

# ANALYZING MICROARRAY GENE EXPRESSION DATA

 WILEY



**Geoffrey J. McLachlan**  
**Kim-Anh Do**  
**Christophe Ambroise**

Wiley Series in Probability and Statistics

# Analyzing Microarray Gene Expression Data Wiley Series In Probability And Statistics

**Saeid Sanei, Hossein Hassani**



## **Analyzing Microarray Gene Expression Data Wiley Series In Probability And Statistics:**

Analyzing Microarray Gene Expression Data Geoffrey J. McLachlan, Kim-Anh Do, Christophe Ambroise, 2005-02-18 A multi discipline hands on guide to microarray analysis of biological processes Analyzing Microarray Gene Expression Data provides a comprehensive review of available methodologies for the analysis of data derived from the latest DNA microarray technologies Designed for biostatisticians entering the field of microarray analysis as well as biologists seeking to more effectively analyze their own experimental data the text features a unique interdisciplinary approach and a combined academic and practical perspective that offers readers the most complete and applied coverage of the subject matter to date Following a basic overview of the biological and technical principles behind microarray experimentation the text provides a look at some of the most effective tools and procedures for achieving optimum reliability and reproducibility of research results including An in depth account of the detection of genes that are differentially expressed across a number of classes of tissues Extensive coverage of both cluster analysis and discriminant analysis of microarray data and the growing applications of both methodologies A model based approach to cluster analysis with emphasis on the use of the EMMIX GENE procedure for the clustering of tissue samples The latest data cleaning and normalization procedures The uses of microarray expression data for providing important prognostic information on the outcome of disease

**Computational Intelligence Methods for Bioinformatics and Biostatistics** Elia Biganzoli, Alfredo Vellido, Federico Ambrogi, Roberto Tagliaferri, 2012-12-11 This book constitutes the thoroughly refereed post proceedings of the 8th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics CIBB 2011 held in Gargnano del Garda Italy in June July 2011 The 19 papers presented together with 2 keynote speeches were carefully reviewed and selected from 24 submissions The papers are organized in topical sections on statistical learning genomics computational intelligence for health at the edge proteomics intelligent clinical decision support systems i CDSS bioinformatics and data clustering

Handbook of Mixture Analysis Sylvia Fruhwirth-Schnatter, Gilles Celeux, Christian P. Robert, 2019-01-04 Mixture models have been around for over 150 years and they are found in many branches of statistical modelling as a versatile and multifaceted tool They can be applied to a wide range of data univariate or multivariate continuous or categorical cross sectional time series networks and much more Mixture analysis is a very active research topic in statistics and machine learning with new developments in methodology and applications taking place all the time The Handbook of Mixture Analysis is a very timely publication presenting a broad overview of the methods and applications of this important field of research It covers a wide array of topics including the EM algorithm Bayesian mixture models model based clustering high dimensional data hidden Markov models and applications in finance genomics and astronomy Features Provides a comprehensive overview of the methods and applications of mixture modelling and analysis Divided into three parts Foundations and Methods Mixture Modelling and Extensions and Selected Applications Contains many worked examples using real data together with computational implementation to illustrate the

methods described Includes contributions from the leading researchers in the field The Handbook of Mixture Analysis is targeted at graduate students and young researchers new to the field It will also be an important reference for anyone working in this field whether they are developing new methodology or applying the models to real scientific problems

**Bayesian Modeling in Bioinformatics** Dipak K. Dey, Samiran Ghosh, Bani K. Mallick, 2010-09-03 Bayesian Modeling in Bioinformatics discusses the development and application of Bayesian statistical methods for the analysis of high throughput bioinformatics data arising from problems in molecular and structural biology and disease related medical research such as cancer It presents a broad overview of statistical inference clustering and c

**Medical Applications of Finite Mixture Models** Peter Schlattmann, 2009-03-02 Patients are not alike This simple truth is often ignored in the analysis of medical data since most of the time results are presented for the average patient As a result potential variability between patients is ignored when presenting e.g. the results of a multiple linear regression model In medicine there are more and more attempts to individualize therapy thus from the author's point of view biostatisticians should support these efforts Therefore one of the tasks of the statistician is to identify heterogeneity of patients and if possible to explain part of it with known explanatory covariates Finite mixture models may be used to aid this purpose This book tries to show that there are a large range of applications They include the analysis of gene expression data pharmacokinetics toxicology and the determinants of beta carotene plasma levels Other examples include disease clustering data from psychophysiology and meta analysis of published studies The book is intended as a resource for those interested in applying these methods

Singular Spectrum Analysis of Biomedical Signals Saeid Sanei, Hossein Hassani, 2015-12-23 Recent advancements in signal processing and computerised methods are expected to underpin the future progress of biomedical research and technology particularly in measuring and assessing signals and images from the human body This book focuses on singular spectrum analysis SSA an effective approach for single channel signal analysis and its

