Book Review

Am. J. Hum. Genet. 71:000, 2002

Quantitative Trait Loci: Methods and Protocols. Edited by Nicola J. Camp and Angela Cox. New Jersey: Humana Press, 2002. Pp. 376. $89.50.

In the past few decades, quantitative-trait approaches to the analysis of genetic disorders have become widely utilized. This type of approach is used in order to better characterize the phenotypic variation in and evolution of human traits. This book is a comprehensive and up-to-date resource for the analysis of quantitative-trait loci (QTL) for any investigator, regardless of his or her background. QTLs in humans, rodents, and agricultural settings are included, although, for the purposes of this review, only the section about humans will be discussed (i.e., Part 1). Included in Part 1 are six chapters, each focusing on a different type of analysis used for the mapping and detection of QTLs.

Because the editors have chosen a group of statistical geneticists who are all studying human QTL analysis, the information in this book is very current for a field that is constantly changing. Not only is the book comprehensive in the sense that it covers the theory behind association studies, parametric and nonparametric linkage analysis, linkage and association tests, and joint linkage and segregation analysis, but included in every chapter is a demonstration of that particular analysis, using available computer software.

Each chapter begins with a discussion of the theoretical basis of a particular analysis, followed by an applied section in which an example using available software is executed, using real study data. The theoretical discussions are well written and easy to read for the nonmathematician. The applied section of each chapter provides explicit details about how to prepare the files for each piece of software being demonstrated, as well as how to interpret the results. At the end of each chapter is a notes section, in which specific theoretical issues are elaborated upon and helpful hints are given for more efficient use of the software used in that chapter.

Of particular interest is the fourth chapter of Part 1, entitled “Nonparametric Linkage Analysis: II. Variance Components,” written by Angela J. Marlow, in which three of the predominant software packages (GENEHUNTER, SOLAR, and ACT) for variance components analysis are compared and contrasted through use of simulated data from Genetic Analysis Workshop 10. Even though all other chapters (i.e., chapters 1–3, 5, and 6) mention that there are multiple software packages available for use, only one program is used in each chapter for that specific analysis. For the researcher interested in choosing an appropriate program to use for his or her study, a software comparison for each type of analysis would have been helpful.

On the whole, this is an excellent resource for the mathematician wishing to review QTL analysis, as well as for the nonmathematician with no experience in this type of analysis.

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0002-9297/2002/7104-00XX$15.00