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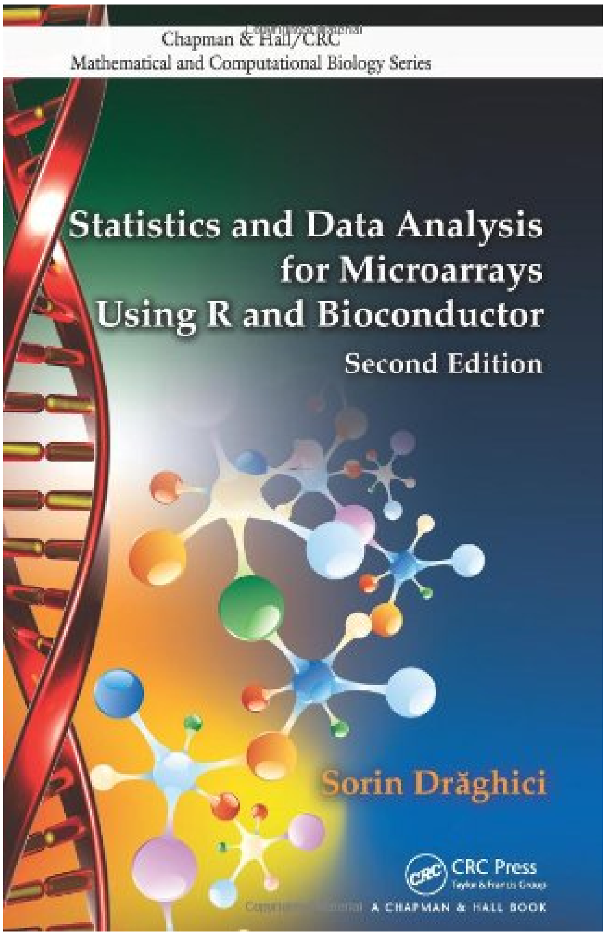

