

Sandrine Dudoit · Mark J. van der Laan

Multiple Testing Procedures with Applications to Genomics

Multiple Testing Procedures With Applications To Genomics Springer Series In Statistics

**Xinping Cui, Thorsten Dickhaus, Ying
Ding, Jason C. Hsu**



Multiple Testing Procedures With Applications To Genomics Springer Series In Statistics:

Multiple Testing Procedures with Applications to Genomics Sandrine Dudoit, Mark J. van der Laan, 2007-12-18 This book establishes the theoretical foundations of a general methodology for multiple hypothesis testing and discusses its software implementation in R and SAS These are applied to a range of problems in biomedical and genomic research including identification of differentially expressed and co expressed genes in high throughput gene expression experiments tests of association between gene expression measures and biological annotation metadata sequence analysis and genetic mapping of complex traits using single nucleotide polymorphisms The procedures are based on a test statistics joint null distribution and provide Type I error control in testing problems involving general data generating distributions null hypotheses and test statistics

Handbook of Multiple Comparisons Xinping Cui, Thorsten Dickhaus, Ying Ding, Jason C. Hsu, 2021-11-17 Written by experts that include originators of some key ideas chapters in the Handbook of Multiple Testing cover multiple comparison problems big and small with guidance toward error rate control and insights on how principles developed earlier can be applied to current and emerging problems Some highlights of the coverages are as follows Error rate control is useful for controlling the incorrect decision rate Chapter 1 introduces Tukey's original multiple comparison error rates and point to how they have been applied and adapted to modern multiple comparison problems as discussed in the later chapters Principles endure While the closed testing principle is more familiar Chapter 4 shows the partitioning principle can derive confidence sets for multiple tests which may become important as the profession goes beyond making decisions based on p values Multiple comparisons of treatment efficacy often involve multiple doses and endpoints Chapter 12 on multiple endpoints explains how different choices of endpoint types lead to different multiplicity adjustment strategies while Chapter 11 on the MCP Mod approach is particularly useful for dose finding To assess efficacy in clinical trials with multiple doses and multiple endpoints the reader can see the traditional approach in Chapter 2 the Graphical approach in Chapter 5 and the multivariate approach in Chapter 3 Personalized precision medicine based on targeted therapies already a reality naturally leads to analysis of efficacy in subgroups Chapter 13 draws attention to subtle logical issues in inferences on subgroups and their mixtures with a principled solution that resolves these issues This chapter has implication toward meeting the ICH E9 R1 Estimands requirement Besides the mere multiple testing methodology itself the handbook also covers related topics like the statistical task of model selection in Chapter 7 or the estimation of the proportion of true null hypotheses or in other words the signal prevalence in Chapter 8 It also contains decision theoretic considerations regarding the admissibility of multiple tests in Chapter 6 The issue of selected inference is addressed in Chapter 9 Comparison of responses can involve millions of voxels in medical imaging or SNPs in genome wide association studies GWAS Chapter 14 and Chapter 15 provide state of the art methods for large scale simultaneous inference in these settings

Simultaneous Statistical Inference Thorsten Dickhaus, 2014-01-23 This monograph will provide an in depth mathematical treatment of modern multiple test procedures

controlling the false discovery rate FDR and related error measures particularly addressing applications to fields such as genetics proteomics neuroscience and general biology The book will also include a detailed description how to implement these methods in practice Moreover new developments focusing on non standard assumptions are also included especially multiple tests for discrete data The book primarily addresses researchers and practitioners but will also be beneficial for graduate students

Bioinformatics and Human Genomics Research Diego A. Forero,2021-12-22 Advances in high throughput biological methods have led to the publication of a large number of genome wide studies in human and animal models In this context recent tools from bioinformatics and computational biology have been fundamental for the analysis of these genomic studies The book Bioinformatics and Human Genomics Research provides updated and comprehensive information about multiple approaches of the application of bioinformatic tools to research in human genomics It covers strategies analysis of genome wide association studies genome wide expression studies and genome wide DNA methylation among other topics It provides interesting strategies for data mining in human genomics network analysis prediction of binding sites for miRNAs and transcription factors among other themes Experts from all around the world in bioinformatics and human genomics have contributed chapters in this book Readers will find this book as quite useful for their in silico explorations which would contribute to a better and deeper understanding of multiple biological processes and of pathophysiology of many human diseases

Computational Methods for Time-Series Analyses in Earth Sciences Silvio José Gumiere,Hossein Bonakdari,2025-06-27 Computational Methods for Time Series Analyses in Earth Sciences bridges the gap between theoretical knowledge and practical application offering a deep dive into the utilization of R programming for managing analyzing and forecasting time series data within the realm of Earth sciences It systematically unfolds the layers of data manipulation graphical representation and sampling to prepare the reader for complex analyses and predictive modeling from the basics of signal processing to the nuances of machine learning It presents cutting edge techniques such as neural networks kernel based methods and evolutionary algorithms specifically tailored to tackle challenges and provides practical case studies to aid readers with utilizing the techniques covered Computational Methods for Time Series Analyses in Earth Sciences is a valuable resource for scientists researchers and students delving into the intricacies of Earth s environmental patterns and cycles through the lens of computational analysis and guides readers through various computational approaches to deciphering spatial and temporal data Focuses on the use of R for time series analysis and the application of these methods directly to Earth and environmental datasets Integrates Machine Learning techniques enabling readers to explore advanced computational methods for forecasting and modeling Includes case studies with real world applications providing readers with examples on how to translate computational skills into tangible outcomes

