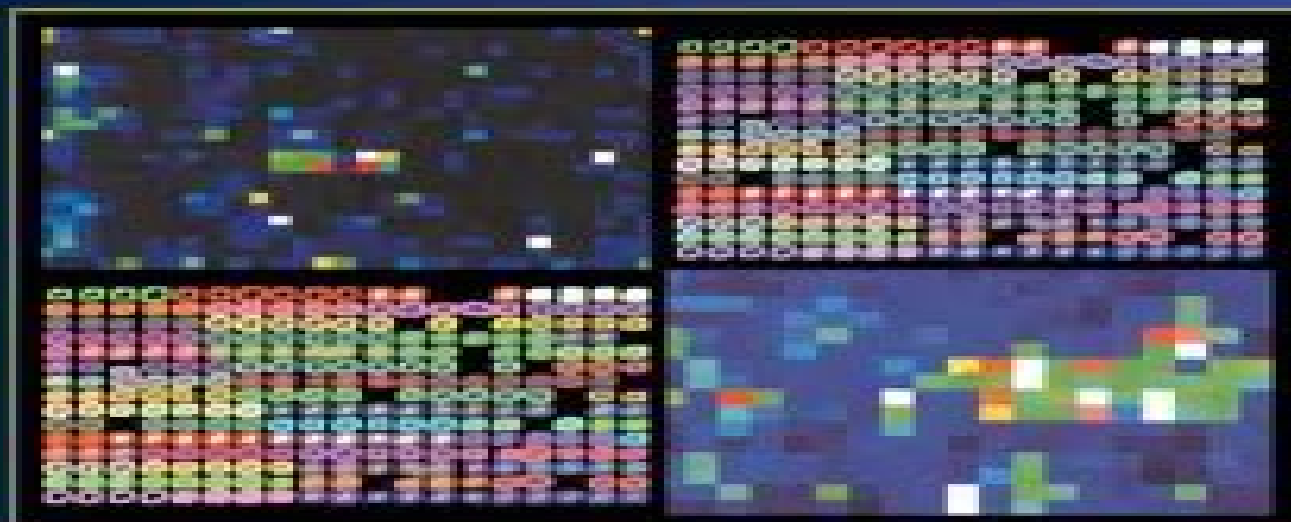


Interdisciplinary Statistics
**STATISTICAL ANALYSIS
of GENE EXPRESSION
MICROARRAY DATA**



Edited by
Terry Speed



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Statistical Analysis Of Gene Expression Microarray Data

Xiaohong Huang



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Statistical Analysis of Gene Expression Microarray Data Terry Speed, 2003-03-26 Although less than a decade old the field of microarray data analysis is now thriving and growing at a remarkable pace Biologists geneticists and computer scientists as well as statisticians all need an accessible systematic treatment of the techniques used for analyzing the vast amounts of data generated by large scale gene expression studies

Analysis of Microarray Gene Expression Data Mei-Ling Ting Lee, 2007-05-08 After genomic sequencing microarray technology has emerged as a widely used platform for genomic studies in the life sciences Microarray technology provides a systematic way to survey DNA and RNA variation With the abundance of data produced from microarray studies however the ultimate impact of the studies on biology will depend heavily on data mining and statistical analysis The contribution of this book is to provide readers with an integrated presentation of various topics on analyzing microarray data

Statistics and Data Analysis for Microarrays Using R and Bioconductor Sorin Drăghici, 2016-04-19 Richly illustrated in color Statistics and Data Analysis for Microarrays Using R and Bioconductor Second Edition provides a clear and rigorous description of powerful analysis techniques and algorithms for mining and interpreting biological information Omitting tedious details heavy formalisms and cryptic notations the text takes a hands on example based approach that teaches students the basics of R and microarray technology as well as how to choose and apply the proper data analysis tool to specific problems 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 downloadable resource With all the necessary prerequisites included this best selling book guides students from very basic notions to advanced analysis techniques in R and Bioconductor The first half of the text presents an overview of microarrays and the statistical elements that form the building blocks of any data analysis The second half introduces the techniques most commonly used in the analysis of microarray data

