Applied Statistical Genetics with R: For Population-based Association Studies (Use R!)

Andrea S. Foulkes
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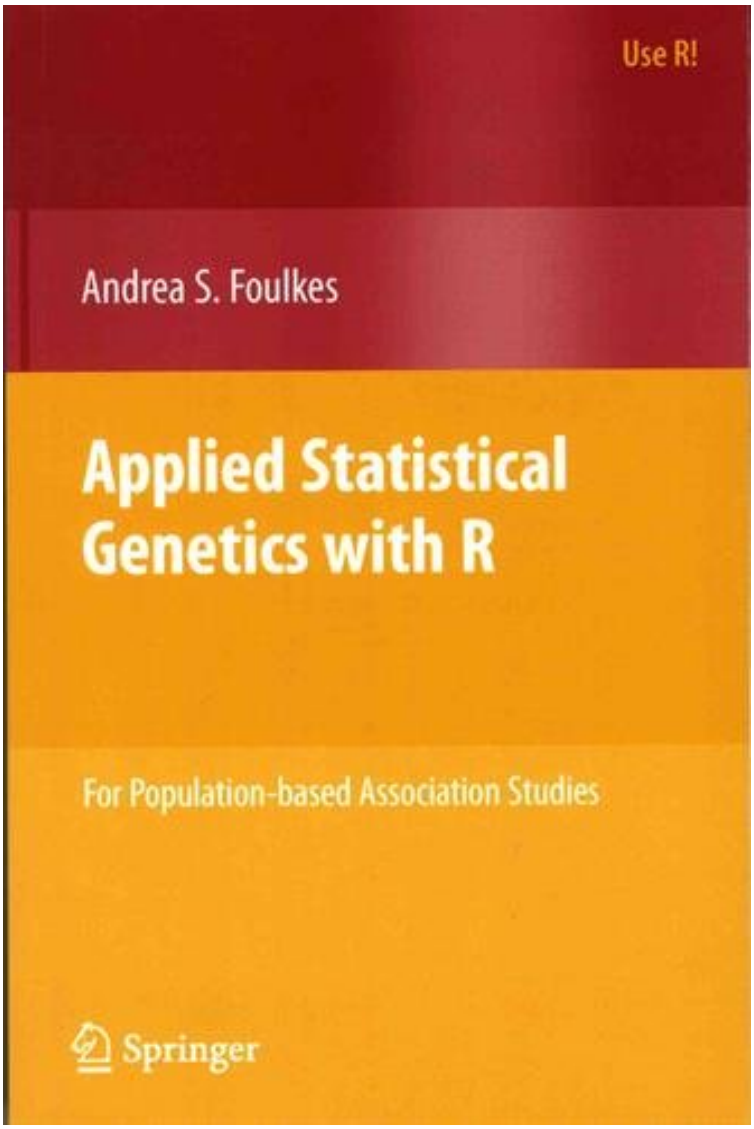

#1046852 in Books Andrea S Foulkes 2009-04-17Ingredients: Example IngredientsOriginal language:EnglishPDF # 1 9.25 x .63 x 6.10l, .90 #File Name: 0387895531252 pagesApplied Statistical Genetics with R For Population based Association Studies | File size: 24.Mb

Andrea S. Foulkes : Applied Statistical Genetics with R: For Population-based Association Studies (Use R!) before purchasing it in order to gage whether or not it would be worth my time, and all praised Applied Statistical Genetics with R: For Population-based Association Studies (Use R!):

0 of 0 people found the following review helpful. Fills The GapBy William Carrol"Applied Statistical genetics With

R" is a good follow up to classic texts like Falconer or Weir's books on quantitative genetics. Although it does not cover QTL analysis specifically, association testing is covered extensively, making it is a good companion to "A Guide to QTL Mapping with R/qtl." Then it has a couple chapters on regression trees and forests.The introduction to contingency tables needs to be revised because it reads like it got tacked on at the last second. Luckily, readers can easily find PowerPoint presentations online that cover the topic in a couple slides.The Springer books are good, although this one is a little short at around 220 pages, which is probably why this is one of the cheaper titles in this series. It feels like there will be a longer second edition some day.0 of 2 people found the following review helpful. Good reference book - not enough up to dateBy Sagi PolaniGood reference book, but not enough up to date, and does not relate to available R packages that are extendedly used today.10 of 10 people found the following review helpful. A solid text with interest beyond statistical geneticsBy David R. GagnonApplied Statistical Genetics with R For Population-based Association Studies is by Andrea S. Foulkesof the University of Massachusetts and is meant for an audience with some understanding of both genetics and statistics, though the level of understanding in both areas need not be extensive. The statistical knowledge required would be covered in one or two undergraduate courses and an introductory genetics course would be helpful. Lacking this background, the first three chapters provide a well written review of the required knowledge and also provide extensive references for further reading. Indeed, the entire book provides plenty of references for further study of all of the topics covered.For genetic studies, this book covers several basic topics, including linkage disequilibrium, Hardy-Weinberg equilibrium, and haplotypic phase as well as methods for identifying associations between single genetic polymorphisms and a trait. Subjects that are not covered include family studies, population genetics or gene expression analysis.One of the great strengths of this book is the presentation of topics that while relevant to genetics studies are also relevant to the general statistical reader. There are very good chapters and sections on missing data, multiple comparisons, cross-validation, the EM algorithm, classification and regression trees [CART] and random forests as well as several Bayesian techniques. While some statistical notation and formulas are used throughout, each topic is presented in clear fashion that is understandable to the less mathematically inclined. Algorithms are laid out in a step-by-step fashion that makes topics such as the EM algorithm and Gibbs sampling understandable. Indeed, this is one of the few statistical texts, beyond the most basic introductory texts, that can be read cover-to-cover. If not for the extensive use of examples with a genetics focus, I would recommend this as a general text on advanced statistics.This book makes extensive use of the freely available R programming language and publicly available data sets, with many worked-out examples throughout the text. A web site provides download-able data sets and code. While there is an appendix that introduces the R language, some working familiarity with R beyond this text will be necessary for most readers.In all, I found this to be a very readable introduction to the use of statistics in genetics. It would make a very good text for an introductory course on statistical genetics. I also recommend this book to the general statistics reader because of its very readable presentation of some complex statistical topics.

