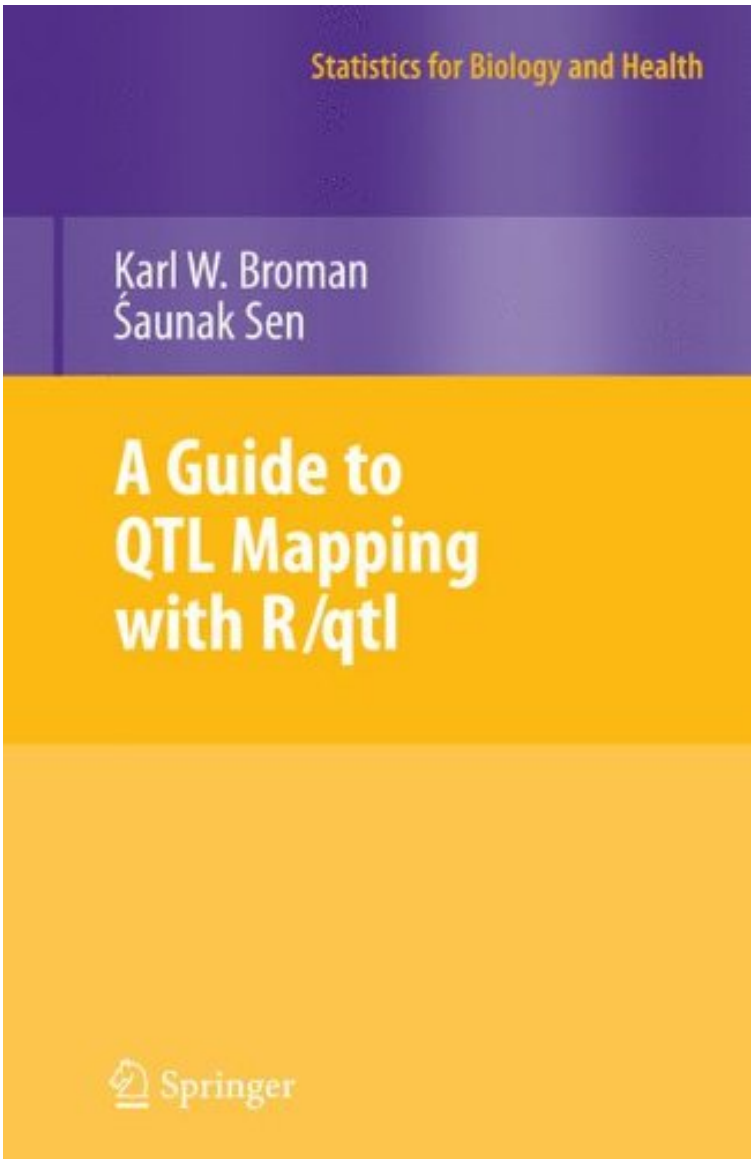
A Guide to QTL Mapping with R/qtl (Statistics for Biology and Health)

Karl W. Broman, Saunak Sen



#2338148 in Books Karl W Broman Saunak Sen 2009-07-20Original language:EnglishPDF # 1 9.21 x .94 x 6.14l, 1.85 #File Name: 0387921249400 pagesA Guide to QTL Mapping with R qtl Statistics for Biology and Health | File size: 56.Mb

Karl W. Broman, Saunak Sen : A Guide to QTL Mapping with R/qtl (Statistics for Biology and Health) before purchasing it in order to gage whether or not it would be worth my time, and all praised A Guide to QTL Mapping with R/qtl (Statistics for Biology and Health):

