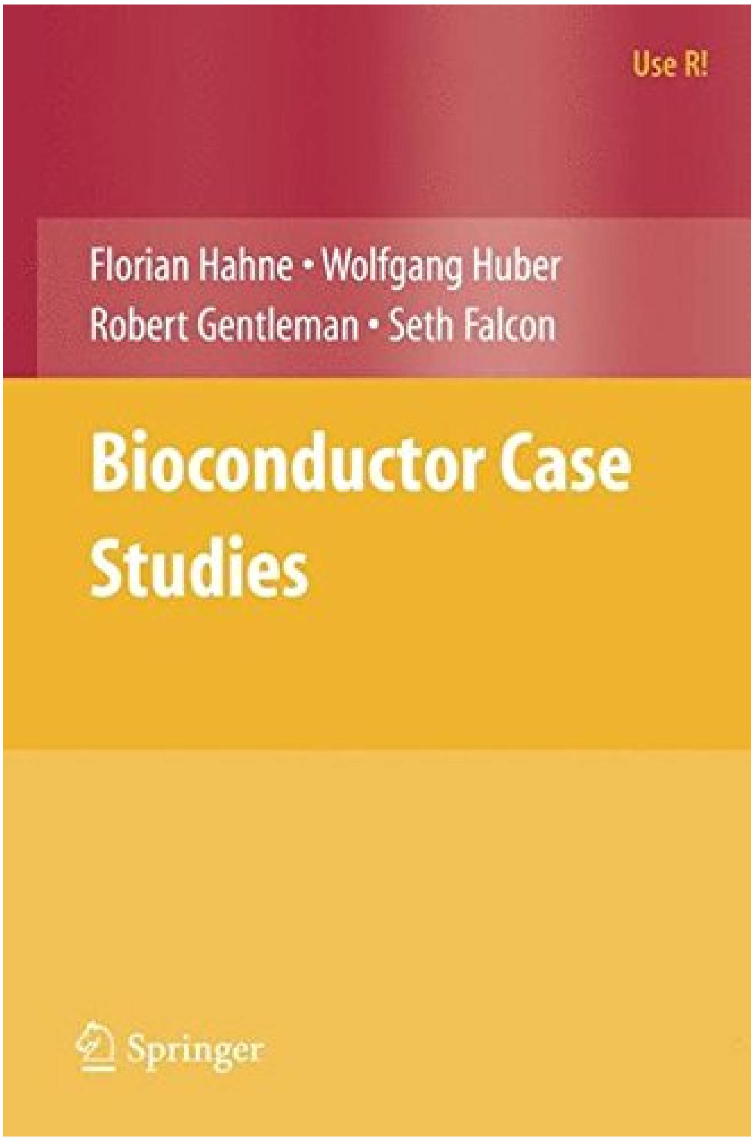
Bioconductor Case Studies (Use R!)

Florian Hahne, Wolfgang Huber, Robert Gentleman, Seth Falcon
*ePub | *DOC | audiobook | ebooks | Download PDF*



#2230113 in Books Florian Hahne 2008-08-15Original language:EnglishPDF # 1 9.25 x .71 x 6.10l, .85
#File Name: 0387772391284 pagesBioconductor Case Studies | File size: 56.Mb

Florian Hahne, Wolfgang Huber, Robert Gentleman, Seth Falcon : Bioconductor Case Studies (Use R!) before purchasing it in order to gage whether or not it would be worth my time, and all praised Bioconductor Case Studies (Use R!):

7 of 8 people found the following review helpful. Awful book, period!By CustomerI am loathe to write this review, but I feel compelled to. This is really an awful, awful book. There is no plan for the book in terms of trying to teach the reader the methods of analysis of Bioconductor in a structured way. All the chapters of the book seem like a

patchwork which begin somewhere and end abruptly without any consistency. It is highly puzzling for me since the Bioconductor package seems to relatively well thought out overall. When it comes to writing books, all the authors associated with the Bioconductor seem to abruptly and inexplicably fail. This leads to conclude TWO things 1) The authors do not want the general reader to learn the analysis 2) They are just awful writers. I have used the other official "Bioconductor" books too and they are equally awful too. 0 out of 3 is not a good record. Rather than try to make money off gullible public by peddling incremental and useless books, please try to write a book which will truly educate someone. Please give it a try. I assure you, you will better about yourselves. The 2 stars are for the effort. That's all. I understand this is a scathing review. But I assure you, I am a genuine student who wanted to learn the analysis and feels extremely cheated after shelling over $70 for this book. I am no dummy either. I have a Doctoral degree in Engineering. But this is just an awful book. Period.

