

BOOK REVIEW

Statistical Genetics

By PREM NARAIN; Wiley Eastern Limited, New Delhi, 1990; 599 pages; Rs 300

This book covers two areas of genetics traditionally known as 'population genetics' and 'quantitative genetics'. While there is some overlap, these two areas of genetics remain quite distinct. About 40 per cent of the book deals with population genetics; the remaining deals with quantitative genetics. Several pages are devoted to biological concepts and definitions that are necessary for understanding the statistical formulation and treatment.

The book is most useful to students and researchers who have graduated with a statistics major. A prior course in genetics will be helpful, but is not a prerequisite. While the major portion of the book may be difficult for biologists without training in statistics, several sections of the book will be helpful to those biologists who are quantitatively minded. The breadth of the book makes it very useful as a reference book to researchers in the field of biostatistics. The book is well written and the statistical treatment is sound. The author has often given multiple approaches to solving a problem, which adds to the flavour and usefulness of the book. In many instances, estimators of parameters are derived using alternative methods of statistical estimation, viz. least-squares, minimum chi-square and maximum likelihood.

The book has 18 chapters and an appendix. It begins with a brief introduction to the principles of Mendelian genetics. In chapter 2, the problems of studying segregation of alleles at a single locus and of cosegregation of alleles at two loci are formulated statistically, parameters identified, and estimates of parameters based on different data structures obtained. In chapters 3 and 4, the behaviours of gene and genotype frequencies are studied under different mating systems in large ('infinite-size') populations and when various evolutionary forces (e.g. mutation, natural selection, migration) are in action either singly or jointly. Chapter 5 deals with the stochastic problems encountered when population size is finite. In chapter 6, the author discusses how continuous variation can arise from genes with discrete effects, and makes statistical assessments of these effects. Different genetic models for a trait yield different levels of correlation between relatives; these are discussed in chapter 7. Chapters 8 through 17 belong primarily to the domain of 'quantitative genetics'. In these chapters, the author discusses many issues that are of importance in plant and animal breeding. These include genotype–environment interactions (chapter 8); estimation of heritability (chapter 9); intensity, limits and responses to selection (chapters 10 and 11); evaluation of testing and selection schemes (chapters 12 and 13); methods and evaluation of strategies for improving multiple characters (chapter 14); retention of genetic diversity under breeding schemes for improvement (chapter 15); diallele and partial diallele crosses (chapters 16 and 17). The book ends with a 'Summary and conclusions' chapter. Some optimal breeding plans are included in an appendix.

Data structures in humans often lead to interesting and difficult statistical problems

(e.g. in linkage detection), some of which could have been discussed in this book. Some other aspects, e.g. estimation of effective population size, also deserve more elaborate discussion. The topic of migration as an evolutionary force is inadequately discussed. While it is easy to list the various topics that the book does not cover, it must be stated that the author has done a commendable job of putting together enormous material in a very readable and statistically sound manner. The book should find a place on the bookshelf of every statistical geneticist; at the stated price, it is a bargain.

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