Modern Issues and Methods in Biostatistics (Statistics for Biology and Health)

Mark Chang
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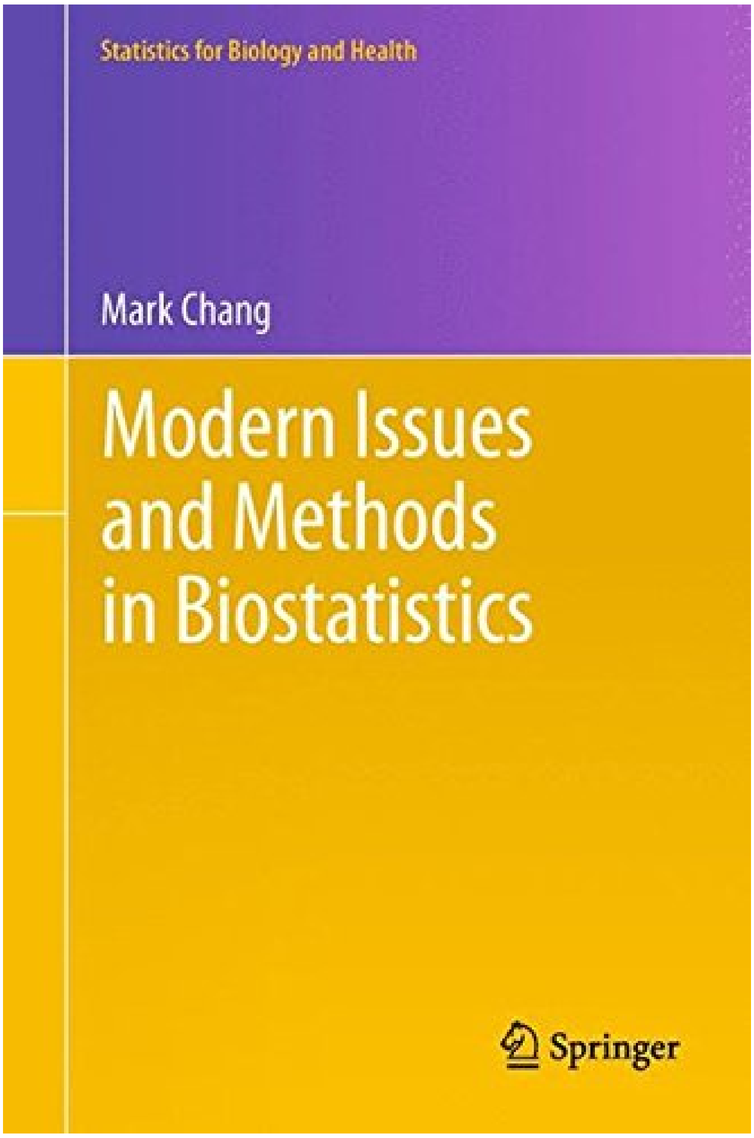

#5190817 in Books Chang Mark 2011-07-15Original language:EnglishPDF # 1 9.21 x .75 x 6.14l, 1.35 #File Name: 1441998411307 pagesModern Issues and Methods in Biostatistics | File size: 75.Mb

Mark Chang : Modern Issues and Methods in Biostatistics (Statistics for Biology and Health) before purchasing it in order to gage whether or not it would be worth my time, and all praised Modern Issues and Methods in Biostatistics (Statistics for Biology and Health):

4 of 4 people found the following review helpful. a nice advanced treatment of modern issues and statistical methodology in biostatisticsBy Michael R. ChernickThere are many things that I like about this book but also several

