Statistical and Computational Pharmacogenomics (Chapman Hall/CRC Interdisciplinary Statistics)

Rongling Wu, Min Lin
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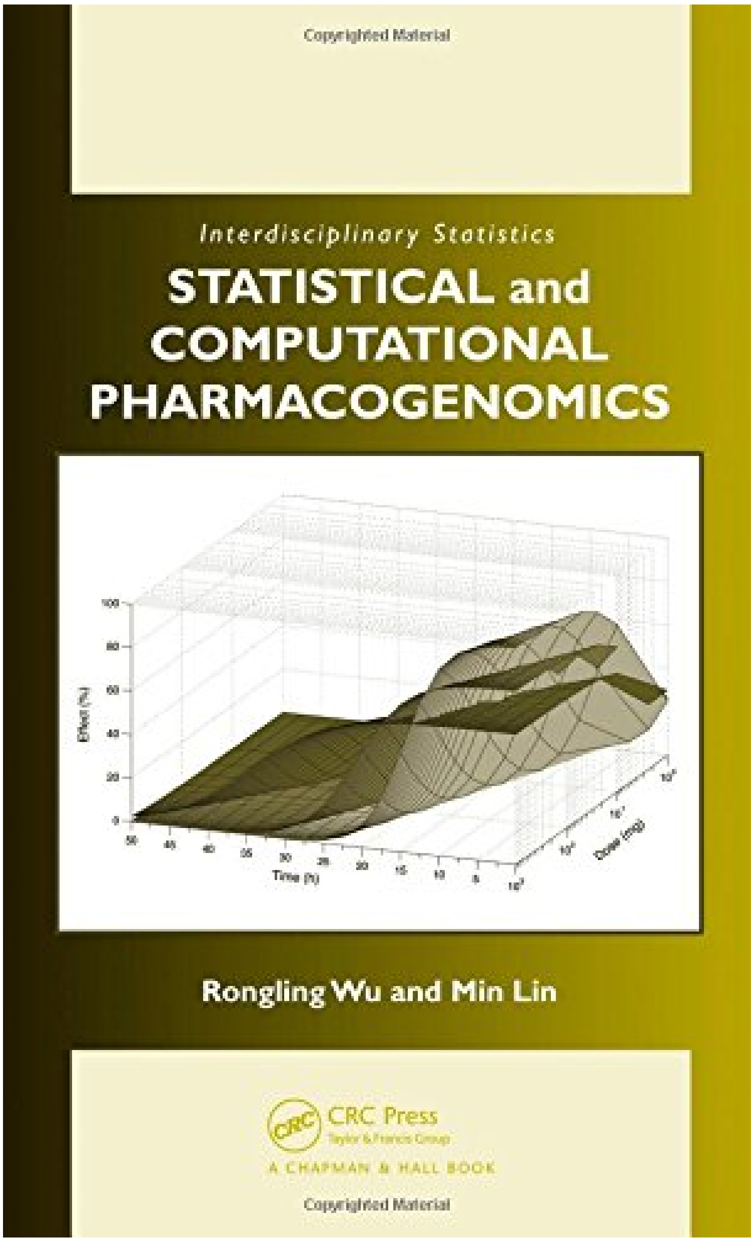

#5797719 in Books Chapman and Hall/CRC 2008-08-08Original language:EnglishPDF # 1 9.30 x 1.00 x 6.30l, 1.50 #File Name: 1584888288368 pages | File size: 52.Mb

Rongling Wu, Min Lin : Statistical and Computational Pharmacogenomics (Chapman Hall/CRC Interdisciplinary Statistics) before purchasing it in order to gage whether or not it would be worth my time, and all praised Statistical and Computational Pharmacogenomics (Chapman Hall/CRC Interdisciplinary Statistics):

