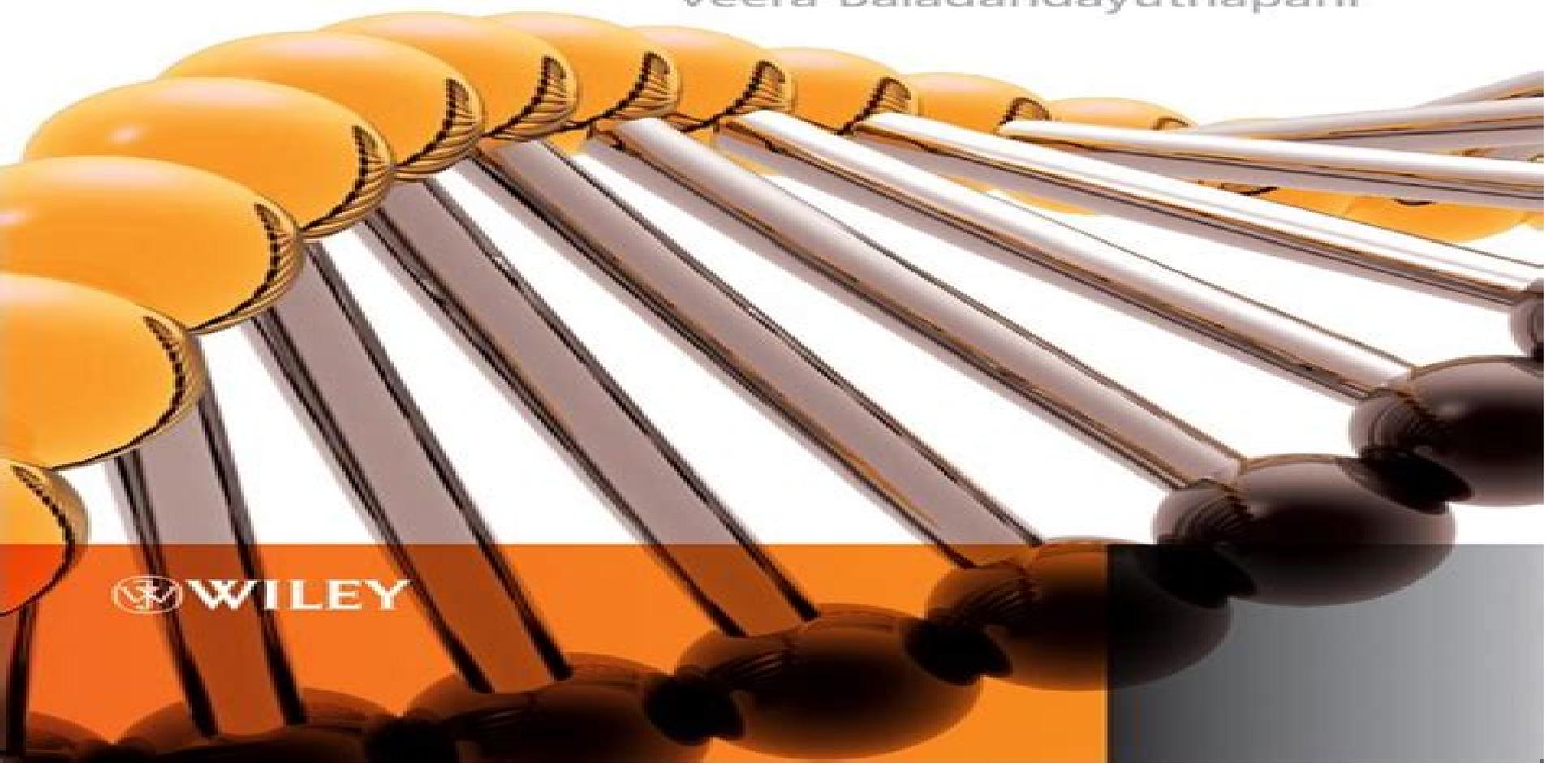


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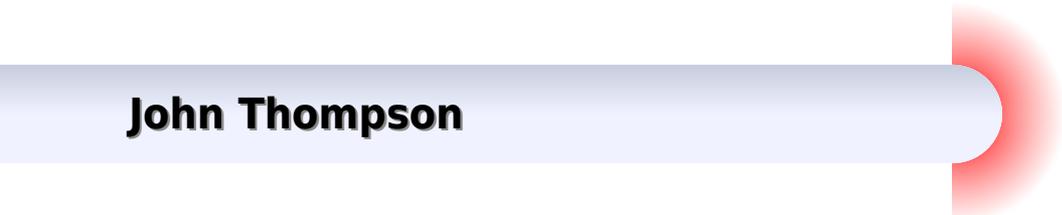
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Analysis of Gene Expression Data Using Hierarchical Bayesian and Gene Set Enrichment Procedures Haibo Wan,2007 Bayesian Statistics 9 José M. Bernardo, M. J. Bayarri, James O. Berger, A. P. Dawid, David Heckerman, Adrian F. M. Smith, Mike West, 2011-10-06 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

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 in existence 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

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