

Statistics for Biology and Health

**David Siegmund
Benjamin Yakir**

The Statistics of Gene Mapping

 Springer

The Statistics Of Gene Mapping Statistics For Biology And Health

Didier Musso



The Statistics Of Gene Mapping Statistics For Biology And Health:

The Statistics of Gene Mapping David Siegmund, Benjamin Yakir, 2007-05-27 This book details the statistical concepts used in gene mapping first in the experimental context of crosses of inbred lines and then in outbred populations primarily humans It presents elementary principles of probability and statistics which are implemented by computational tools based on the R programming language to simulate genetic experiments and evaluate statistical analyses Each chapter contains exercises both theoretical and computational some routine and others that are more challenging The R programming language is developed in the text

Statistical Genetics of Quantitative Traits Rongling Wu, Changxing Ma, George Casella, 2007-07-17 Most traits in nature and of importance to agriculture are quantitatively inherited These traits are difficult to study due to the complex nature of their inheritance However recent developments of genomic technologies provide a revolutionary means for unraveling the secrets of genetic variation in quantitative traits Genomic technologies allow the molecular characterization of polymorphic markers throughout the entire genome that are then used to identify and map the genes or quantitative trait loci QTLs underlying a quantitative trait based on linkage analysis Statistical analysis is a crucial tool for analyzing genome data which are now becoming increasingly available for a variety of species and for giving precise explanations regarding genetic variation in quantitative traits occurring among species populations families and individuals In 1989 Lander and Botstein published a landmark methodological paper for interval mapping that enables geneticists to detect and estimate individual QTL that control the phenotype of a trait Today interval mapping is an important statistical tool for studying the genetics of quantitative traits at the molecular level and has led to the discovery of thousands of QTLs responsible for a variety of traits in plants animals and humans In a recent study published in Science Li Zhou and Sang 2006 311 1936 1939 were able to characterize the molecular basis of the reduction of grain shattering a fundamental selection process for rice domestication at the detected QTL by interval mapping

[Encyclopedia of Biopharmaceutical Statistics - Four Volume Set](#) Shein-Chung Chow, 2018-09-03 Since the publication of the first edition in 2000 there has been an explosive growth of literature in biopharmaceutical research and development of new medicines This encyclopedia 1 provides a comprehensive and unified presentation of designs and analyses used at different stages of the drug development process 2 gives a well balanced summary of current regulatory requirements and 3 describes recently developed statistical methods in the pharmaceutical sciences Features of the Fourth Edition 1 78 new and revised entries have been added for a total of 308 chapters and a fourth volume has been added to encompass the increased number of chapters 2 Revised and updated entries reflect changes and recent developments in regulatory requirements for the drug review approval process and statistical designs and methodologies 3 Additional topics include multiple stage adaptive trial design in clinical research translational medicine design and analysis of biosimilar drug development big data analytics and real world evidence for clinical research and development 4 A table of contents organized by stages of biopharmaceutical

development provides easy access to relevant topics About the Editor Shein Chung Chow Ph D is currently an Associate Director Office of Biostatistics U S Food and Drug Administration FDA Dr Chow is an Adjunct Professor at Duke University School of Medicine as well as Adjunct Professor at Duke NUS Singapore and North Carolina State University Dr Chow is the Editor in Chief of the Journal of Biopharmaceutical Statistics and the Chapman Hall CRC Biostatistics Book Series and the author of 28 books and over 300 methodology papers He was elected Fellow of the American Statistical Association in 1995

Analyzing Ecological Data Alain Zuur,Elena N. Ieno,Graham M. Smith,2007-08-29 Which test should I apply During the many years of working with ecologists biologists and other environmental scientists this is probably the question that the authors of this book hear the most often The answer is always the same and along the lines of What are your underlying questions What do you want to show The answers to these questions provide the starting point for a detailed discussion on the ecological background and purpose of the study This then gives the basis for deciding on the most appropriate analytical approach Therefore a better start ing point for an ecologist is to avoid the phrase test and think in terms of analy sis A test refers to something simple and unified that gives a clear answer in the form of a p value something rarely appropriate for ecological data In practice one has to apply a data exploration check assumptions validate the models per haps apply a series of methods and most importantly interpret the results in terms of the underlying ecology and the ecological questions being investigated Ecology is a quantitative science trying to answer difficult questions about the complex world we live in Most ecologists are aware of these complexities but few are fully equipped with the statistical sophistication and understanding to deal with them

