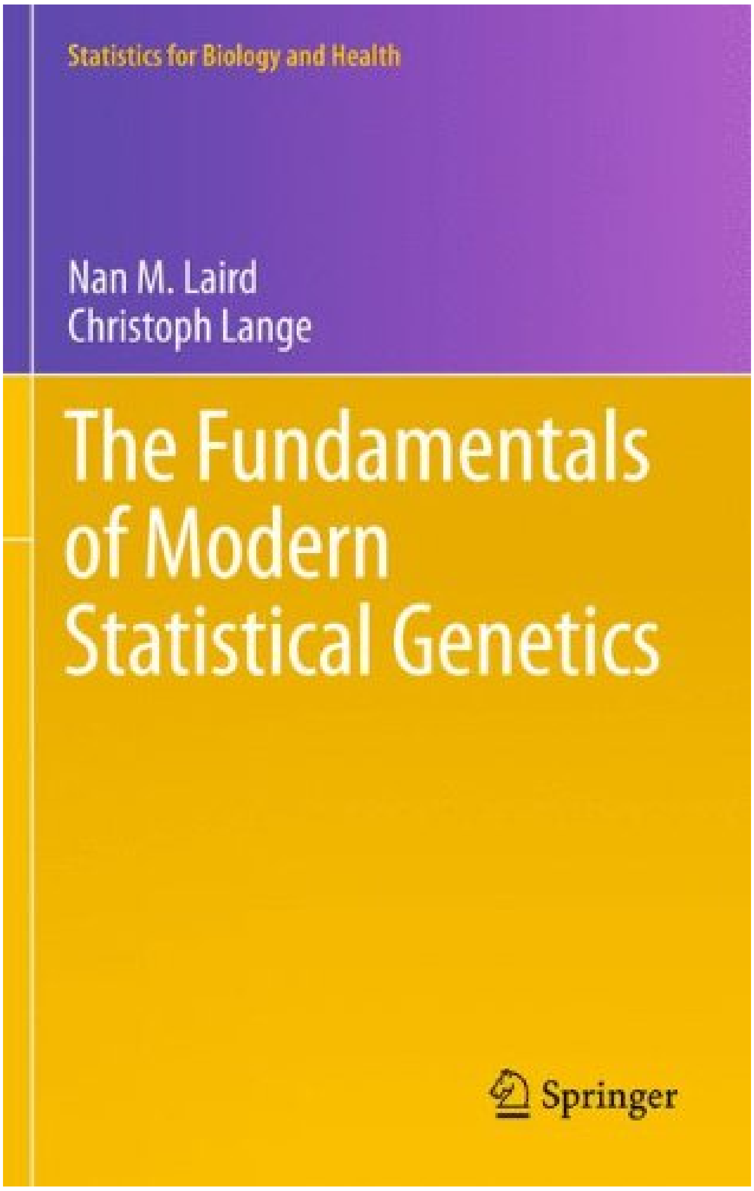
The Fundamentals of Modern Statistical Genetics (Statistics for Biology and Health)

Nan M. Laird, Christoph Lange



#1454389 in Books Springer New York 2010-12-02Original language:EnglishPDF # 1 9.36 x .91 x 6.54l, 1.05 #File Name: 1441973370226 pages | File size: 18.Mb

Nan M. Laird, Christoph Lange : The Fundamentals of Modern Statistical Genetics (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 Fundamentals of Modern Statistical Genetics (Statistics for Biology and Health):

2 of 2 people found the following review helpful. SloppyBy RamanLaird and Lange is a compelling book on first glance: it covers genetic linkage and association analysis in a sufficiently short and focused book that a working professional could hope to read it cover to cover in a reasonable amount of time.Unfortunately, it is sloppy and full of errors. It targets a person with a pretty high level of previous statistics knowledge, but even so, inconsistencies in notation are sufficiently ubiquitous that it makes the presentation and derivations hard to follow. Ambiguous symbols are everywhere. Clear errors abound as well; data quoted in case studies change from table to table (compare Table 3.1 and Box 3.5), and some statements fail very basic consistency checks (note Figure 4.1, which shows dominant and recessive recurrence risk ratios having identical scaling on a log-log plot while the preceding derivation shows the ratios having different scaling). After reading about 30% of the book, I began the search for a better text.The book resembles the LaTeX rough drafts that grad students sometimes hand me; the problem is that in this relationship, I am the student, and I'm not even allowed to ask questions and push the authors to fix them.0 of 0 people found the following review helpful. Many mathematical formulas and equations are missing from the text ...By J. MucsiMany mathematical formulas and equations are missing from the text. In some places, the text is accidentally repeated. Overall, the Kindle edition is low quality.3 of 4 people found the following review helpful. Stats for geneticsBy kwysockiThe book provides great fundamentals for genetic analysis. Although I have not completed the entire book I find that there are few worked out examples in the chapters making the exercises in the back of the chapters difficult to perform given the information in that or previous chapters. Would be great to have answers available (even for odd exercises) to facilitate self learning.