Bioconductor software has become a standard tool for the analysis and comprehension of data from high-throughput genomics experiments. Its application spans a broad field of technologies used in contemporary molecular biology. In this volume, the authors present a collection of cases to apply Bioconductor tools in the analysis of microarray gene expression data. Topics covered include: (1) import and preprocessing of data from various sources; (2) statistical modeling of differential gene expression; (3) biological metadata; (4) application of graphs and graph rendering; (5) machine learning for clustering and classification problems; (6) gene set enrichment analysis. Each chapter of this book describes an analysis of real data using hands-on example driven approaches. Short exercises help in the learning process and invite more advanced considerations of key topics. The book is a dynamic document. All the code shown can be executed on a local computer, and readers are able to reproduce every computation, figure, and table.

From the reviews: "This work has extended R substantially and is an important tool for research. All the code, including solutions to the exercises, is available for downloading on the Web and-this is well worth mentioning-it runs straight out of the box. The book describes various analysis, provides the code for them and discusses the output. This makes for an easy read and anyone who works through the book will gain confidence that they can carry out analysis on their own data. The discussion of analysis is generally sound and practical. In particular the interpretation of the results of clustering is more sensible then you often see. This book is strongly recommended for learning more about Bioconductor." (Antony Unwin, Journal of Statistical Software, January 2009, Volume 29, Book 1). "The readership of this book will be specialized but the text deserves to be read more widely within the statistics and computer science communities as there is much to interest the inquiring mind. Exercises for private study and their solutions are provided as an integral part of the text. "(C.M. OBrien, International Statistical , 2009, 77, 1) One of the great advantages of the R language is its dynamic nature, where code and other resources are continuously generated in order to address novel analytical challenges. Microarray gene expression data present such a challenge, and the Bioconductor project has risen over the years to become the foremost central repository of R-implemented approaches for such data. However, while individual packages within Bioconductor are usually well documented, it is often hard to know which packages to use in what circumstances, especially when tools from several packages are best used in concert. This text aims to fill that void by offering a collection of case studies derived from the authors own Bioconductor courses, covering the topics of processing raw intensities; correcting for background noise and variation across chips; differential expression analysis; machine learning for clustering and classification; graph creation; and gene set enrichment. All in all, this text is an excellent, well-written reference for many of the common tasks that arise during the analysis of microarray gene expression datasets, as implemented by Bioconductor. It is well worth the modest sum required for its purchase. (The American Statistician, May 2010, Vol. 64, No. 2)From the Back CoverBioconductor software has become a standard tool for the analysis and comprehension of data from high-throughput genomics experiments. Its application spans a broad field of technologies used in contemporary molecular biology. In this volume, the authors present a collection of cases to apply Bioconductor tools in the analysis of microarray gene expression data. Topics covered include * import and preprocessing of data from various sources * statistical modeling of differential gene expression * biological metadata * application of graphs and graph rendering * machine learning for clustering and classification problems * gene set enrichment analysis Each chapter of this book describes an analysis of real data using hands-on example driven approaches. Short exercises help in the learning process and invitemore advanced considerations of key topics. The book is a dynamic document. All the code shown can be executed on a local computer, and readers are able to reproduce every computation, figure, and table. The authors of this book have longtime experience in teaching introductory and advanced courses to the application of Bioconductor software. Florian Hahne is a Postdoc at the Fred Hutchinson Cancer Research Center in Seattle, developing novel methodologies for the analysis of high-throughput cell-biological data. Wolfgang Huber is a research group leader in the European Molecular Biology Laboratory at the European Bioinformatics Institute in Cambridge. He has wide-ranging experience in the development of methods for the analysis of functional genomics experiments. Robert Gentleman is Head of the Program in Computational Biology at the Fred Hutchinson Cancer Research Center in Seattle, and he is one of the two authors of the original R system. Seth Falcon is a member of the R core team and former project manager and developer for the Bioconductor project.