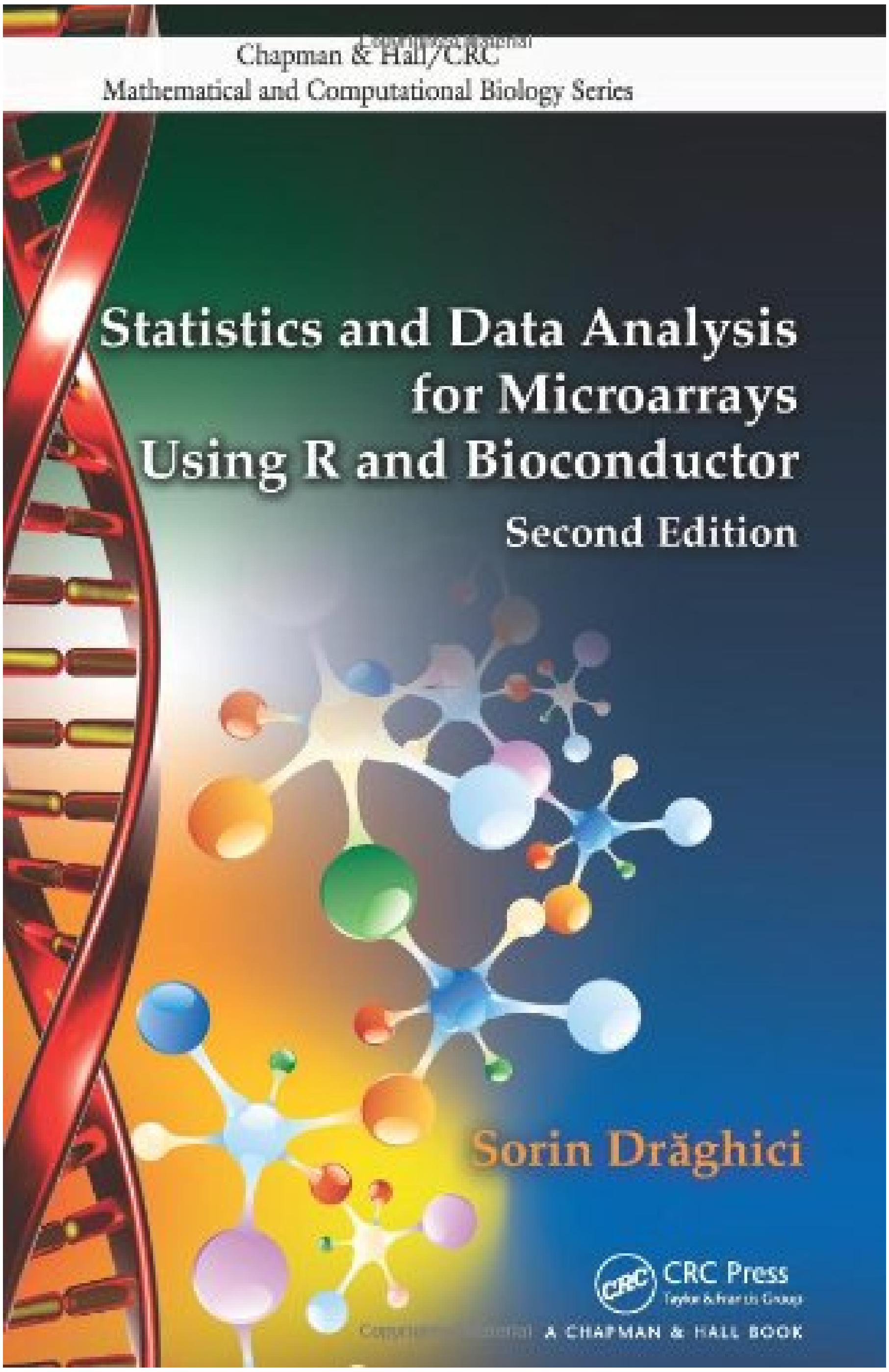

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Praise for the First Edition
The book by Draghici is an excellent choice to be used as a textbook for a graduate-level bioinformatics course. This well-written book with two accompanying CD-ROMs will create much-needed enthusiasm among statisticians.
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New to the Second Edition
Completely updated and double the size of its predecessor, this timely second edition replaces the commercial software with the open source R and Bioconductor environments. Fourteen new chapters cover such topics as the basic mechanisms of the cell, reliability and reproducibility issues in DNA microarrays, basic statistics and linear models in R, experiment design, multiple comparisons, quality control, data pre-processing and normalization, Gene Ontology analysis, pathway analysis, and machine learning techniques. Methods are illustrated with toy examples and real data and the R code for all routines is available on an accompanying CD-ROM.

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thorough, rich, and readable
By Rebecca L. Tagett
This book is extremely rich yet readable. It covers a lot of different topics, and chapters can be read in order or referred to as needed.
However, if you take the time to read it through carefully, you will enjoy yourself, because the author is a master of pedagogy, and often humorous.

While expression microarrays are the platforms covered by this book, most of the material has much broader application beyond that. Cell biology, R, statistics, experiment design, molecular pathways, and machine learning are all covered. Even if you don't work with microarrays, there is something in this book for you, anyway you should know the basics of microarray analysis.

Computer scientists or other non biologists may want to start at the beginning, which is an introduction to the cell and its basic mechanisms. It may seem like a lot of memorization and daunting to those who have never learned biology, but this chapter is well written with plenty of color images. It gives all of the fundamental biology needed to understand microarrays.

The author knows which topics need to be covered in more depth than other authors are generally willing to do. I especially appreciated the section on degrees of freedom. If you never really had a grasp on this topic (but used it anyway) you will be grateful for section 8.4!

Another chapter that I especially appreciated was "Experiment Design", which is so critical to any scientist of molecular biology and bioinformatics. How many of us in bioinformatics have been asked to analyze data from poorly designed experiments? Thanks to the extremely thorough preceding chapter on ANOVA, the chapter on experiment design is naturally set up for a straightforward and clear presentation of the rules, guidelines and concepts of experiment design. It presents the classic design models and several examples used by professionals in the field. The reader will feel confident designing basic experiments without having to refer the big hard core texts on the subject.

Throughout the book, very essential snippets of R code are revealed. You won't need much more or less than what you see here, once you have a little R under your belt. Dr Draghici's specialty is pathway analysis, and he is the coauthor of the R package "SPIA", available on bioconductor. The pros and cons of the different pathway analysis methods are discussed in detail.

5 of 5 people found the following review helpful.
Thank you, Sorin
By minijen
Thank you, Sorin. It is a fantastic book, funny, easy to follow and extremely useful for my work.
I have a very strong biological/biochemical background (PhD + postdoc), but I switched to bioinformatics several years ago. I've never got any formal training in bioinformatics, just reading a lot of books, publications, taking courses, attending lectures and talking to experts. This book has structured and organized my knowledge, cleared up some terms and conceptions, advanced my R skills.

4 of 4 people found the following review helpful.
The book is very good book!!!!!
By Leandro de Mattos Pereira
Very good this book, excellent! it covers various aspects of the basic statistics and methods of data mining and steps for data microarray analysis.

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