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BOOK REVIEWS

Analysis of Human Genetic Linkage. By JURG OTT. Baltimore: Johns Hopkins University Press. 1985. 223 pages. £33.60. ISGN 0 8018 2485 0.

Anyone who has been involved in human genetic linkage over the past few years will appreciate how complex the field has become. Although there are several excellent textbooks available which give a full account of the basic concepts, they do not cover the more complex situations arising today. I was therefore quite excited to learn that Jurg Ott's book was now available. Here was an opportunity for all the new ideas to be brought together.

The book is prefaced with a note to the reader explaining the purposes of the book. One is to provide a guide to practitioners, to assist them in their analyses and to highlight possible pitfalls, and the other is to present a unified likelihood approach to linkage analysis. The main emphasis is on the detection and measurement of linkage and on the formation of linkage maps. However, very little is said about the practical applications of genetic counselling. Inevitably, the book begins with a brief summary of Mendelian inheritance, genetic linkage and gene mapping. The second chapter introduces the statistical concepts required, such as maximum-likelihood estimation, hypothesis testing and lod scores. A chapter on numerical methods outlines the calculation of lod scores, using examples, but points out that explicit formulation of the likelihood is only feasible for small families and simple modes of inheritance. Relevant computer programs in use at various places are described, including one, available from the author, which runs on an IBM personal computer. The remainder of the book concentrates on recent developments. There are many situations where standard assumptions no longer hold, and each is discussed. For example, the recombination rate may depend on sex or age, or may show interfamilial differences requiring heterogeneity tests. Inconsistencies may be found in the recombination rate owing to ascertainment, misclassification or misspecificion of the model. Penetrance may be reduced, age or sex dependent, or the loci may be epistatic. Marker loci may even need special consideration as in the HLA system. Finally, multipoint linkage and the practical problems of sample size and genetic counselling are covered. An appendix gives Fortran listings of programs which find maximum-likelihood estimates of the recombination rate and confidence intervals from lod-score data and conduct heterogeneity tests.

The book provides an excellent and remarkably up-to-date summary of the techniques used in linkage analysis currently fragmented throughout the literature. The more mathematically demanding sections are said to be highlighted so that they can be omitted by those with more practical objectives. Despite this I found the tone of the book very mathematical throughout and more suited to quantitative geneticists than medical practitioners. Many of the sections are also relevant to those working with other species.

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General and Quantitative Genetics (*World Animal Science*, *A4*). Edited by A. B. CHAPMAN. Amsterdam. 1985. xiv+408 pages. US $92.50/Dfl. 250.00. ISBN 0 444 42203 X.

Although much practical animal breeding is common sense – if you want to improve a population, select the best animals – it is based on a firm theory of quantitative genetics. This theory, and results obtained from many selection experiments, enable the breeder to be confident that the selection he practises is likely to bring reward, and it enables him to design his improvement programme and to use data collected in an optimal way. There has been little need for the student or practitioner to know any genetics other than basic Mendelism and advanced quantitative genetics. We are now at a stage where there may be a major revolution in methodology through the use of recombinant DNA techniques; and even if the revolution never comes, the student requires much more knowledge and understanding of molecular genetics if he is to keep up with the new literature.