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Statistics and Data Analysis for Microarrays Using R and Bioconductor, Second EditionMicroarray DataStatistics and Data Analysis for Microarrays Using R and BioconductorUnderstanding Lipid Metabolism with Microarrays and Other Omic ApproachesStatistics for MicroarraysDNA Methylation MicroarraysMicroarray Image and Data AnalysisBayesian Modeling in BioinformaticsBiosensors and Molecular Technologies for Cancer DiagnosticsA Gene-microarray based Approach to the Detection of Recombinant Human Erythropoietin Doping in AthletesDNA MicroarraysMultiple Testing in MicroarraysMicroarraysDNA MicroarraysTissue MicroarraysArray-based Comparative Genomic Hybridization in Phylogenetics and Its Application for Discovery of Rapidly Evolving GenesMultivariate Empirical Bayes Models for Replicated Microarray Time Course DataMicroarrays and Combinatorial Technologies for Biomedical ApplicationsStatistical Issues in Detection of Biological Signals in the Analysis of Microarray Gene Expression DataDNA Microarrays, Part B: Databases and Statistics Sorin Drăghici Shailaja R. Deshmukh Sorin Drăghici Alvin Berger Ernst Wit Sun-Chong Wang Luis Rueda Dipak K. Dey Keith E. Herold Tushar Chatterji David Bowtell Yongchao Ge Society of Photo-optical Instrumentation Engineers Mark Schena Ronald Simon Luz Beatriz Gilbert Yu Chuan Tai Dan V. Nicolau Ruixiao Lu

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A Gene-microarray based Approach to the Detection of Recombinant Human Erythropoietin Doping in Athletes DNA Microarrays Multiple Testing in Microarrays Microarrays DNA Microarrays Tissue Microarrays Array-based Comparative Genomic Hybridization in Phylogenetics and Its Application for Discovery of Rapidly Evolving Genes Multivariate Empirical Bayes Models for Replicated Microarray Time Course Data Microarrays and Combinatorial Technologies for Biomedical Applications Statistical Issues in Detection of Biological Signals in the Analysis of Microarray Gene Expression Data DNA Microarrays, Part B: Databases and Statistics Sorin Drăghici Shailaja R. Deshmukh Sorin Drăghici Alvin Berger Ernst Wit Sun-Chong Wang Luis Rueda Dipak K. Dey Keith E. Herold Tushar Chatterji David Bowtell Yongchao Ge Society of Photo-optical Instrumentation Engineers Mark Schena Ronald Simon Luz Beatriz Gilbert Yu Chuan Tai Dan V. Nicolau Ruixiao Lu

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 cd rom 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

functional genomics a branch of bioinformatics is essentially an interdisciplinary subject in which biologists statisticians and computer experts

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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

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 editioncompletely 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

reviewing current studies and previously unpublished research from leading laboratories around the world unravelling lipid metabolism with microarrays demonstrates the use of microarrays and transcriptomic approaches to clarify the biological function of lipids it provides an extensive overview of statistical approaches to microarray data as well as discussions on how microarrays can be used to understand the role of lipids in the

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initiation or prevention of disorders such as cancer diabetes and obesity of particular note is a chapter by the only group known to study the effect of lipids on transcriptomics in multiple brain regions

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 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

providing an interface between dry bench bioinformaticians and wet lab biologists dna methylation microarrays experimental design and statistical analysis presents the statistical methods and tools to analyze high throughput epigenomic data in particular dna methylation microarray data since these microarrays share the same under

microarray image and data analysis theory and practice is a compilation of the latest and greatest microarray image and data analysis methods from the multidisciplinary international research community delivering a detailed discussion of the biological aspects and applications of microarrays the book describes the key stages of image processing gridding segmentation compression quantification and normalization features cutting edge approaches to clustering biclustering and the reconstruction of regulatory networks covers different types of microarrays such as dna

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protein tissue and low and high density oligonucleotide arrays examines the current state of various microarray technologies including their availability and affordability explains how data generated by microarray experiments are analyzed to obtain meaningful biological conclusions an essential reference for academia and industry microarray image and data analysis theory and practice provides readers with valuable tools and techniques that extend to a wide range of biological studies and microarray platforms