This book covers the statistical models and methods that are used to understand human genetics, following the historical and recent developments of human genetics. Starting with Mendels first experiments to genome-wide association studies, the book describes how genetic information can be incorporated into statistical models to discover disease genes. All commonly used approaches in statistical genetics (e.g. aggregation analysis, segregation, linkage analysis, etc), are used, but the focus of the book is modern approaches to association analysis. Numerous examples illustrate key points throughout the text, both of Mendelian and complex genetic disorders. The intended audience is statisticians, biostatisticians, epidemiologists and quantitatively- oriented geneticists and health scientists wanting to learn about statistical methods for genetic analysis, whether to better analyze genetic data, or to pursue research in methodology. A background in intermediate level statistical methods is required. The authors include few mathematical derivations, and the exercises provide problems for students with a broad range of skill levels. No background in genetics is assumed.

From the reviews:The book covers the historical perspective, covering the standard models and methods. The presentation of the material is carefully thought through. There are lots of figures, many in colour, a large number of examples, numerous boxes that highlight particular derivations and computations, and exercises at the ends of the chapters. All topics are clearly discussed with due detail. I would say that, for the budding statistical geneticist, this is a must-have. (Martin Crowder, International Statistical , Vol. 79 (3), 2011)A book that focuses on statistical methods for finding links between genes and diseases is timely. the authors steer us gently and diligently through material that was developed originally for postgraduate students at the Harvard School of Public Health . ideal for a statistician intending to research in this area or simply for a curious, sufficiently qualified reader. a lovely book, and essential reading if you are a budding GWASer, or simply interested in where your next disease will come from. (G. Wood, Australian New Zealand Journal of Statistics, Vol. 53 (4), 2011)The Fundamentals of Modern Statistical Genetics, by Dr. Nan M. Laird and Dr. Christoph Lange, is a timely reference for both researchers and students. the book is clearly written, and it is useful for colleagues who are interested in the association analysis. Although the book primarily covers the interesting topic of association analysis, it does touch other interesting topics such as joint linkage and association mapping of complex traits. (Ruzong Fan, Journal of the American Statistical Association, March, 2013)From the Back CoverThis book covers the statistical models and methods that are used to understand human genetics, following the historical and recent developments of human genetics. Starting with Mendels first experiments to genome-wide association studies, the book describes how genetic information can be incorporated into statistical models to discover disease genes. All commonly used approaches in statistical genetics (e.g. aggregation analysis, segregation, linkage analysis, etc), are used, but the focus of the book is modern approaches to association analysis. Numerous examples illustrate key points throughout the text, both of Mendelian and complex genetic disorders. The intended audience is statisticians, biostatisticians, epidemiologists and quantitatively- oriented geneticists and health scientists wanting to learn about statistical methods for genetic analysis, whether to better analyze genetic data, or to pursue research in methodology. A background in intermediate level statistical methods is required. The authors include few mathematical derivations, and the exercises provide problems for students with a broad range of skill levels. No background in genetics is assumed. Dr. Laird is a Professor of Biostatistics in the Biostatistics Department at the Harvard School of Public Health. Dr. Laird has contributed to methodology in many different fields, including missing data, EM-algorithm, meta-analysis, statistical genetics, and has coauthored a book with Garrett Fitzmaurice and James Ware on Applied Longitudinal Analysis. She is the recipient of many awards and prizes, including Fellow of the American Statistical Association, the American Association for the Advancement of Science, the Florence Nightingale Award, and the Janet Norwood Award. Dr. Lange is an Associate Professor in the Biostatistics Department at the Harvard School of Public Health. After his PhD in Statistics at the University of Reading (UK), he has worked extensively in the field of statistical genetics. Dr. Lange has been the director of the Institute of Genome Mathematics at the University of Bonn and has received several awards in mathematics and genetics. Dr. Lange is the developer of the PBAT package.About the AuthorDr. Laird is a Professor of Biostatistics in the Biostatistics Department at the Harvard School of Public Health. Dr. Laird has contributed to methodology in many different fields, including missing data, EM-algorithm, meta-analysis, statistical genetics, and has coauthored a book with Garrett Fitzmaurice and James Ware on Applied Longitudinal Analysis. She is the recipient of many awards and prizes, including Fellow of the American Statistical Association, the American Association for the Advancement of Science, the Florence Nightingale Award, and the Janet Norwood Award. Dr. Lange is an Associate Professor in the Biostatistics Department at the Harvard School of Public Health. After his PhD in Statistics at the University of Reading (UK), he has worked extensively in the field of statistical genetics. Dr. Lange has been the director of the Institute of Genome Mathematics at the University of Bonn and has received several awards in mathematics and genetics. Dr. Lange is the developer of the PBAT package.