

# DNA Microarrays and Gene Expression

From Experiments to Data Analysis and Modeling

Pierre Baldi and G. Wesley Hamfield



# Dna Microarrays And Gene Expression From Experiments To Data Analysis And Modeling

**Simon M. Lin, Kimberly F. Johnson**



## **Dna Microarrays And Gene Expression From Experiments To Data Analysis And Modeling:**

**DNA Microarrays and Gene Expression** Pierre Baldi,G. Wesley Hatfield,2011-04-28 Massive data acquisition technologies such as genome sequencing high throughput drug screening and DNA arrays are in the process of revolutionizing biology and medicine This concise user friendly and interdisciplinary guide to DNA microarray technology is an introduction and a reference for both biologists and computational scientists The authors describe the underlying technologies and offer an awareness of the noise and pitfalls present in the data generated They also provide an idea of the different data mining techniques and algorithms that are available to interpret data and the advantages and disadvantages of each in differing situations *DNA Microarrays and Gene Expression* Pierre Baldi,G. Wesley Hatfield,2011-04-28 Massive data acquisition technologies such as genome sequencing high throughput drug screening and DNA arrays are in the process of revolutionizing biology and medicine Using the mRNA of a given cell at a given time under a given set of conditions DNA microarrays can provide a snapshot of the level of expression of all the genes in the cell Such snapshots can be used to study fundamental biological phenomena such as development or evolution to determine the function of new genes to infer the role individual genes or groups of genes may play in diseases and to monitor the effect of drugs and other compounds on gene expression Originally published in 2002 this inter disciplinary introduction to DNA arrays will be of value to anyone with an a interest in this powerful technology **DNA Microarrays and Gene Expression** Pierre Baldi,2002 **A Practical Approach to Microarray Data Analysis** Daniel P. Berrar,Werner Dubitzky,Martin Granzow,2007-05-08 In the past several years DNA microarray technology has attracted tremendous interest in both the scientific community and in industry With its ability to simultaneously measure the activity and interactions of thousands of genes this modern technology promises unprecedented new insights into mechanisms of living systems Currently the primary applications of microarrays include gene discovery disease diagnosis and prognosis drug discovery pharmacogenomics and toxicological research toxicogenomics Typical scientific tasks addressed by microarray experiments include the identification of coexpressed genes discovery of sample or gene groups with similar expression patterns identification of genes whose expression patterns are highly differentiating with respect to a set of discerned biological entities e g tumor types and the study of gene activity patterns under various stress conditions e g chemical treatment More recently the discovery modeling and simulation of regulatory gene networks and the mapping of expression data to metabolic pathways and chromosome locations have been added to the list of scientific tasks that are being tackled by microarray technology Each scientific task corresponds to one or more so called data analysis tasks Different types of scientific questions require different sets of data analytical techniques Broadly speaking there are two classes of elementary data analysis tasks predictive modeling and pattern detection Predictive modeling tasks are concerned with learning a classification or estimation function whereas pattern detection methods screen the available data for interesting previously unknown regularities or relationships Methods of Microarray

Data Analysis III Kimberly F. Johnson, Simon M. Lin, 2003-09-30 As microarray technology has matured data analysis methods have advanced as well *Methods Of Microarray Data Analysis III* is the third book in this pioneering series dedicated to the existing new field of microarrays While initial techniques focused on classification exercises volume I of this series and later on pattern extraction volume II of this series this volume focuses on data quality issues Problems such as background noise determination analysis of variance and errors in data handling are highlighted Three tutorial papers are presented to assist with a basic understanding of underlying principles in microarray data analysis and twelve new papers are highlighted analyzing the same CAMDA 02 datasets the Project Normal data set or the Affymetrix Latin Square data set A comparative study of these analytical methodologies brings to light problems solutions and new ideas This book is an excellent reference for academic and industrial researchers who want to keep abreast of the state of art of microarray data analysis     **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     *Methods of Microarray Data Analysis* Simon M. Lin, Kimberly F. Johnson, 2012-12-06 Microarray technology is a major experimental tool for functional genomic explorations and will continue to be a major tool throughout this decade and beyond The recent explosion of this technology threatens to overwhelm the scientific community with massive quantities of data Because microarray data analysis is an emerging field very few analytical models currently exist *Methods of Microarray Data Analysis* is one of the first books dedicated to this exciting new field In a single reference readers can learn about the most up to date methods ranging from data normalization feature selection and discriminative analysis to machine learning techniques Currently there are no standard procedures for the design and analysis of microarray experiments *Methods of Microarray Data Analysis* focuses on two well known data sets using a different method of analysis in each chapter Real examples expose the strengths and weaknesses of each method for a given situation aimed at helping readers choose appropriate protocols and utilize them for their own data set In addition web links are provided to the

programs and tools discussed in several chapters This book is an excellent reference not only for academic and industrial researchers but also for core bioinformatics genomics courses in undergraduate and graduate programs

**Methods of Microarray Data Analysis II** Simon M. Lin, Kimberly F. Johnson, 2002-06-30 Contains papers from the second CAMDA conference 2001