0 of 0 people found the following review helpful. Very niceBy maria pilar sanchezA issue very important for pharmacist, treated in a comprehensively way. I like a second part with specifics of pharmacogenetics analysis.2 of 2 people found the following review helpful. great book for biostatisticians maybe scientists tooBy Michael R. ChernickI have provided a more detailed review for Technometrics but I would like to explain here why I like the book and encourage biostatisticians to read it and keep it on their book shelf.This text is one of the first books written by statisticians for statisticians who need to know the basics of genetic markers based on genomic mapping and haplotyping. Since I have worked for many years and current work in the pharmaceutical industry, I know that as we learn more and more about the human genome and the processes that create individual genetic responses we are learning how to identify subgroups that respond well to a drug or have fewer side effects. If genetic markers can accurately identify individuals that respond well to a drug as well as those that do not, more drugs may be come available that can treat a subset of the population that has a certain disease without creating hazardous side effect. Often drugs have failed to reach market because of serious complications found on a small but significant portion of the population even though they could potential benefit many others. Getting more drugs to market that are safe and effective in a targeted population is the goal that has great potential and is beginning to bear fruit.The authors' goals are (1) to summarize in one place the scattered literature that has developed over the past 5 years in a very readable way, (2) to expose the statistician who works in the pharmaceutical field the underlying theory that motivates the statistical methods that are employed, (3) to show the biologists, geneticists, chemists, and clinicians the value of some very powerful statistical techniques that encompass functional mappping. I can be very positive about the authors' acheiving goals 1 and 2. Goal 3 is difiuclt for me to access since I am a statistician and not a biologist, geneticist or chemist who might have limited statsistcal background.0 of 0 people found the following review helpful. Do not read that book if you don't like mathematics, it has detailed all the formulas to ...By Beatriz Sonja KanzkiDo not read that book if you don't like mathematics, it has detailed all the formulas to help compute in that field

Due to the tremendous accumulation of data for genetic markers, pharmacogenomics, the study of the functions and interactions of all genes in the overall variability of drug response, is one of the hottest areas of research in biomedical science. Statistical and Computational Pharmacogenomics presents recent developments in statistical methodology with a number of detailed worked examples that outline how these methods can be applied. This comprehensive volume provides key tools needed to understand and model the genetic variation for drug response and equips statisticians with a thorough understanding of this complex field and how computational skills can be employed.

a statistically rigorous text that gives a systematic exposition of the subject of pharmacogenomics, the related analytical methods and the corresponding computational algorithms. a good basis for further methodological, empirical and applied investigation into the field.Statistics in Medicine, 2011, 30 This text is one of the first books written by statisticians and for statisticians who need to know the basics of genetic markers based on genomic mapping and haplotyping. this book is a welcome addition that will help me learn pharmacogenomics to the extent that I need it to apply appropriate statistical methodology in microarray analysis and classification problems. I can recommend it for the statisticians . I also hope that it will be successful at getting the chemists, biologists, and geneticists interested in the important statistical methods and mathematical modeling described in this book.Michael R. Chernick, Technometrics, February 2011 This book covers advanced topics in statistical genetics focusing on applications of interest in pharmacogenomics. The difficulties in estimating haplotype frequencies and their effects on quantitative trait loci (QTLs) are covered in detail for a variety of experimental designs. of most interest for statisticians working in the pharmaceutical area that need to incorporate genetic variables into consideration in their studies.ISCB News, No. 50, December 2010 [Pharmacogenomics] can address questions such as whether individuals with different versions of a gene are more or less likely to respond to a particular drug. However, Wu and Lin go well beyond this and discuss methods for relating genetic variation to dynamic pharmacokinetic and pharmacodynamic profiles of drugs. They refer to this as functional mapping. One of the main clinical applications of these methods will be in predicting efficacy and toxicity of drugs, allowing treatment to be tailored to an individuals genetic background, and this book makes a valuable contribution towards this.Significance, June 2010 a volume that can be recommended to both statisticians and life scientists. Yes, theres plenty of heavy-duty math for the theory lovers, but there are also many sections of explanations for the biologist. These explanations are not highly theoretical and give the scientist a better understanding of what the analysis is doing and why it is needed.John A. Wass, Ph.D., Scientific Computing, 2009About the AuthorUniversity of Florida, Gainsville, USA Duke Clinical Research Institute, Durham, North Carolina, US University of Kent, UK University of Copenhagen, Denmark Utrecht University, The Netherlands University of California, Berkeley, USA