The Analysis of Gene Expression Data Giovanni Parmigiani, Elizabeth S. Garrett, Rafael A. Irizarry, Scott L. Zeger, 2003-04-08 This book presents practical approaches for the analysis of data from gene expression micro arrays It describes the conceptual and methodological underpinning for a statistical tool and its implementation in software The book includes coverage of various packages that are part of the Bioconductor project and several related R tools The materials presented cover a range of software tools designed for varied audiences

Methods for Incorporating Biological Information Into the Statistical Analysis of Gene Expression Microarray Data Debbie Leader, 2009 Microarray technology has made it possible for researchers to simultaneously

measure the expression levels of tens of thousands of genes. It is believed that most human diseases and biological phenomena occur through the interaction of groups of genes that are functionally related. To investigate the feasibility of incorporating functional information and/or constraints based on biological and technical needs into the classification process, two approaches were examined in this thesis. The first of these approaches investigated the effect of incorporating a pre filter into the gene selection step of the classifier construction process. Both simulated and real microarray datasets were used to assess the utility of this approach. The pre filter was based on an early method for determining if a gene had undergone a biologically relevant level of differential expression between two classes. The genes retained by the pre filter were ranked using one of five standard statistical ranking methods and the most highly ranked were used to construct a predictive classifier. To generate the simulated data, a selection of different parametric and non-parametric techniques were employed. The results from these analyses showed that when the constraints that the pre filter contains were placed on the classification analysis, the predictive performance of the classifiers was similar to when the pre filter was not used. The second approach explored the feasibility of incorporating sets of functionally related genes into the classification process. Three publicly available datasets obtained from studies into breast cancer were used to assess the utility of this approach. A summary of each gene set was derived by reducing the dimensionality of each gene set via the use of Principal Component Analysis. The reduced gene sets were then ranked based on their ability to distinguish between the two classes via Hotelling's T^2 and those most highly ranked were used to construct a classifier via logistic regression. The results from the analyses undertaken for this approach showed that it was possible to incorporate function information into the classification process whilst maintaining an equivalent if not higher level of predictive performance as well as improving the biological interpretability of the classifier.

Statistical Analysis Using Microarray Gene Expression Data Xiaohong Huang, 2004

Statistical Analysis of Gene Expression Data from DNA Microarrays Based on Partial Least Squares and Related Dimension Reduction Methods Danh V. Nguyen (Ph. D. in statistics), 2000

Statistical Analysis of Microarray Data -- Topics in Gene Expression Xin Victoria Wang, 2009

Statistics for Microarrays Ernst Wit, John McClure, 2004-07-23

Interest in microarrays has increased considerably in the last ten years. This increase in the use of microarray technology has led to the need for good standards of microarray experimental notation, data representation and the introduction of standard experimental controls as well as standard data normalization and analysis techniques. *Statistics for Microarrays: Design, Analysis and Inference* is the first book that presents a coherent and systematic overview of statistical methods in all stages in the process of analysing microarray data, from getting good data to obtaining meaningful results. It provides an overview of statistics for microarrays including experimental design, data preparation, image analysis, normalization, quality control and statistical inference. Features many examples throughout using real data from microarray experiments. Computational techniques are integrated into the text. Takes a very practical approach suitable for statistically minded biologists. Supported

by a Website featuring colour images software and data sets Primarily aimed at statistically minded biologists bioinformaticians biostatisticians and computer scientists working with microarray data the book is also suitable for postgraduate students of bioinformatics **Microarray Data** Shailaja R. Deshmukh, Sudha G. Purohit, 2007 Functional Genomics a branch of bioinformatics is essentially an interdisciplinary subject in which biologists statisticians and computer experts interact to analyze the microarray data This book caters to the needs of all the three disciplines For biologists and computer scientists it explains concepts of statistics and statistical inference For Biologists and Statisticians it provides annotated R programs to analyze microarray data For Statisticians and Computer scientists it explains basics of biology relevant to microarray experiment Thus the book will be useful to scientists from all the three disciplines with not much knowledge of other disciplines to analyze microarray data and interpret the results

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