

Bayesian Analysis of Gene Expression Data

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John Thompson



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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

Bayesian Inference for Differential Gene Expression Data Dabao Zhang, 2003

Robust Bayesian Analysis of Gene Expression Microarray Data Raphael Gottardo, 2005

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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

Bayesian Statistics 7 J. M. Bernardo, 2003-07-03 This volume contains the proceedings of the 7th Valencia International Meeting on Bayesian Statistics This conference is held every four years and provides the main forum for researchers in the area of Bayesian statistics to come together to present and discuss frontier developments in the field

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

Handbook of Statistical Genetics David J. Balding, Martin Bishop, Chris Cannings, 2008-06-10 The Handbook for Statistical Genetics is widely regarded as the reference work in the field However the field has developed considerably over the past three years In particular the modeling of genetic networks has advanced considerably via the evolution of microarray analysis As a consequence the 3rd edition of the handbook contains a much expanded section on Network Modeling including 5 new chapters covering metabolic networks graphical modeling and inference and simulation of pedigrees and genealogies Other chapters new to the 3rd edition include Human Population Genetics Genome wide Association Studies Family based Association Studies Pharmacogenetics Epigenetics Ethic and Insurance As with the second Edition the Handbook includes a glossary of terms acronyms and abbreviations and features extensive cross referencing between the chapters tying the different areas together With heavy use of up to date examples real life case studies and references to web based resources this continues to be must have reference in a vital area of research Edited by the leading international authorities in the field David Balding Department of Epidemiology Public Health Imperial College An advisor for our Probability Statistics series Professor Balding is also a previous Wiley author having

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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

Bayesian Statistics 8
J.M. Bernardo, 2007-07-19 The Valencia International Meetings on Bayesian Statistics provide the main forum for researchers in Bayesian Statistics This eighth proceedings offers the reader a wide perspective of the developments in Bayesian statistics over the last four years

[Bayesian Analysis with Stata](#) John Thompson, 2014-05-06 Bayesian Analysis with Stata is a compendium of Stata user written commands for Bayesian analysis

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John Wang, 2008

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