0 of 0 people found the following review helpful. If you need a free QTL mapper...By JoshThis book has everything you need if you want to know how to map a QTL (Quantitative Trait Loci) trait. It has some genetic and statistical backgrounds, but a basic knowledge of statistics and genetics would benefit the reader. Previous experience with R is highly recommended, but there are also many step-by-step codings to show you what to do. Mapping a QTL is not so much a linear pathway, but an involved process and this book covers them all. After reading through the book and doing many of the examples in R, the reader would have a very good background in QTL mapping and would be able to design a good experiment with high power, and then analyze the experiment. Also good if the reader has marker data from an experiment and wants to know what to do next. Highly recommended!0 of 0 people found the following review helpful. Hits the sweet spotBy William CarrolIt is what title says, QTL analysis with R/qtl, with just enough background. Hard cover, nice color illustrations of graphics outputs from R that tie in nicely with the text.Descriptions of genetics and crosses are well written and clear. It's not meant to be a comprehensive explanation of inheritance or quantitative genetics, but the book provides just enough background to support their rationale for picking specific crosses and experimental designs.Many books try to fill the gap between introductory texts and theory, but often not enough effort goes into them. This book seems to find the sweet spot, and it was a good purchase.0 of 0 people found the following review helpful. Five StarsBy Hongxu DongThis book is really good. Love it!

Comprehensive discussion of QTL mapping concepts and theory Detailed instructions on the use of the R/qtl software, the most featured and flexible software for QTL mapping Two case studies illustrate QTL analysis in its entirety

From the reviews:The book by Broman and Sen gives a practical review of statistical QTL mapping in experimental crosses with step-by-step instructions to the use of the R package qtl. has a wide coverage of topics, from experimental design and data input, to single-QTL mapping, mapping with covariates and multiple-GTL scans, organized into 11 chapters according to the logic flow of a QTL analysis. The authors made a good compromise between statistical methodology and real-data illustration with R code, so that different readers may easily focus on the parts that are more interesting to them. A researcher can follow the code in the examples of the book to study real-data applications of the qtl package. this is a well-written book with carefully chosen and nicely organized topics. It can serve as a good introduction to QTL mapping methodology and a useful practical guide to the R package. (Journal of Statistical Software, Vol. 32, Book 5, January 2010)The book gives an overview of the practical aspects of the analysis of QTL mapping experiments . Most of the chapters start with a short introduction and finish with a summary and suggestions of further reading listing numerous review articles connected with the discussed subject. There are 150 figures, including 90 in full color. We recommend it, first of all, to scientists who use QTL mapping analysis, and also to postdoctoral researchers and graduated students interested in exploring applications of statistics. (I. Czyczyo-Mysza and I. Marciska, Acta Physiologiae Plantarum, Vol. 32, March, 2010)From the Back CoverQuantitative trait locus (QTL) mapping is used to discover the genetic and molecular architecture underlying complex quantitative traits. It has important applications in agricultural, evolutionary, and biomedical research. R/qtl is an extensible, interactive environment for QTL mapping in experimental crosses. It is implemented as a package for the widely used open source statistical software R and contains a diverse array of QTL mapping methods, diagnostic tools for ensuring high-quality data, and facilities for the fit and exploration of multiple-QTL models, including QTL x QTL and QTL x environment interactions. This book is a comprehensive guide to the practice of QTL mapping and the use of R/qtl, including study design, data import and simulation, data diagnostics, interval mapping and generalizations, two-dimensional genome scans, and the consideration of complex multiple-QTL models. Two moderately challenging case studies illustrate QTL analysis in its entirety. The book alternates between QTL mapping theory and examples illustrating the use of R/qtl. Novice readers will find detailed explanations of the important statistical concepts and, through the extensive software illustrations, will be able to apply these concepts in their own research. Experienced readers will find details on the underlying algorithms and the implementation of extensions to R/qtl. There are 150 figures, including 90 in full color. Karl W. Broman is Professor in the Department of Biostatistics and Medical Informatics at the University of Wisconsin-Madison, and is the chief developer of R/qtl. Saunak Sen is Associate Professor in Residence in the Department of Epidemiology and Biostatistics and the Center for Bioinformatics and Molecular Biostatistics at the University of California, San Francisco.