Statistical genetics has become a core course in many graduate programs in public health and medicine. This book presents fundamental concepts and principles in this emerging field at a level that is accessible to students and researchers with a first course in biostatistics. Extensive examples are provided using publicly available data and the open source, statistical computing environment, R.

From the reviews:"This book aims at filling a real gap in the literature. After three introductory chapters on basic statistical and genetic concepts and association studies, the book deals with the problems of multiple comparison, unknown phase, and model building and predictions in high dimension: topic choices that I find relevant and stimulating. This textbook, then, serves as a starting point for further reading, and this is a great way of introducing statistical genetics problems to a general audience. From this point of view, and in many ways, the book feels like the transcription of lecture notes of an introductory class. This is certainly the way in which many great texts were developed. (Chiara Sabatti, Journal of Statistical Software, September 2009, Volume 31)"This book provides a gentle introduction to genome-wide association studies (GWAS) within both a theoretical and methodological perspective. It will especially be a useful resource to those interested in the ever growing interdisciplinary approach to genetic epidemiology. This new book in the Springer Use R! series certainly fills the lacking R resources on this rapidly evolving field in statistical genetics" (Christopher Lalanne, Journal of Statistical Software, September 2009, Volume 31)Applied Statistical Genetics With R is written at a level accessible to non-experts in statistical genetics. The author does not assume the reader is familiar with statistical techniques and hence introduces techniques s required. Examples are accompanied by R scripts typical of the Use R! book series which encourages hands-on experimentation by the readers. Re-using existing packages is characteristic of open-source software development, such as R, and encourages transparency and reproducibility whole minimizing redundancy. The author invokes functionalities from readily available R packages and provides supplemental R scripts as required. Overall, the book provides a nice introduction to the area of statistical genetics concepts using R. (American Statistician, August 2010, Vol. 64, No. 3)This book is addressed to a wide readership. Researcher with medical background will learn about the statistical fundamentals in

this field, whereas statisticians will see how established methods can be used in this modern research area. a book written about this topic often has to satisfy particular needs and interests. This is well done in this book. The book is a useful help for researchers and students who are interested in an applied approach to statistical genetics in population-based association studies. (Daniel Fischer, International Statistical , Vol. 78 (1), 2010)From the Back CoverThe vast array of molecular level information now available presents exciting opportunities to characterize the genetic underpinnings of complex diseases while discovering novel biological pathways to disease progression. In this introductory graduate level text, Dr. Foulkes elucidates core concepts that undergird the wide range of analytic techniques and software tools for the analysis of data derived from population-based genetic investigations. Applied Statistical Genetics with R offers a clear and cogent presentation of several fundamental statistical approaches that researchers from multiple disciplines, including medicine, public health, epidemiology, statistics and computer science, will find useful in exploring this emerging field. Couched in the language of biostatistics, this text can be easily adopted for public health and medical school curricula. The text covers key genetic data concepts and statistical principles to provide the reader with a strong foundation in methods for candidate gene and genome-wide association studies. These include methods for unobservable haplotypic phase, multiple testing adjustments, and high-dimensional data analysis. Emphasis is on analysis of data arising from studies of unrelated individuals and the potential interplay among genetic factors and more traditional, epidemiological risk factors for disease. While theoretically rigorous, the analytic techniques are presented at a level that will appeal to researchers and students with limited knowledge of statistical genetics. The text assumes the reader has completed a first course in biostatistics, uses publicly available data sets for illustration, and provides extensive examples using the open source, publicly available statistical software environment R. Dr. Foulkes is an Associate Professor of Biostatistics at the University of Massachusetts, Amherst, where she has been recognized for teaching excellence. Her active research program includes the development of methods for characterizing the relationships among high-dimensional molecular and cellular level data and measures of disease progression. She has authored numerous technical manuscripts in this field and currently serves as the principal investigator of an individual research award from the National Institute of Allergy and Infectious Diseases, a division of the National Institutes of Health.