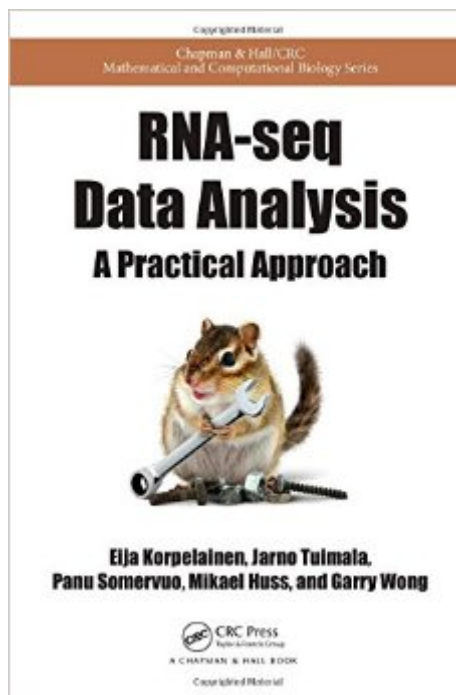# RNA-seq Data Analysis: A Practical Approach (Chapman & Hall/CRC Mathematical And Computational Biology)

Synopsis

The State of the Art in Transcriptome AnalysisRNA sequencing (RNA-seq) data offers unprecedented information about the transcriptome, but harnessing this information with bioinformatics tools is typically a bottleneck. RNA-seq Data Analysis: A Practical Approach enables researchers to examine differential expression at gene, exon, and transcript levels and to discover novel genes, transcripts, and whole transcriptomes. Balanced Coverage of Theory and PracticeEach chapter starts with theoretical background, followed by descriptions of relevant analysis tools and practical examples. Accessible to both bioinformaticians and nonprogramming wet lab scientists, the examples illustrate the use of command-line tools, R, and other open source tools, such as the graphical Chipster software. The Tools and Methods to Get Started in Your LabTaking readers through the whole data analysis workflow, this self-contained guide provides a detailed overview of the main RNA-seq data analysis methods and explains how to use them in practice. It is suitable for researchers from a wide variety of backgrounds, including biology, medicine, genetics, and computer science. The book can also be used in a graduate or advanced undergraduate course.

Book Information

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Customer Reviews

Having now purchased a few other books on this topic from , I have to say this one is the best if you need an introduction to the field. The others could be 1) downloaded from your university journal

subscription, and 2) focus much more on theory and suited better suited for those already familiar with the topic. They could still be useful but I doubt you would use them by themselves - you would probably find yourself looking up a lot of other information online or consulting other books.In contrast, this book is very self-contained. It covers all the basics of RNAseq analysis with a pretty detailed look at a typical pipeline. It covers many different available tools and even has a step-by-step code approach for using many of the common/popular tools. Most of the book uses either R or Bash for the code. It covers, RNA isolation techniques/QC, library prep methods, different sequencing platforms and how to choose, overview of RNAseq applications, preprocessing reads/QC, alignment, transcriptome assembly (including de novo), quantitation, Bioconductor packages, differential gene expression, differential exon usage analysis, annotation, visualization, and small/noncoding RNAseq analysis. I was happy to see that it covers a lot of the QC metrics, what they mean, and in what context they are important. Overall, this is a very thorough book.As a beginners guide it will get you the furthest compared to the other books currently available as of this writing. It will easily get you to that point where you are comfortable enough with the terminology and general pipeline for you to easily search for the answer to more detailed and specific questions online which is the biggest hurdle for this field.

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