

Book Reviews

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Mathematical and Statistical Methods for Genetic Analysis.

By Kenneth Lange. Springer Series in Statistics for Biology and Health. New York: Springer-Verlag, 1997. Pp. 265. \$54.95 (cloth).

Ever since Gregor Mendel deduced the probabilistic “laws” of heredity, mathematical and statistical methods have proved to be essential for genetic analyses. To keep pace both with the flood of genetic information pouring into journals and public databases and with our evolving knowledge of the complexity of genetic mechanisms, new models of genetic analysis are continually needed, particularly for traits measured in observational studies of humans. *Mathematical and Statistical Methods for Genetic Analysis* provides a solid bridge between modern genetics and advanced statistical methods, and it is filled with mathematical and statistical insights into the development of new genetic models. This book can be used not only as an advanced textbook for graduate students in statistics and mathematical modeling but also as a superb synthesis of recent statistical-genetics developments that any practitioner in this field will find immensely useful.

As implied by the title and explicitly stated in the preface, this book is not intended as a cookbook for performing a genetic study; rather, the anticipated audience of this book is students who are already sophisticated in theoretical statistics, as well as in calculus and linear algebra. Readers with a suitable background are guided through fundamental statistical and mathematical concepts and then through a keen demonstration of how these methods can be adapted for genetic research.

The book is composed of 13 chapters, of which the first describes the basic principles of population genetics; a brief appendix gives a summary of molecular genetics. Although these are nice summaries, I suspect that they would be too brief for mathematicians who have no background in biology; serious students of statistical genetics should look elsewhere for a fuller introduction to basic genetics. Chapter 2 covers the EM algorithm, with applications to ascertainment correction for segregation analysis. Chapter 3 discusses Newton’s Method and Scoring, which are indispensable methods for obtaining maximum-likelihood estimates, and it illustrates their application for empirical Bayes estimation of allele frequencies. Some topics related to categorical data analysis, such as the transmission/disequilibrium test and tests for clustering of multinomial data, are covered in chapter 4. Kinship coefficients and their generalizations to more than two people are clearly

presented in chapter 5, along with efficient recursive computational methods. These ideas of probabilistic descriptions of genetic relationships are key to genetic applications and are further expanded in chapter 6—for example, by partitioning the covariances of a pedigree into their genetic contributions.

Chapter 7 covers computational methods for pedigree analyses, a topic on which Lange has published extensively. Although this chapter is full of key ideas that will prove useful for both segregation and linkage analyses, it was disappointing to not see more discussion of the hidden Markov methods that are the basis of the Lander-and-Green algorithm used in popular genetic-analysis software. Nonetheless, the breadth of topics covered is impressive, and generous insights appear throughout. Chapters 8–13 cover the polygenic model (with novel approximations), Markov-Chain Monte Carlo methods, evolutionary trees, radiation-hybrid mapping, models of recombination, and Poisson approximation. The explanations offered for the Markov-Chain Monte Carlo approach and for Poisson approximation, two highly active areas of research, are self-contained and worth reading for any statistician interested in these topics. The general steps needed to derive a genetic model are provided in each chapter, but readers who wish to get the most out of this book should plan to sit down with pencil and paper to fill in the details. Each chapter includes 10–12 problems to work through that reinforce the mathematical concepts.

Mathematical and Statistical Methods for Genetic Analysis synthesizes many of the key statistical and mathematical topics that are used for genetic analyses. Lange indicates that this book represents his polished notes from years of teaching at UCLA and the University of Michigan, as well as a synthesis of his own published work. This bias toward Lange’s own work is perhaps the book’s greatest strength, because it allows him to offer deeper statistical and mathematical explanations for genetic analyses than are found in most other sources. This book is a must-read for students wishing to move into the field of statistical genetics, as well as for practicing statisticians who wish to adapt familiar statistical methods for genetic analyses.

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