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

*International Journal of Bioinformatics Research and Applications* ,2005

**Encyclopedia of Biopharmaceutical Statistics - Four Volume Set** Shein-Chung Chow, 2018-09-03 Since the publication of the first edition in 2000 there has been an explosive growth of literature in biopharmaceutical research and development of new medicines This encyclopedia 1 provides a comprehensive and unified presentation of designs and analyses used at different stages of the drug development process 2 gives a well balanced summary of current regulatory requirements and 3 describes recently developed statistical methods in the pharmaceutical sciences Features of the Fourth Edition 1 78 new and revised entries have been added for a total of 308 chapters and a fourth volume has been added to encompass the increased number of chapters 2 Revised and updated entries reflect changes and recent developments in regulatory requirements for the drug review approval process and statistical designs and methodologies 3 Additional topics include multiple stage adaptive trial design in clinical research translational medicine design and analysis of biosimilar drug development big data analytics and real world evidence for clinical research and development 4 A table of contents organized by stages of biopharmaceutical development provides easy access to relevant topics About the Editor Shein Chung Chow Ph D is currently an Associate Director Office of Biostatistics U S Food and Drug Administration FDA Dr Chow is an Adjunct Professor at Duke University School of Medicine as well as Adjunct Professor at Duke NUS Singapore and North Carolina State University Dr Chow is the Editor in Chief of the Journal of Biopharmaceutical Statistics and the Chapman Hall CRC Biostatistics Book Series and the author of 28 books and over 300 methodology papers He was elected Fellow of the American Statistical Association in 1995

*Environmental Health Perspectives* ,1993

**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

**Modeling Dose-Response Microarray Data in Early Drug Development Experiments Using R** Dan Lin, Ziv Shkedy, Daniel Yekutieli, Dhammika Amaratunga, Luc Bijns, 2012-08-27 This book focuses on the analysis of dose response microarray data in pharmaceutical settings the goal

being to cover this important topic for early drug development experiments and to provide user friendly R packages that can be used to analyze this data It is intended for biostatisticians and bioinformaticians in the pharmaceutical industry biologists and biostatistics bioinformatics graduate students Part I of the book is an introduction in which we discuss the dose response setting and the problem of estimating normal means under order restrictions In particular we discuss the pooled adjacent violator PAV algorithm and isotonic regression as well as inference under order restrictions and non linear parametric models which are used in the second part of the book Part II is the core of the book in which we focus on the analysis of dose response microarray data Methodological topics discussed include Multiplicity adjustment Test statistics and procedures for the analysis of dose response microarray data Resampling based inference and use of the SAM method for small variance genes in the data Identification and classification of dose response curve shapes Clustering of order restricted but not necessarily monotone dose response profiles Gene set analysis to facilitate the interpretation of microarray results Hierarchical Bayesian models and Bayesian variable selection Non linear models for dose response microarray data Multiple contrast tests Multiple confidence intervals for selected parameters adjusted for the false coverage statement rate All methodological issues in the book are illustrated using real world examples of dose response microarray datasets from early drug development experiments

Pacific Symposium on Biocomputing ,2004      **Mixture Models for Microarray Data Analysis** Zhenyu Jia,2006      *DNA Microarrays and Related Genomics Techniques* David B. Allison,Grier P. Page,T. Mark Beasley,Jode W. Edwards,2005-11-14 Considered highly exotic tools as recently as the late 1990s microarrays are now ubiquitous in biological research Traditional statistical approaches to design and analysis were not developed to handle the high dimensional small sample problems posed by microarrays In just a few short years the number of statistical papers providing approaches

**Assessments of Plant and Microbial Interactions of Escherichia Coli O157:H7 and Salmonella on Romaine Lettuce and Development of Molecular Tools for Detection and Source Matching of Pathogenic and Commensal Escherichia Coli Applied to Regional Investigations Relevant to Sources of Lettuce Outbreaks** Wendy Anne Maduff,2008      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 **Methods of Microarray Data Analysis IV** Jennifer S.

Shoemaker, Simon M. Lin, 2006-01-16 As studies using microarray technology have evolved so have the data analysis methods used to analyze these experiments The CAMDA conference plays a role in this evolving field by providing a forum in which investors can analyze the same data sets using different methods Methods of Microarray Data Analysis IV is the fourth book in this series and focuses on the important issue of associating array data with a survival endpoint Previous books in this series focused on classification Volume I pattern recognition Volume II and quality control issues Volume III In this volume four lung cancer data sets are the focus of analysis We highlight three tutorial papers including one to assist with a basic understanding of lung cancer a review of survival analysis in the gene expression literature and a paper on replication In addition 14 papers presented at the conference are included This book is an excellent reference for academic and industrial researchers who want to keep abreast of the state of the art of microarray data analysis Jennifer Shoemaker is a faculty member in the Department of Biostatistics and Bioinformatics and the Director of the Bioinformatics Unit for the Cancer and Leukemia Group B Statistical Center Duke University Medical Center Simon Lin is a faculty member in the Department of Biostatistics and Bioinformatics and the Manager of the Duke Bioinformatics Shared Resource Duke University Medical Center

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