Book Review

Am. J. Hum. Genet. 66:1725, 2000

Analysis of Human Genetic Linkage, Third Edition. By Jurg Ott. Baltimore and London: The Johns Hopkins University Press, 1999. Pp. 405. $55.00.

The golden age of linkage analysis continues, as disease gene mapping and cloning move forward at an unprecedented rate. Dense maps of microsatellite markers are in common use, and much denser maps of single nucleotide polymorphisms soon will be available. Although mapping genes for common familial (complex) diseases remains a daunting task, the anticipated completion of the human DNA sequence, the growing human transcript map, and the prospect of a near-complete catalog of common human genetic variants all offer hope for more rapid success. Improved statistical methods and more-powerful computational resources also are playing an important role in moving the field of gene mapping forward. With these continuing changes, the appearance of the third edition of Dr. Ott's now classic text is most welcome.

The goal of the book remains the same: to provide a concise, easy-to-read introduction to human linkage analysis. Like the revised edition, the third edition includes chapters on basic genetic principles, genetic loci and genetic polymorphisms, aspects of statistical inference, basics of linkage analysis, the informativeness of family data, multipoint linkage analysis, penetrance, variability of the recombination fraction, numerical and computerized methods, and inconsistencies. Although the titles are the same, additions and modifications have been made in each of these chapters. The reference list also has been updated to reflect the substantial advances in the field in the past 8 years. A larger, more-readable typeface and judicious use of subheadings make for a more reader-friendly text.

In response to the growing emphasis on complex diseases, the author has replaced the chapter on linkage analysis with disease loci with chapters on linkage analysis with Mendelian disease loci, nonparametric methods, two-locus inheritance, complex traits, and quantitative phenotypes. The result is a much more extensive treatment of sib-pair and relative-pair methods of linkage analysis (including both current nonparametric and semiparametric approaches) and inclusion of two-trait locus methods and tests of linkage disequilibrium.

Just as for the first two editions, an understanding of basic algebra and equations is required. Some knowledge of single-variable calculus and probability is necessary to follow the mathematical arguments. However, the book is well signposted, so that the mathematically less inclined reader can skip the more mathematically challenging sections. The book remains informal rather than technically rigorous. The more mathematically inclined reader might wish to consult other books, including those by Lange (1997), Weir (1996), and Thompson (1986). However, none of these other books specifically focuses on linkage analysis, so that even for the mathematically inclined, Dr. Ott's book continues to fill an important niche.

The author is to be commended for his efforts to improve the book not only at times of publication of a new edition but also in between, by use of the internet. He encourages reader comments and keeps a list of corrections on his web site (http://linkage.rockefeller.edu/ott/corr-ott3.htm). Also notable is a page with remarks on new developments and relevant references (http://linkage.rockefeller.edu/ott/booknotes.html).

As with any book, one can quarrel with details of emphasis. Although the chapter on quantitative traits is a welcome addition, the subject is treated only briefly, and, in particular, modern variance-components methods of linkage analysis are given less than a page. Even the rather extensive new material on complex traits only scratches the surface of a very important area.

In summary, a good and useful book has been updated and improved. Dr. Ott's book remains the standard reference on human gene mapping, and the new edition merits a place in the library of anyone with a serious interest in the topic.

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0002-9297/2000/6605-0032$02.00