From References: 19 From Reviews: 0

MR1224677 (94i:92006) 92D10 92-01 Nagylaki, Thomas (1-CHI-EV)

★Introduction to theoretical population genetics. (English summary) Biomathematics, 21.

Springer-Verlag, Berlin, 1992. xii+369 pp. \$59.00. ISBN 3-540-53344-3

As the author states at the beginning of his preface, this book covers those areas of theoretical population genetics that can be investigated rigorously by elementary mathematical methods. Fortunately, these areas include several of the most important ones. The major mathematical theme of the book is the dynamical analysis of recursion relations. Many exact and approximate techniques for investigating linear and nonlinear recursion relations in one dimension and in several dimensions are developed and applied. Although only linear algebra, calculus, and a little bit of differential equations and probability theory are required as mathematical prerequisites, and although the presentation is very clear (and concise), the book is not easy to read. In many places some skill in algebraic manipulations is required, and the reader should always have pencil and paper at hand.

Here is a short overview of the contents of the book. The introductory chapter gives some background in elementary genetics, and in evolutionary theory. Chapter 2 presents the basic equations for selection, mutation, migration, and random drift in asexual haploid populations, as well as their analyses. In Chapter 3, panmictic populations in the absence of evolutionary forces are treated (the Hardy-Weinberg law, X-linkage, population subdivision, finite populations). Of central importance is Chapter 4, which investigates selection at an autosomal locus (multiple alleles, discrete- and continuoustime models, inbreeding, mutation and selection, density and frequency dependence are some of the topics). The next three chapters are devoted to nonrandom mating, migration and selection, and X-linkage, respectively. Chapter 8 studies selection at two loci, beginning with a formulation of the general *n*-locus model. Two multiallelic and two diallelic loci are studied in detail, and the continuous-time model is derived rigorously. Inbreeding and random drift are studied in Chapter 9. Topics include calculations of the inbreeding coefficient from pedigrees, identity relations between relatives, regular systems of inbreeding, concepts of effective population size, etc. The final Chapter 10 is devoted to quantitative genetics. It treats the decomposition of variance, the correlation between relatives (with panmixia and assortative mating), the change in variance due to assortative mating, and finally, selection, and mutation-selection balance.

The first eight chapters are a thoroughly revised, extended, and updated version of another book by the author [Selection in one- and two-locus systems, Lecture Notes in Biomath., 15, Springer, Berlin, 1977; MR0490041 (58 #9402)]. Chapters 9 and 10 are completely new. An important part of the book is the problem sections which include many illuminating examples, and provide hints and references to further results and literature. The comprehensive subject index is very useful.

This book is a valuable addition to the literature on mathematical population genetics and is warmly recommended to students and researchers in biomathematics.

Reinhard Bürger

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