things to criticize. First, although the title is "Modern Issues and Methods in Biostatistics", it is really primarily about the aspects of biostatistics that pertain to clinical trials and drug development (which are areas the author is very familiar with and has great expertise in).I like that this book is well-suited for biostatisticians both as a source for great examples and references and for the nice technical treatment of important issues including multiple testing, superiority vs non-inferiority trials, group sequential and adaptive trial designs, missing data and imputation, survival modeling and meta-analysis. Also it is somewhat unique in its coverage of statistical decision/game theory, data mining and the discussion of Bayesian methods and their applications.One problem with the book is the author's intention to make this book available to researchers and scientists as well as statisticians. The level of the book is very uneven. Much of the development of methods is highly mathematical and technical and probably too advanced for many of these intended readers. On the other hand, the author clearly has interesting things to say to a general audience in the discussion sections of the chapters, particularly the chapters with sections on controversies and challenges. While the entire book is appealing to me I doubt that the scientists and researchers will be able to follow some of the very technical sections.I also think that the organization could be better. Bootstrapping and Bayesian methods are mentioned and allude to far before they are formally introduced. For example, the introduction to the Bayesian paradigm does not come until the final chapter (Chapter 10). Yet Bayesian methods are discussed throughout (Bayesian approach to multiplicity, page 1, Bayesian methods in imputation, pages 126 and 137, Bayesian confidence propagation, page 223 and Bayesian networks, page 245). A better approach would be to split the Baysian chapter with the introductory material on pages 261-268 and put it into a separate chapter between the current chapters 1 and 2 with the remainder from the middle of page 268 to page 289 as the new concluding chapter.Bootstrap methods are introduced in Section 9.2.3, pages 240-242, but bootstrap aggregation is mentioned on pages 212 and 227 and the Bayesian bootstrap on page 137. I think it is discomforting to the reader to have terms mentioned before they are formally defined. Putting section 9.2.3 into a section in an early chapter would solve the problem.At times the discussion sounds like the author is having a dialogue with fellow statisticians as for example when he writes on page 110 "Jennison and Turnbull (2006) raised the question as to when an adaptive design using nonsufficient statistics can be improved upon by a nonadaptive group sequential design. Tsiatis and Mehta (2003) have proved that for any SSR adaptive design there exists a more powerful group sequential design. On the other hand, the weighted method (or MINP) provides great flexibility, and when the sample size does not change, it has the same power as the classical group sequential design."Mark is making an important point here. Some statisticians used the result of Tsiatis and Mehta to claim that adaptive designs provide no advantage over group sequential methods and Mark is trying to explain that this is not the case. However, although this argument may be comprehensible to some statisticians I think it would be confusing to other audiences.To summarize: this book is a gem for statisticians as a reference source on modern biostatistical methods. However, the highly technical exposition makes it inaccessible to many researchers and scientists that are claimed to be part of the intended audience. The organization and, at times, the exposition could be improved upon. I highly recommend this book for statisticians in the pharmaceutical industry and those statisticians that are particularly interested in biostatistics. For the book to be accessible to researchers and scientists, the level of the text would need to be lowered and most of the mathematical exposition would need to be removed and be replaced with simple explanations. I think this could best be achieved in a separate book specifically designed for the research audience.

Classic biostatistics, a branch of statistical science, has as its main focus the applications of statistics in public health, the life sciences, and the pharmaceutical industry. Modern biostatistics, beyond just a simple application of statistics, is a confluence of statistics and knowledge of multiple intertwined fields. The application demands, the advancements in computer technology, and the rapid growth of life science data (e.g., genomics data) have promoted the formation of modern biostatistics. There are at least three characteristics of modern biostatistics: (1) in-depth engagement in the application fields that require penetration of knowledge across several fields, (2) high-level complexity of data because they are longitudinal, incomplete, or latent because they are heterogeneous due to a mixture of data or experiment types, because of high-dimensionality, which may make meaningful reduction impossible, or because of extremely small or large size; and (3) dynamics, the speed of development in methodology and analyses, has to match the fast growth of data with a constantly changing face. This book is written for researchers, biostatisticians/statisticians, and scientists who are interested in quantitative analyses. The goal is to introduce modern methods in biostatistics and help researchers and students quickly grasp key concepts and methods. Many methods can solve the same problem and many problems can be solved by the same method, which becomes apparent when those topics are discussed in this single volume.

From the book reviews:There are 10 chapters, each one covering a major topic in biostatistics in about 30 pages. Each chapter is reasonably self-contained, so a reader does not necessarily need to read all prior chapters to understand a given one. this is a useful book for upper-level graduate students and Ph.D. statisticians. (Charles Heckler, Technometrics, Vol. 55 (1), February, 2013)This is a first class book. It discusses a wide range of deep issues in statistics, and although focused on topics arising in biostatistics, pharmaceuticals, and clinical trials it would make stimulating and thought-provoking reading for any statistician. There are exercises at the end of each chapter, and I am certainly tempted to use the book as the basis for a short course for beginning postgraduate students since it would open their eyes to some challenging and indeed fascinating aspects of modern statistics. (David J. Hand, International Statistical , Vol. 80 (1), 2012)From the Back CoverClassic biostatistics, a branch of statistical science, has as its main focus the applications of statistics in public health, the life sciences, and the pharmaceutical industry. Modern biostatistics, beyond just a simple application of statistics, is a confluence of statistics and knowledge of multiple intertwined fields. The application demands, the advancements in computer technology, and the rapid growth of life science data (e.g., genomics data) have promoted the formation of modern biostatistics. There are at least three characteristics of modern biostatistics: (1) in-depth engagement in the application fields that require penetration of knowledge across several fields, (2) high-level complexity of data because they are longitudinal, incomplete, or latent because they are heterogeneous due to a mixture of data or experiment types, because of high-dimensionality, which may make meaningful reduction impossible, or because of extremely small or large size; and (3) dynamics, the speed of development in methodology and analyses, has to match the fast growth of data with a constantly changing face. This book is written for researchers, biostatisticians/statisticians, and scientists who are interested in quantitative analyses. The goal is to introduce modern methods in biostatistics and help researchers and students quickly grasp key concepts and methods. Many methods can solve the same problem and many problems can be solved by the same method, which becomes apparent when those topics are discussed inthis single volume.About the AuthorMark Chang Ph.D. is the executive director, Biostatistics and Data Management, AMAG Pharmaceuticals, with over 15 years of experience as a statistician in the field of clinical trials. He is a co-founder of the International Society for Biopharmaceutical Statistics, an executive member of ASA Biopharmaceutical Section, and a member of Expert Panel for the Networks of Centres of Excellence, Canada. He is a co-chair of Biotechnology Industry Organization Adaptive Design Working Group.