Bayesian Analysis
of Gene Expression
Data

Bani Mallick
David Lee Gold and
Veera Baladandayuthapani

WILEY

Bayesian Analysis Of Gene Expression Data

Lauren Gardner

Bayesian Analysis Of Gene Expression Data:

   Bayesian Analysis of Gene Expression Data Bani K. Mallick,David Gold,Veera Baladandayuthapani,2009-08-24 The field of high throughput genetic experimentation is evolving rapidly with the advent of new technologies and new venues for data mining Bayesian methods play a role central to the future of data and knowledge integration in the field of Bioinformatics This book is devoted exclusively to Bayesian methods of analysis for applications to high throughput gene expression data exploring the relevant methods that are changing Bioinformatics Case studies illustrating Bayesian analyses of public gene expression data provide the backdrop for students to develop analytical skills while the more experienced readers will find the review of advanced methods challenging and attainable This book Introduces the fundamentals in Bayesian methods of analysis for applications to high throughput gene expression data Provides an extensive review of Bayesian analysis and advanced topics for Bioinformatics including examples that extensively detail the necessary applications Accompanied by website featuring datasets exercises and solutions Bayesian Analysis of Gene Expression Data offers a unique introduction to both Bayesian analysis and gene expression aimed at graduate students in Statistics Biomedical Engineers Computer Scientists Biostatisticians Statistical Geneticists Computational Biologists applied Mathematicians and Medical consultants working in genomics Bioinformatics researchers from many fields will find much value in this book   Bayesian Inference for Gene Expression and Proteomics Kim-Anh Do,Peter Müller,Marina Vannucci,2006-07-24 Expert overviews of Bayesian methodology tools and software for multi platform high throughput experimentation   **Literature Based Bayesian Analysis of Gene Expression Data** Lijing Xu,2010   **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   Bayesian Inference for Differential Gene Expression Data Dabao Zhang,2003   **Robust Bayesian Analysis of Gene Expression Microarray Data** Raphael Gottardo,2005   **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   *Bayesian Thinking, Modeling and Computation* ,2005-11-29 This volume describes how to develop Bayesian thinking modelling and computation both from philosophical methodological and application point of view It further describes parametric and nonparametric Bayesian methods for modelling and how to use modern computational methods to summarize inferences using simulation The book covers wide range of topics including objective and subjective Bayesian inferences with a variety of applications in modelling categorical survival spatial spatiotemporal

Epidemiological software reliability small area and micro array data The book concludes with a chapter on how to teach Bayesian thoughts to nonstatisticians Critical thinking on causal effects Objective Bayesian philosophy Nonparametric Bayesian methodology Simulation based computing techniques Bioinformatics and Biostatistics **Bayesian Methods for High-throughput Gene Expression Data in Bioinformatics** Fang Yu,2007 **Analysis of Gene Expression Data Using Hierarchical Bayesian and Gene Set Enrichment Procedures** Haibo Wan,2007 *On Bayesian Modeling and Design for Microarray Gene Expression Data* Yuan Ji,2003 **Bayesian Statistics 9** José M. Bernardo,M. J. Bayarri,James O. Berger,A. P. Dawid,David Heckerman,Adrian F. M. Smith,Mike West,2011-10-06 The Valencia International Meetings on Bayesian Statistics established in 1979 and held every four years have been the forum for a definitive overview of current concerns and activities in Bayesian statistics These are the edited Proceedings of the Ninth meeting and contain the invited papers each followed by their discussion and a rejoinder by the authors s In the tradition of the earlier editions this encompasses an enormous range of theoretical and applied research high lighting the breadth vitality and impact of Bayesian thinking in interdisciplinary research across many fields as well as the corresponding growth and vitality of core theory and methodology The Valencia 9 invited papers cover a broad range of topics including foundational and core theoretical issues in statistics the continued development of new and refined computational methods for complex Bayesian modelling substantive applications of flexible Bayesian modelling and new developments in the theory and methodology of graphical modelling They also describe advances in methodology for specific applied fields including financial econometrics and portfolio decision making public policy applications for drug surveillance studies in the physical and environmental sciences astronomy and astrophysics climate change studies molecular biosciences statistical genetics or stochastic dynamic networks in systems biology **Genomics Data Analysis** David R. Bickel,2019-09-24 Statisticians have met the need to test hundreds or thousands of genomics hypotheses simultaneously with novel empirical Bayes methods that combine advantages of traditional Bayesian and frequentist statistics Techniques for estimating the local false discovery rate assign probabilities of differential gene expression genetic association etc without requiring subjective prior distributions This book brings these methods to scientists while keeping the mathematics at an elementary level Readers will learn the fundamental concepts behind local false discovery rates preparing them to analyze their own genomics data and to critically evaluate published genomics research Key Features dice games and exercises including one using interactive software for teaching the concepts in the classroom examples focusing on gene expression and on genetic association data and briefly covering metabolomics data and proteomics data gradual introduction to the mathematical equations needed how to choose between different methods of multiple hypothesis testing how to convert the output of genomics hypothesis testing software to estimates of local false discovery rates guidance through the minefield of current criticisms of p values material on non Bayesian prior p values and posterior p values not previously published **Statistical Methods for Analysis of Microarray Time Course**

