Statistical Diagnostics for Cancer: Analyzing High-Dimensional Data (Quantitative and Network Biology (VCH))

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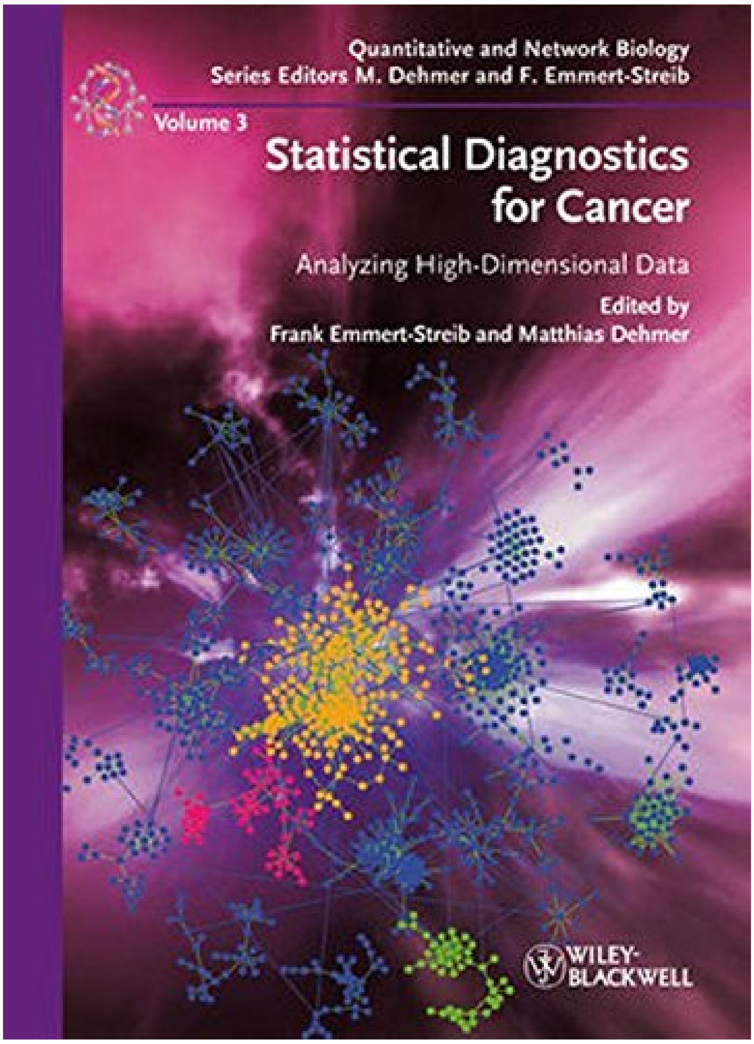

#7202999 in Books 2013-02-25Original language:EnglishPDF # 1 9.70 x .83 x 7.00l, 1.80 #File Name: 3527332626312 pages | File size: 33.Mb

From Wiley-Blackwell : Statistical Diagnostics for Cancer: Analyzing High-Dimensional Data (Quantitative and Network Biology (VCH)) before purchasing it in order to gage whether or not it would be worth my time, and all praised Statistical Diagnostics for Cancer: Analyzing High-Dimensional Data (Quantitative and Network Biology (VCH)):

This ready reference discusses different methods for statistically analyzing and validating data created with high-throughput methods. As opposed to other titles, this book focusses on systems approaches, meaning that no single gene or protein forms the basis of the analysis but rather a more or less complex biological network. From a methodological point of view, the well balanced contributions describe a variety of modern supervised and unsupervised statistical methods applied to various large-scale datasets from genomics and genetics experiments. Furthermore, since the availability of sufficient computer power in recent years has shifted attention from parametric to nonparametric methods, the methods presented here make use of such computer-intensive approaches as Bootstrap, Markov Chain Monte Carlo or general resampling methods. Finally, due to the large amount of information available in public databases, a chapter on Bayesian methods is included, which also provides a systematic means to integrate this information. A welcome guide for mathematicians and the medical and basic research communities.

From the Back CoverThis ready reference discusses different methods for statistically analyzing and validating cancer data generated from high-throughput methods. In contrast to other titles, this book focuses on systems approaches, meaning that no single gene or protein forms the basis of the analysis but rather a more orless complex biological network. Due to the complex nature of cancer, such approaches are very appropriate.From a methodological point of view, the well-balanced contributions describe a variety of modern supervised and unsupervised statistical methods applied to various large-scale datasets from genomics and genetics experiments. Furthermore, since the availability of sufficient computer power in the recent years has shifted attention from parametric to nonparametric methods, the methods presented here make use of such computer-intensive approaches such as Bootstrap, Markov Chain Monte Carlo or general resampling methods. Finally, Bayesian methods are discussed, because these are particularly useful for a systematic data integration. Thus, the book serves as a useful guide for methods-oriented scientists and the medical and basic research community.About the AuthorFrank Emmert-Streib studied physics at the University of Siegen (Germany) and received his Ph.D. in Theoretical Physics from the University of Bremen (Germany). He was a postdoctoral research associate at the Stowers Institute for Medical Research (Kansas City, USA) in the Department for Bioinformatics and a Senior Fellow at the University of Washington (Seattle, USA) in the Department of Biostatistics and the Department of Genome Sciences. Currently, he is Lecturer/Assistant Professor at the Queen's University Belfast at the Center for Cancer Research and Cell Biology (CCRCB) leading the Computational Biology and Machine Learning Lab. His research interests are in the field of computational biology, machine learning and biostatistics in the development and application of methods from statistics and machine learning for the analysis of high-throughput data from genomics and genetics experiments. Matthias Dehmer studied mathematics at the University of Siegen (Germany) and received his PhD in computer science from the Technical University of Darmstadt (Germany). Afterwards, he was a research fellow at Vienna Bio Center (Austria), Vienna University of Technology and University of Coimbra (Portugal). Currently, he is Professor at UMIT - The Health and Life Sciences University (Austria). His research interests are in bioinformatics, cancer analysis, chemical graph theory, systems biology, complex networks, complexity, statistics and information theory. In particular, he is also working on machine learning-based methods to design new data analysis methods for solving problems in computational biology and medicinal chemistry.