Exploration and Analysis of DNA Microarray and Protein Array Data Dhammika Amaratunga, Javier Cabrera, 2004 A cutting edge guide to the analysis of DNA microarray data Genomics is one of the major scientific revolutions of this century and the use of microarrays to rapidly analyze numerous DNA samples has enabled scientists to make sense of mountains of genomic data through statistical analysis Today microarrays are being used in biomedical research to study such vital areas as a drug's therapeutic value or toxicity and cancer spreading patterns of gene activity Exploration and Analysis of DNA Microarray and Protein Array Data answers the need for a comprehensive cutting edge overview of this important and emerging field The authors seasoned researchers with extensive experience in both industry and academia effectively outline all phases of this revolutionary analytical technique from the preprocessing to the analysis stage Highlights of the text include A review of basic molecular biology followed by an introduction to microarrays and their preparation Chapters on processing scanned images and preprocessing microarray data Methods for identifying differentially expressed genes in comparative microarray experiments Discussions of gene and sample clustering

and class prediction Extension of analysis methods to protein array data Numerous exercises for self study as well as data sets and a useful collection of computational tools on the authors Web site make this important text a valuable resource for both students and professionals in the field

### **Exploration and Analysis of DNA Microarray and Other**

**High-Dimensional Data** Dhammika Amaratunga,Javier Cabrera,Ziv Shkedy,2014-01-27 Praise for the First Edition extremely well written a comprehensive and up to date overview of this important field Journal of Environmental Quality Exploration and Analysis of DNA Microarray and Other High Dimensional Data Second Edition provides comprehensive coverage of recent advancements in microarray data analysis A cutting edge guide the Second Edition demonstrates various methodologies for analyzing data in biomedical research and offers an overview of the modern techniques used in microarray technology to study patterns of gene activity The new edition answers the need for an efficient outline of all phases of this revolutionary analytical technique from preprocessing to the analysis stage Utilizing research and experience from highly qualified authors in fields of data analysis Exploration and Analysis of DNA Microarray and Other High Dimensional Data Second Edition features A new chapter on the interpretation of findings that includes a discussion of signatures and material on gene set analysis including network analysis New topics of coverage including ABC clustering biclustering partial least squares penalized methods ensemble methods and enriched ensemble methods Updated exercises to deepen knowledge of the presented material and provide readers with resources for further study The book is an ideal reference for scientists in biomedical and genomics research fields who analyze DNA microarrays and protein array data as well as statisticians and bioinformatics practitioners Exploration and Analysis of DNA Microarray and Other High Dimensional Data Second Edition is also a useful text for graduate level courses on statistics computational biology and bioinformatics

### **Markov Decision**

**Processes** Martin L. Puterman,2005-03-03 The Wiley Interscience Paperback Series consists of selected books that have been made more accessible to consumers in an effort to increase global appeal and general circulation With these new unabridged softcover volumes Wiley hopes to extend the lives of these works by making them available to future generations of statisticians mathematicians and scientists This text is unique in bringing together so many results hitherto found only in part in other texts and papers The text is fairly self contained inclusive of some basic mathematical results needed and provides a rich diet of examples applications and exercises The bibliographical material at the end of each chapter is excellent not only from a historical perspective but because it is valuable for researchers in acquiring a good perspective of the MDP research potential Zentralblatt fur Mathematik it is of great value to advanced level students researchers and professional practitioners of this field to have now a complete volume with more than 600 pages devoted to this topic Markov Decision Processes Discrete Stochastic Dynamic Programming represents an up to date unified and rigorous treatment of theoretical and computational aspects of discrete time Markov decision processes Journal of the American Statistical Association

*Statistical Meta-Analysis with Applications* Joachim Hartung (Prof. Dr.),Guido Knapp,Bimal K.

Sinha,2008-08-11 An accessible introduction to performing meta analysis across various areas of research The practice of meta analysis allows researchers to obtain findings from various studies and compile them to verify and form one overall conclusion Statistical Meta Analysis with Applications presents the necessary statistical methodologies that allow readers to tackle the four main stages of meta analysis problem formulation data collection data evaluation and data analysis and interpretation Combining the authors expertise on the topic with a wealth of up to date information this book successfully introduces the essential statistical practices for making thorough and accurate discoveries across a wide array of diverse fields such as business public health biostatistics and environmental studies Two main types of statistical analysis serve as the foundation of the methods and techniques combining tests of effect size and combining estimates of effect size Additional topics covered include Meta analysis regression procedures Multiple endpoint and multiple treatment studies The Bayesian approach to meta analysis Publication bias Vote counting procedures Methods for combining individual tests and combining individual estimates Using meta analysis to analyze binary and ordinal categorical data Numerous worked out examples in each chapter provide the reader with a step by step understanding of the presented methods All exercises can be computed using the R and SAS software packages which are both available via the book s related Web site Extensive references are also included outlining additional sources for further study Requiring only a working knowledge of statistics Statistical Meta Analysis with Applications is a valuable supplement for courses in biostatistics business public health and social research at the upper undergraduate and graduate levels It is also an excellent reference for applied statisticians working in industry academia and government