Unified Methods for Censored Longitudinal Data and Causality Mark J. van der Laan,James M Robins,2012-11-12 During the last decades there has been an explosion in computation and information technology This development comes with an expansion of complex observational studies and clinical trials in a variety of fields such as medicine biology epidemiology sociology and economics among many others which involve collection of large amounts of data on subjects or organisms over time The goal of such studies can be formulated as estimation of a finite dimensional parameter of the population distribution corresponding to the observed time dependent process Such estimation problems arise in survival analysis causal inference and regression analysis This book provides a fundamental statistical framework for the analysis of complex longitudinal data It provides the first comprehensive description of optimal estimation techniques based on time dependent data structures subject to informative censoring and treatment assignment in so called semiparametric models Semiparametric models are particularly attractive since they allow the presence of large unmodeled nuisance parameters These techniques include estimation of regression parameters in the familiar multivariate generalized linear regression and multiplicative intensity models They go beyond standard statistical approaches by incorporating all the observed data to allow for informative censoring to obtain maximal efficiency and by developing estimators of causal effects It can be used to teach masters and Ph D students in biostatistics and statistics and is suitable for researchers in statistics

with a strong interest in the analysis of complex longitudinal data The Statistical Analysis of Recurrent Events Richard J. Cook, Jerald Lawless, 2007-08-02 This book presents models and statistical methods for the analysis of recurrent event data The authors provide broad detailed coverage of the major approaches to analysis while emphasizing the modeling assumptions that they are based on More general intensity based models are also considered as well as simpler models that focus on rate or mean functions Parametric nonparametric and semiparametric methodologies are all covered with procedures for estimation testing and model checking *Mathematical Reviews* ,2007 **National Library of Medicine Current Catalog** National Library of Medicine (U.S.),1989 **Mathematical and Statistical Methods for Genetic Analysis** Kenneth Lange,2003-06-03 Written to equip students in the mathematical sciences to understand and model the epidemiological and experimental data encountered in genetics research This second edition expands the original edition by over 100 pages and includes new material Sprinkled throughout the chapters are many new problems **AMSTAT News** American Statistical Association,2002 *American Book Publishing Record* ,2007 Current Catalog National Library of Medicine (U.S.), First multi year cumulation covers six years 1965 70 **Biology Digest** ,1994 **Energy Research Abstracts** ,1988 Includes all works deriving from DOE other related government sponsored information and foreign nonnuclear information **Heterogeneity in Statistical Genetics** Derek Gordon,Stephen J. Finch,Wonkuk Kim,2020-12-16 Heterogeneity or mixtures are ubiquitous in genetics Even for data as simple as mono genic diseases populations are a mixture of affected and unaffected individuals Still most statistical genetic association analyses designed to map genes for diseases and other genetic traits ignore this phenomenon In this book we document methods that incorporate heterogeneity into the design and analysis of genetic and genomic association data Among the key qualities of our developed statistics is that they include mixture parameters as part of the statistic a unique component for tests of association A critical feature of this work is the inclusion of at least one heterogeneity parameter when performing statistical power and sample size calculations for tests of genetic association We anticipate that this book will be useful to researchers who want to estimate heterogeneity in their data develop or apply genetic association statistics where heterogeneity exists and accurately evaluate statistical power and sample size for genetic association through the application of robust experimental design **Science** John Michels (Journalist),2003 A weekly record of scientific progress **Journal of the Japanese Society of Computational Statistics** ,2002 **Dissertation Abstracts International** ,2004 *Genome Research* ,1998
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