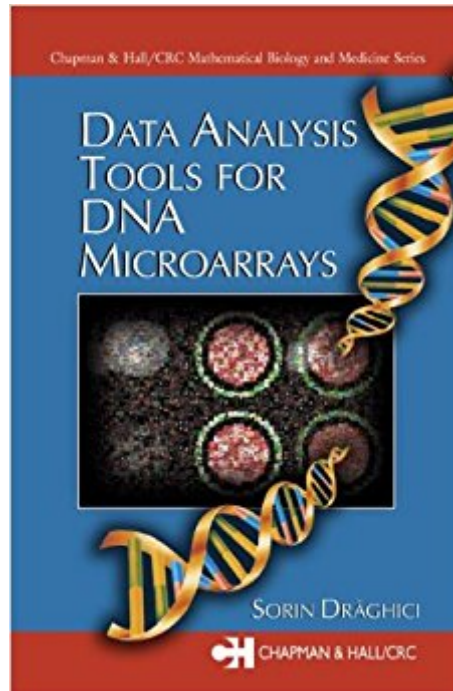




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Data Analysis Tools For DNA Microarrays



Synopsis

Technology today allows the collection of biological information at an unprecedented level of detail and in increasingly vast quantities. To reap real knowledge from the mountains of data produced, however, requires interdisciplinary skills—a background not only in biology but also in computer science and the tools and techniques of data analysis. To help meet the challenges of DNA research, *Data Analysis Tools for DNA Microarrays* builds the foundation in the statistics and data analysis tools needed by biologists and provides the overview of microarrays needed by computer scientists. It first presents the basics of microarray technology and more importantly, the specific problems the technology poses from the data analysis perspective. It then introduces the fundamentals of statistics and the details of the techniques most commonly used to analyze microarray data. The final chapter focuses on commercial applications with sections exploring various software packages from BioDiscovery, Insightful, SAS, and Spotfire. The book is richly illustrated with more than 230 figures in full color and comes with a CD-ROM containing full-feature trial versions of software for image analysis (ImaGene, BioDiscovery Inc.) and data analysis (GeneSight, BioDiscovery Inc. and S-Plus Array Analyzer, Insightful Inc.). Written in simple language and illustrated in full color, *Data Analysis Tools for DNA Microarrays* lowers the communication barrier between life scientists and analytical scientists. It prepares those charged with analyzing microarray data to make informed choices about the techniques to use in a given situation and contribute to further advances in the field.

Book Information

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Customer Reviews

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. -Journal of Statistical Computation and Simulation, Vol. 74I really like Draghici's book. As the author explains in the Preface, the book is intended to serve both the statistician who knows very little about DNA microarrays and the biologist who has no expertise in data analysis. The author lays out a study plan for the statistician that excludes 5 of the 17 chapters (4-8). These chapters present the basics of statistical distributions, estimation, hypothesis testing, ANOVA, and experimental design. What that leaves for the statistician is the three-chapter primer on microarrays and image processing, plus all of the data analysis tools specific to the microarray situation. The softcover book is reasonably priced, and it includes two CDs with trial versions of several specialised software packages. Anyone who uses microarray data should certainly own a copy. -Technometrics, Vol. 47, No. 1, February 2005

Being a book worm, as soon as I started working with microarrays I bought a bunch of books on the subject. After six months working with this technique and reading chapters on all the books I've bought I can say with certainty that Draghici's is the best introductory book on microarrays. Other books around are better at describing protocols or explaining the math involved in microarray data analysis but Draghici's book does a very good job at explaining how to analyse microarray data for the biologist (and maybe for other publics but statisticians). Everytime some friend ask me for hints on chapters or books to read for learning (or re-learning) statistics I suggest this book. The first chapters are an excellent review of the basics of statistics necessary for day to day practice. The only complain I have is that the shareware software that comes with the book does not work anymore (it's trial period has already expired and therefore it is not possible to install it even if you get a brand new book). I read this book from cover to cover and I think that, considering how readable it is, anyone could do it.

