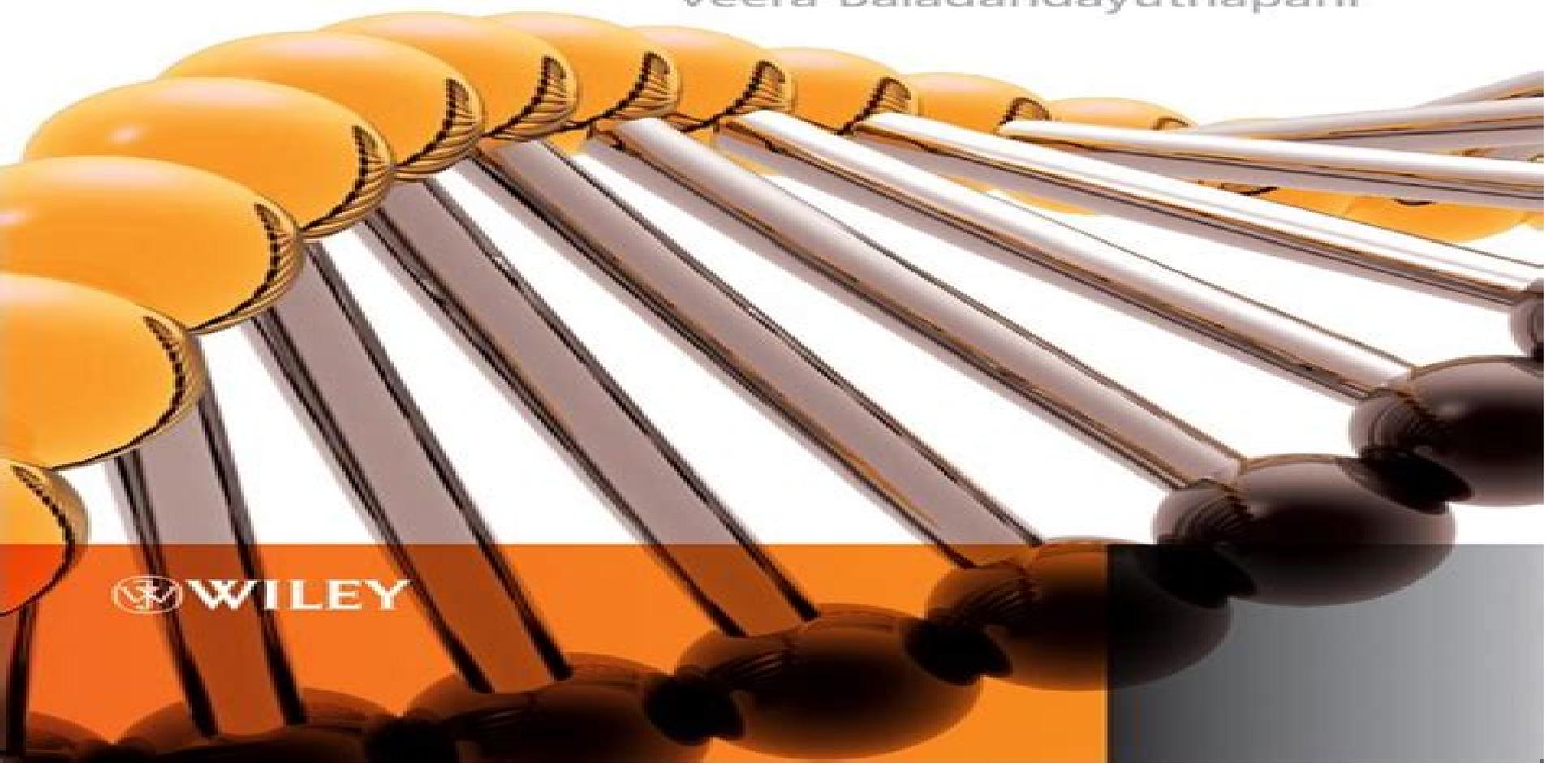


Bayesian Analysis of Gene Expression Data

Bani Mallick
David Lee Gold and
Veera Baladandayuthapani



 WILEY

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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

Literature Based Bayesian Analysis of Gene Expression Data Lijing Xu, 2010

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 *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

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Robust Bayesian Analysis of Gene Expression Microarray Data Raphael Gottardo, 2005 *Bayesian Methods for High-throughput Gene Expression Data in Bioinformatics* Fang Yu, 2007

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
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Expression Data Using Hierarchical Bayesian and Gene Set Enrichment Procedures** Haibo Wan,2007 **On
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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
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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
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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 *Handbook of Statistical Genomics* David J. Balding,Ida Moltke,John
Marioni,2019-09-10 A timely update of a highly popular handbook on statistical genomics This new two volume edition of a
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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 *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

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Bayesian Analysis with Stata John

Thompson,2014-05-06 Bayesian Analysis with Stata is a compendium of Stata user written commands for Bayesian analysis

Bayesian Methods for Gene Expression Analysis from High-throughput Sequencing Data Peter Glaus,2014

Encyclopedia of Data Warehousing and Mining John Wang,2006 Provides a comprehensive critical and descriptive examination of concepts issues trends and challenges in this rapidly expanding field of data warehousing and mining DWM consists of more than 350 contributors from 32 countries Publisher **Journal of the American Statistical Association** ,2008

Bayesian and Meta- Analyses of Cell-Cycle Gene Expression Data Mehmet Kocak,2011 Gene expression experiments conducted under a variety of conditions can allow for concurrent tests of more than one hypothesis It is common for such experiments to be conducted independently by different researchers using possibly different microarray platforms In the second and fourth chapter of this thesis we propose a differential meta analytic procedure to pool the data from various sources and test the relative significance of the hypotheses under consideration The specific application made in this thesis is to 10 time course cell cycle experiments on fission yeast *S Pombe* Oliva et al 2005 Peng et al 2005 Rustici et al 2004 and the hypotheses of interest concern the question of differential expression and periodic regulation of genes Besides addressing the above differential meta analysis issue we explore how time course gene expression data can be used to test for periodicity In this context the commonly used procedures for testing include the Permutation test by de Lichtenberg et al 2005 and the G test by Fisher 1929 both of which are designed to evaluate periodicity against noise however it is possible that a given gene may have expression that is neither cyclic nor just noise In the third chapter we introduce an Empirical

Bayes approach to test for periodicity and compare its performance in terms of sensitivity and specificity with that of the other two methods through simulations and by application to the S Pombe cell cycle gene expression data We use conserved and cycling genes by Lu et al 2007 to assess the sensitivity and CESR genes by Chen et al 2003 to assess the specificity of our method Kocak M Zhang G Narasimhan G George E O Pyne S 2010 use George and Mudholkar 1983 Difference of Two Logit Sums method to pool bivariate P values across independent experiments assuming independence within a pair We propose a Bayesian approach for pooling bivariate P values across independent experiments which accounts for potential correlation between paired P values We will investigate the operating characteristics of the Bayesian method through simulations and apply it to the S Pombe cell cycle data

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