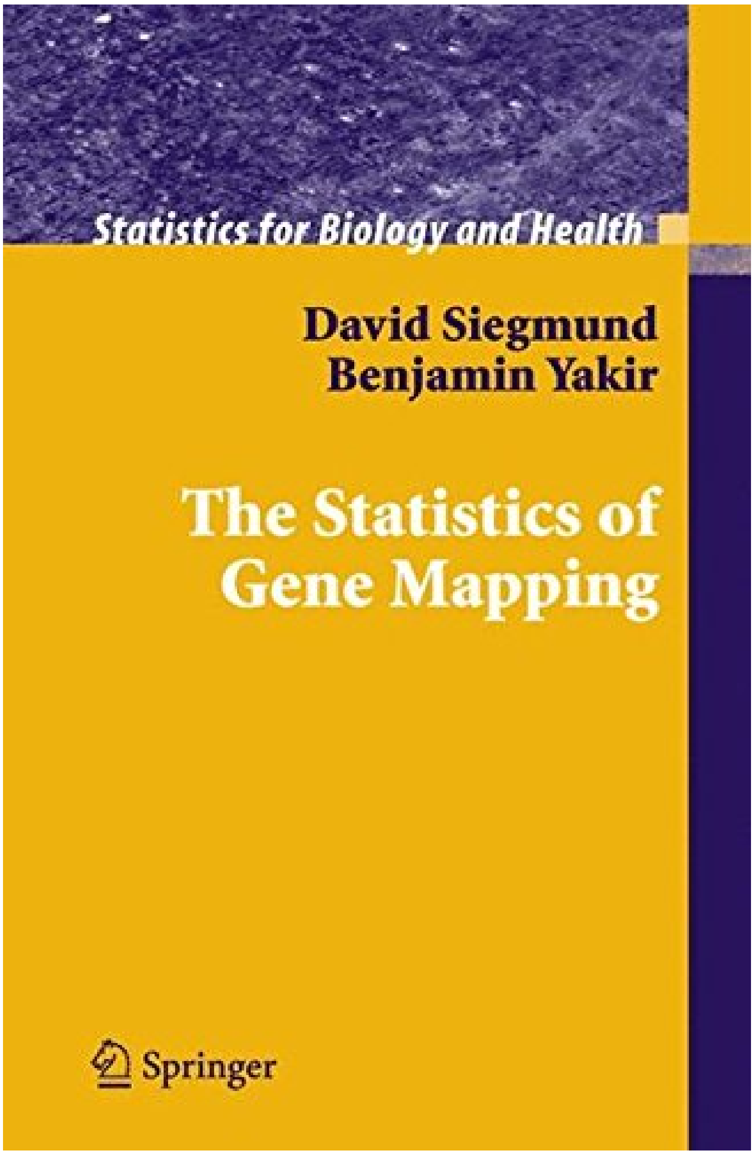
The Statistics of Gene Mapping (Statistics for Biology and Health)

David Siegmund, Benjamin Yakir



#3906314 in Books 2007-03-12Original language:EnglishPDF # 1 9.21 x .81 x 6.14l, 1.35 #File Name: 038749684X334 pages | File size: 67.Mb

David Siegmund, Benjamin Yakir : The Statistics of Gene Mapping (Statistics for Biology and Health) before purchasing it in order to gage whether or not it would be worth my time, and all praised The Statistics of Gene Mapping (Statistics for Biology and Health):

3 of 3 people found the following review helpful. Marginal treatmentBy Dennis OneillThe Statistics of Gene Mapping leaves a great deal to be desired. The authors are not very explicit about how they arrive at many of the equations they use often not showing any derivations whatsoever. They also provide a great deal of code in R with very little

explanation of what the code does. For a much better treatment of quantitative genetics there are two excellent sources: "Genetics and Analysis of Quantitative Traits," by Michael Lynch and Bruce Walsh and "Introduction to Quantitative Genetics," by Falconer and Mackay. Both are far superior to this.32 of 32 people found the following review helpful. another great book by SiegmundBy Michael R. ChernickDavid Siegmund is a famous probabilist who is both a great lecturer and writer. I personally audited his advanced probability course at Stanford. He coauthored a book on optimal stopping with Herb Robbins and has written other fine books on sequential analysis and repeated significance testing. In recent years he as well as Brad Efron and other Stanford and Berkeley statistics professors has studied the mathematics, probability theory and statistics associated with human genetics and microarray data. This book presents the theory and application of the appropriate probabilistic methods. Anyone with a serious interest in this topic should get the book.The book assumes some knowledge of probability and statistics. So a novice in the field of statistics could have trouble with the text and require more development. Also for the statistician it may assume a little too much knowledge of genetics. But I think it is the perfect book for the intended audience and makes a great reference.Another text that is rigorous in terms of statistics and assume less knowledge of statistics and genetics is "Analyzing Microarray Gene Expression Data" by G. J. McLachlan, k.-A. Do and C. Amboise. You will find that I have also reviewed that text on .

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.

From the reviews: "The Statistics of Gene Mapping...is a welcome addition to the statistical genetics literature, that in fact includes a very small number of textbooks. ...The exercises at the end of the chapters will provide a useful pedagogical tool, with their mix of computer implementation and conceptual questions. ...[This book] provides the reader with clar, concises introduction to a number of important topics and I think it will prove to be a useful teaching instrument." Chiara Sabatti, Journal of Statistical Software, August 2007, Vol. 21 "The book is an excellent addition to the statistics-for-biology and health book series. It is also a very good textbook is statistical genetics. All statistical models and methods in the book are illustrated and simulated using R Language. Overall, the book covers both classical and up-to-date important topics in statistical genetics. It is a well-written book for both researchers and graduate students in statistics, biostatistics, statistical genetics, and other related fields." (Xianggui Qu, Technometrics, Vol. 50 (1), 2008) "This book presents an excellent introduction to the basic statistical principles used in gene mapping. Computer algorithms are given . There are numerous challenging problems. This is a rewarding read . those that work through the book will gain a deep understanding of the statistical challenges of the field. With this knowledge they would be prepared for more encyclopedic or data analytic works. I recommend the book to any graduate student who might consider contributing to the field." (David F. Andrews, International Statistical , Vol. 75 (2), 2007)From the Back CoverGene mapping is used in experimental genetics to improve the hardiness or productivity of animals or plants of agricultural value, to explore basic mechanisms of inheritance, or to study animal models of human inheritance. In human populations it is used as a first step to identify genes associated with human health and disease. This book presents a unified discussion of the statistical concepts applied in gene mapping, first in the experimental context of crosses of inbred lines and then in outbred populations, primarily humans. The development involves 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. The viewpoint reflects the modern approach of using anonymous DNA markers distributed throughout the genome to identify regions likely to contain genes of interest. The reader is assumed to have some familiarity with probability/statistics and with elementary genetics. Important topics are reviewed in the first three chapters. The R programming language is developed in the text. Each chapter contains exercises, both theoretical and computational, some routine and others that are more challenging. The book is suitable for upper level undergraduate students or graduate students of genetics or statistics. David Siegmund is the John D. and Sigrid Banks Professor in the Department of Statistics,Stanford University. He has been a visitor at The Hebrew University, the University of Zurich, the University of Heidelberg, the National University of Singapore, and the Free University of Amsterdam. He is a member of the National Academy of Sciences (USA) and the American Academy of Arts and Sciences. Benjamin Yakir is Associate Professor of Statistics at The Hebrew University of Jerusalem and has been a visiting professor at Stanford University, the University of Pennsylvania, and the National University of Singapore.