Gene Expression Data Fangxin Hong,2004 **Bayesian Inference on Complicated Data** Niansheng Tang,2020-07-15 Due to great applications in various fields such as social science biomedicine genomics and signal processing and the improvement of computing ability Bayesian inference has made substantial developments for analyzing complicated data This book introduces key ideas of Bayesian sampling methods Bayesian estimation and selection of the prior It is structured around topics on the impact of the choice of the prior on Bayesian statistics some advances on Bayesian sampling methods and Bayesian inference for complicated data including breast cancer data cloud based healthcare data gene network data and longitudinal data This volume is designed for statisticians engineers doctors and machine learning researchers

Brenner's Encyclopedia of Genetics Stanley Maloy,Kelly Hughes,2013-03-03 The explosion of the field of genetics over the last decade with the new technologies that have stimulated research suggests that a new sort of reference work is needed to keep pace with such a fast moving and interdisciplinary field Brenner s Encyclopedia of Genetics Second Edition Seven Volume Set builds on the foundation of the first edition by addressing many of the key subfields of genetics that were just in their infancy when the first edition was published The currency and accessibility of this foundational content will be unrivalled making this work useful for scientists and non scientists alike Featuring relatively short entries on genetics topics written by experts in that topic Brenner s Encyclopedia of Genetics Second Edition Seven Volume Set provides an effective way to quickly learn about any aspect of genetics from Abortive Transduction to Zygotes Adding to its utility the work provides short entries that briefly define key terms and a guide to additional reading and relevant websites for further study Many of the entries include figures to explain difficult concepts Key terms in related areas such as biochemistry cell and molecular biology are also included and there are entries that describe historical figures in genetics providing insights into their careers and discoveries This 7 volume set represents a 25% expansion from the first edition with over 1600 articles encompassing this burgeoning field Thoroughly up to date with many new topics and subfields covered that were in their infancy or not inexistence at the time of the first edition Timely coverage of emergent areas such as epigenetics personalized genomic medicine pharmacogenetics and genetic enhancement technologies Interdisciplinary and global in its outlook as befits the field of genetics Brief articles written by experts in the field which not only discuss define and explain key elements of the field but also provide definition of key terms suggestions for further reading and biographical sketches of the key people in the history of genetics **Journal of the American Statistical Association** ,2008 *Bayesian Pathway Analysis in Epigenetics* Alan Wright,2013 A typical gene expression data set consists of measurements of a large number of gene expressions on a relatively small number of subjects classified according to two or more outcomes for example cancer or non cancer The identification of associations between gene expressions and outcome is a huge multiple testing problem Early approaches to this problem involved the application of thousands of univariate tests with corrections for multiplicity Over the past decade numerous studies have demonstrated that analyzing gene expression data structured into predefined

gene sets can produce benefits in terms of statistical power and robustness when compared to alternative approaches This thesis presents the results of research on gene set analysis In particular it examines the properties of some existing methods for the analysis of gene sets It introduces novel Bayesian methods for gene set analysis A distinguishing feature of these methods is that the model is specified conditionally on the expression data whereas other methods of gene set analysis and IGA generally make inferences conditionally on the outcome Computer simulation is used to compare three common established methods for gene set analysis In this simulation study a new procedure for the simulation of gene expression data is introduced The simulation studies are used to identify situations in which the established methods perform poorly The Bayesian approaches developed in this thesis apply reversible jump Markov chain Monte Carlo RJMCMC techniques to model gene expression effects on phenotype The reversible jump step in the modelling procedure allows for posterior probabilities for activeness of gene set to be produced These mixture models reverse the generally accepted conditionality and model outcome given gene expression which is a more intuitive assumption when modelling the pathway to phenotype It is demonstrated that the two models proposed may be superior to the established methods studied There is considerable scope for further development of this line of research which is appealing in terms of the use of mixture model priors that reflect the belief that a relatively small number of genes restricted to a small number of gene sets are associated with the outcome

On Some Bayesian and Empirical Bayes Procedures for Analyzing Gene Expression Data Demba Fofana,2016 In this dissertation we propose hybrid testing procedures as a general class of methods that simultaneously addresses the problems of procedure selection and multiple testing At each hierarchical level the results from each testing are summarized as a set of p values and empirical Bayesian probabilities EBPs of the corresponding null hypotheses Prior knowledge of the properties of the primary test statistics is used to construct an algorithm which uses the distributional assumption of the tests to determine weights for combining the EBPs The combined EBPs can be used as a measure of statistical significance that adjusts for multiple testing while accounting for the several assumptions used in the hierarchy of hypothesis testing procedures In the second part of this dissertation we apply the development of the first part for constructing a hybrid testing procedure that incorporates assumptions and information about graphical network relations into the analysis of gene expression data based on the biological knowledge that neighboring genes share biological functions The degree of correlation between genes is taken into account via similar prior probabilities for neighboring genes We show that combining these different elements not only improve statistical power but also provide a better framework through which gene expression can be properly analyzed We use a series of simulations to compare our approach with other published methods and demonstrate that our method has more statistical power   The Analysis of Gene Expression Data Giovanni Parmigiani,Elizabeth S. Garett,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

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