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

bridging the gap between research and clinical application biosensors and molecular technologies for cancer diagnostics explores the use of biosensors as effective alternatives to the current standard methods in cancer diagnosis and detection it describes the major aspects involved in detecting and diagnosing cancer as well as the basic elements

recombinant human erythropoietin r huepo increases haemoglobin and haematocrit levels thereby potentially enhancing aerobic performance this has led to the alleged widespread abuse of r huepo in competition by athletes direct and indirect approaches to r huepo detection endorsed by wada have led to cases of false negatives and false positives requiring an urgent need for these methods to be revised and improved a gene microarray based approach might provide more specific sensitive and robust anti doping testing models to the detection of r huepo doping the objective of this pilot study involving three subjects was to adopt a gene microarray based approach to analyse changes in gene expression associated with r huepo administration subjects were administered r huepo every two days for four weeks microarray data was analysed using both illumina and partek analysis packages the results were combined and a consistent signature pattern of significant differentially expressed genes including alas2 fech tsta3 ca1 tfdp1 and creg1 were identified furthermore using pathway analysis these genes were shown to participate in erythropoiesis and heme

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biosynthesis confirming the functional role of r huepo treatment in all subjects these initial findings while encouraging for developing anti doping tests remain to be replicated

dna microarray technology is a new and powerful means to analyze genomes and characterize patterns of gene expression its applications are widespread across the many fields of plant and animal biological and biomedical research this manual designed to extend and to complement the information in the best selling molecular cloning is a synthesis of the expertise and experience of more than 30 contributors all innovators in a fast moving field dna microarraysprovides authoritative detailed instruction on the design construction and applications of microarrays as well as comprehensive descriptions of the software tools and strategies required for analysis of images and data

covers the very latest in dna microarray technology with a clear focus on how these techniques can be used in the lab to gain the very best results the authors are from some of the leading laboratories in the field and write with real authority on the latest methodology and its applications every chapter provides detailed step by step protocols with valuable hints and tips for success as well as giving typical experimental results and selected literature citations a manual for researchers in all fields of biology medicine and agriculture

today s tissue microarray tma method presents as a modern high tech technology one which allows for the linking of clinical data to the tissues that are combined on one slide in tissue microarrays methods and protocols expert researchers explore the current world of tma making and tma applications providing insight into the inherent and complex aspects of the most popular assays used for in situ tissue analysis chapters examine the range of tma techniques that allow for a large number of tissues to be included in one tma preserve the integrity of donor tissue blocks and present a highly organized array pattern that allows for the reliable allocation of clinical data to individual tissue spots composed in the highly successful methods in molecular biologytm series format each chapter contains a brief introduction step by step methods a list of necessary materials and a notes section which shares tips on troubleshooting and avoiding known pitfalls contemporary and ground breaking tissue microarrays methods and

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protocols serves as an essential handbook for pathologists molecular biologists researchers in the life sciences as well as physicians a reflection of the various applications of current tma technology

modern dna microarray technologies have evolved over the past 25 years to the point where it is now possible to take many million measurements from a single experiment these two volumes parts a b in the methods in enzymology series provide methods that will shepard any molecular biologist through the process of planning performing and publishing microarray results part a starts with an overview of a number of microarray platforms both commercial and academically produced and includes wet bench protocols for performing traditional expression analysis and derivative techniques such as detection of transcription factor occupancy and chromatin status wet bench protocols and troubleshooting techniques continue into part b these techniques are well rooted in traditional molecular biology and while they require traditional care a researcher that can reproducibly generate beautiful northern or southern blots should have no difficulty generating beautiful array hybridizations data management is a more recent problem for most biologists the bulk of part b provides a range of techniques for data handling this includes critical issues from normalization within and between arrays to uploading your results to the public repositories for array data and how to integrate data from multiple sources there are chapters in part b for both the debutant and the expert bioinformatician provides an overview of platforms includes experimental design and wet bench protocols presents statistical and data analysis methods array databases data visualization and meta analysis

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