I'm more than 2/3 through the book and I've never encountered a topic that I feel could have been better presented. My definition of a Great book is that I can understand and follow it, and this definitely is a Great book! Thanks to the author for writing such readable text. This text has not made it to my bookshelf at work, it stays on my desk.

it is very good.fast and excellent

I had to buy this book for a class, but I kept because it has very interesting information about basics of DNA microarrays but also data analysis. It is definitely very useful, I recommend.

For long time I searched for a book on microarray data analysis to be used by my students of the medical School. Finally I found the Sorin Draghici's book: comprehensive and easy to be read.

The targeted audience of this book is biologists who are eager to get an understanding of the analysis tools they use for microarrays. The book does an excellent job addressing this tier of audience. The book has plenty of examples. Almost all the examples, whether fake or real, are microarray-related. Whenever needed, figures or charts are provided to illustrate ideas. A few chapters that introduce basic statistical concepts provide solved problems and exercises. All these efforts are worthwhile making difficult statistical concepts easy to understand in the context of microarrays and making the book especially valuable for biologists who do not have strong background in statistics. This book has an emphasis on major statistical aspects of microarray data analysis. There are 17 chapters in this book. About 8 of them are directly related to statistics. Especially, there is one whole chapter devoted to multiple hypothesis testing, one chapter for ANOVA, and one chapter for experimental design. The above subjects are presented in a thorough, yet easy-to-follow style. Statistical issues are often not well addressed in published papers using microarrays. This book on microarray data analysis does an excellent job emphasizing this aspect. The title of the book indicates "data analysis". However, since this is not a clearly defined term, you should be aware that the book only deals with "the bare minimum" of data analysis. That is routines, such as normalization, transformation, statistical testing, and clustering, that have to be carried out each and every time. Exploratory data visualizing and data mining algorithms are not covered thoroughly in this book. For example, principal component analysis (PCA) is presented as a subsection of a chapter. It does not provide explanations on concepts such as loading factors nor scree test. Series data (e.g. time series) are on two pages only and there is no mention of Fourier transformation. Support vector machine (SVM), which is widely used today as a supervised classification method, is not presented at all. As I mentioned at the beginning, the targeted audience is biologists. If you are a statistician or a bioinformatician who wants to mathematically explore data analysis algorithms, you should look somewhere else. You may be disappointed that many

concepts are not rigorously or accurately defined in this book. For example, the book uses capital letters to denote random variables. But the concept of random variables is not rigorously defined in the book. One of the consequences is the weak definition of mathematical expectation. Another example is the inflation of Type I error rate. On page 220, the author claims that the probability of "drawing the correct conclusion" is $1 - p$, where p is the calculated probability of a statistic versus a parameter. However, if the probability of making a correct conclusion excludes the probability of making Type II errors, $1 - p$ should be stated as the probability of not making Type I errors. In summary, this is a good book on microarray analysis tools for biologists using microarrays. However, people who are seeking in-depth descriptions of these algorithms should look somewhere else.

When entering the minefields of microarray data analysis, one has to understand and keep up with state-of-the-art technologies and interdisciplinary literatures. A background in molecular biology is clearly not enough to evaluate the pro and cons of the various statistical methods for selecting truly modulated candidate genes in a given experimental biological system. Choosing between the available analysis software's is not an easy task either. Draghici presents a complete visit of the microarray underworld by initiating the reader to all the facettes of this domain. From the fundamentals of slide production and target hybridization to image processing, statistical analysis, experimental design, data management and biological interpretation, all aspects treated herein are described with pertinent details. Draghici slowly, but successfully, tames the reticent molecular biologist to the arid world of statistics and even entertains the reader with anecdotes and humoristic citations. Clearly written, with appropriate mathematical examples for each topic, this book even includes exercises at the end of some chapters, for the zealous student sleeping in all of us. It constitutes a very good didactic tool and the included CD's allow a good peek in some of the available image/data analysis software's on the market. As a core facility manager and eternal student, I strongly recommend Draghici's book to life scientists and students who are struggling with statistical analysis and data mining techniques. Brigitte Malette, Ph. D. Project Leader, Microarray Platform Centre for Structural and Functional Genomics Concordia University Montreal

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