**Batch Effects and Noise in Microarray Experiments** Andreas Scherer,2009-11-03 Batch Effects and Noise in Microarray Experiments Sources and Solutions looks at the issue of technical noise and batch effects in microarray studies and illustrates how to alleviate such factors whilst interpreting the relevant biological information Each chapter focuses on sources of noise and batch effects before starting an experiment with examples of statistical methods for detecting measuring and managing batch effects within and across datasets provided online Throughout the book the importance of standardization and the value of standard operating procedures in the development of genomics biomarkers is emphasized Key Features A thorough introduction to Batch Effects and Noise in Microarray Experiments A unique compilation of review and research articles on handling of batch effects and technical and biological noise in microarray data An extensive overview of current standardization initiatives All datasets and methods used in the chapters as well as colour images are available on [www the batch effect book org](http://www.thebatcheffectbook.org) so that the data can be reproduced An exciting compilation of state of the art review chapters and latest research results which will benefit all those involved in the planning execution and analysis of gene expression studies

Uncertainty Analysis with High Dimensional Dependence Modelling Dorota Kurowicka,Roger M. Cooke,2006-03-31 This text provides both the mathematical foundations and practical applications in this rapidly expanding area including an up to date comprehensive overview of the foundations and applications of uncertainty analysis

all the key topics including uncertainty elicitation dependence modelling sensitivity analysis and probabilistic inversion numerous worked examples and applications workbook problems enabling use for teaching software support for the examples using UNICORN a Windows based uncertainty modelling package developed by the authors and a website featuring a version of the UNICORN software tailored specifically for the book as well as computer programs and data sets to support the examples      *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      *Quantitative Trait Linkage Analysis of S.Cerevisiae Gene Expression Data* Xinping Cui,2002

**Microarrays** Society of Photo-optical Instrumentation Engineers,2001      **Biostatistics** George G. Woodworth,2004-09-06 An essential introductory text linking traditional biostatistics with bayesian methods In recent years Bayesian methods have seen an explosion of interest with applications in fields including biochemistry ecology medicine oncology pharmacology and public health As an interpretive system integrating data with observation the Bayesian approach provides a nuanced yet mathematically rigorous means of conceptualizing biomedical statistics from diagnostic tests to DNA evidence Biostatistics A Bayesian Introduction offers a pioneering approach by presenting the foundations of biostatistics through the Bayesian lens Using easily understood classic Dutch Book thought experiments to derive subjective probability from a simple principle of rationality the book connects statistical science with scientific reasoning The author shows how to compute interpret and report Bayesian statistical analyses in practice and illustrates how to reinterpret traditional statistical reporting such as confidence intervals margins of error and one sided p values in Bayesian terms Topics covered include Probability and subjective probability Distributions and descriptive statistics Continuous probability distributions Comparing rates and means Linear models and statistical adjustment Logistic regression and adjusted odds ratios Survival analysis Hierarchical models and meta analysis Decision theory and sample size determination The book includes extensive problem sets and references in each chapter as well as complete instructions on computer analysis with the versatile SAS and WinBUGS software packages as well as the Excel spreadsheet program For professionals and students Biostatistics A Bayesian Introduction offers an unique real world entry point into a remarkable alternative method of interpreting statistical data      **Journal of the American Statistical Association** ,2006      *The EM Algorithm and Extensions* Geoffrey J. McLachlan,Thriyambakam Krishnan,2008-03-14 The only single source now completely updated and revised to offer a unified treatment of the theory methodology and applications of the EM algorithm Complete with updates that capture developments from the past decade The EM Algorithm and Extensions Second Edition successfully provides a basic understanding of the

EM algorithm by describing its inception implementation and applicability in numerous statistical contexts In conjunction with the fundamentals of the topic the authors discuss convergence issues and computation of standard errors and in addition unveil many parallels and connections between the EM algorithm and Markov chain Monte Carlo algorithms Thorough discussions on the complexities and drawbacks that arise from the basic EM algorithm such as slow convergence and lack of an in built procedure to compute the covariance matrix of parameter estimates are also presented While the general philosophy of the First Edition has been maintained this timely new edition has been updated revised and expanded to include New chapters on Monte Carlo versions of the EM algorithm and generalizations of the EM algorithm New results on convergence including convergence of the EM algorithm in constrained parameter spaces Expanded discussion of standard error computation methods such as methods for categorical data and methods based on numerical differentiation Coverage of the interval EM which locates all stationary points in a designated region of the parameter space Exploration of the EM algorithm s relationship with the Gibbs sampler and other Markov chain Monte Carlo methods Plentiful pedagogical elements chapter introductions lists of examples author and subject indices computer drawn graphics and a related Web site The EM Algorithm and Extensions Second Edition serves as an excellent text for graduate level statistics students and is also a comprehensive resource for theoreticians practitioners and researchers in the social and physical sciences who would like to extend their knowledge of the EM algorithm

**Biomedical Applications of Micro- and Nanoengineering** ,2006

**Mathematical and Computational Methods in Biology** Alejandro Maass, Salomé Martínez, Élisabeth Pécou, 2006

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