Multiple Testing Procedures with Applications to Genomics Sandrine Dudoit,Mark J. van der Laan,2008-11-01 This book establishes the theoretical foundations of a general methodology for multiple hypothesis testing and discusses its

software implementation in R and SAS These are applied to a range of problems in biomedical and genomic research including identification of differentially expressed and co expressed genes in high throughput gene expression experiments tests of association between gene expression measures and biological annotation metadata sequence analysis and genetic mapping of complex traits using single nucleotide polymorphisms The procedures are based on a test statistics joint null distribution and provide Type I error control in testing problems involving general data generating distributions null hypotheses and test statistics

Computational Epigenetics and Diseases, 2019-02-06 Computational Epigenetics and Diseases written by leading scientists in this evolving field provides a comprehensive and cutting edge knowledge of computational epigenetics in human diseases In particular the major computational tools databases and strategies for computational epigenetics analysis for example DNA methylation histone modifications microRNA noncoding RNA and ceRNA are summarized in the context of human diseases This book discusses bioinformatics methods for epigenetic analysis specifically applied to human conditions such as aging atherosclerosis diabetes mellitus schizophrenia bipolar disorder Alzheimer disease Parkinson disease liver and autoimmune disorders and reproductive and respiratory diseases Additionally different organ cancers such as breast lung and colon are discussed This book is a valuable source for graduate students and researchers in genetics and bioinformatics and several biomedical field members interested in applying computational epigenetics in their research Provides a comprehensive and cutting edge knowledge of computational epigenetics in human diseases Summarizes the major computational tools databases and strategies for computational epigenetics analysis such as DNA methylation histone modifications microRNA noncoding RNA and ceRNA Covers the major milestones and future directions of computational epigenetics in various kinds of human diseases such as aging atherosclerosis diabetes heart disease neurological disorders cancers blood disorders liver diseases reproductive diseases respiratory diseases autoimmune diseases human imprinting disorders and infectious diseases

Permutation Tests for Complex Data Luigi Salmaso, Fortunato Pesarin, 2025-09-09 Timely update of a popular edition on permutation testing with numerous case studies included throughout The newly revised and updated Second Edition of Permutation Tests for Complex Data describes permutation tests from the point of view of experimental design with methodological details and illustrating the process of devising an appropriate permutation test through case studies In addition to the text this book includes two open source packages for permutation tests in Python and R which include a comprehensive code base to implement common permutation tests as well as code to implement each of the book s case studies The focus of this book is the permutation approach to a variety of univariate and multivariate problems of hypothesis testing in a typical nonparametric framework The book examines the most up to date methodologies of univariate and multivariate permutation testing includes real case studies from both experimental and observational studies and presents and discusses solutions to the most important and frequently encountered real problems in multivariate analyses Written by two highly qualified authors in the field of nonparametrics and

applied statistics Permutation Tests for Complex Data includes information on sample topics including Theory of one dimensional and multi dimensional permutation tests covering test statistics arguments for selecting permutation tests and examples of one sample and multi sample problems Multiplicity control and closed testing covering raw and adjusted p values the MinP Bonferroni Holm procedure and weighted methods for controlling FWE and FDR Multivariate categorical variables covering stochastic ordering tests on moments for ordered variables and heterogeneity comparisons NPC tests for survival analysis and shape analysis covering analysis of PERC data and analysis with correlated landmarks Presenting a thorough overview of permutation testing with both formal description and proofs Permutation Tests for Complex Data is an excellent introduction to permutation tests for graduate level statistics or data science courses and will be ideal as a handbook for researchers hoping to use the open source code

Computational Network Analysis with R Matthias Dehmer, Yongtang Shi, Frank Emmert-Streib, 2016-08-09 This new title in the well established Quantitative Network Biology series includes innovative and existing methods for analyzing network data in such areas as network biology and chemoinformatics With its easy to follow introduction to the theoretical background and application oriented chapters the book demonstrates that R is a powerful language for statistically analyzing networks and for solving such large scale phenomena as network sampling and bootstrapping Written by editors and authors with an excellent track record in the field this is the ultimate reference for R in Network Analysis

Encyclopedia of Bioinformatics and Computational Biology, 2018-08-21 Encyclopedia of Bioinformatics and Computational Biology ABC of Bioinformatics Three Volume Set combines elements of computer science information technology mathematics statistics and biotechnology providing the methodology and in silico solutions to mine biological data and processes The book covers Theory Topics and Applications with a special focus on Integrative omics and Systems Biology The theoretical methodological underpinnings of BCB including phylogeny are covered as are more current areas of focus such as translational bioinformatics cheminformatics and environmental informatics Finally Applications provide guidance for commonly asked questions This major reference work spans basic and cutting edge methodologies authored by leaders in the field providing an invaluable resource for students scientists professionals in research institutes and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries Brings together information from computer science information technology mathematics statistics and biotechnology Written and reviewed by leading experts in the field providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images multimedia tools and crosslinking to further resources and databases

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