

The present book by Tom Nagylaki provides an excellent complement to the existing literature, as it concentrates on in-depth treatments of some of the most important models. Its main emphasis is on deterministic models, that is, on recursion and differential equations as they are used, for example, to describe gene frequency changes in large populations. 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. Let me now present a short overview of the contents of the present 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 continuous-time 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 thoroughly revised, extended and updated version of the author's Springer Lecture Notes *Selection in One- and Two-Locus Systems*, published in 1977. Chapters 9 and 10 are completely new. An important part of the book consists of the problem sections, which include many illuminating examples, and provide hints to further results and literature. The comprehensive subject index is very useful.

Of course, there are important areas of theoretical population genetics that are not covered by this book, or only treated in an introductory way. Among these are the advanced theory of gene frequency change in finite populations (e.g. diffusion approximations), the neutral theory and related topics, various areas of quantitative genetics, or the theory of geographical

variation. This list is somewhat arbitrary but includes fields to which the author provided contributions in the past, and/or fields that would deserve a similar careful treatment.

In my opinion, the main strengths of Nagylaki's book are that it (i) provides precise, general formulations of some of the most important models in population genetics, and states the assumptions explicitly, (ii) investigates the models by rigorous mathematical methods, and (iii) explains and demonstrates abstract and more complicated results in terms of simple, well-chosen examples.

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. At many places some skill in algebraic manipulations is required, and the reader should always have pencil and paper at hand.

To summarize, I recommend this book to every student and researcher in population genetics who feels some need for an in-depth understanding of some of the basic models in population genetics, or who is looking for more recent developments in theoretical population genetics than those covered by the books of Crow and Kimura, and Ewens.

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#### **New gene and karyotype standards: Livestock, horse, fish**

We draw the attention of our readers to the following new standards for karyotypes of domestic animals and the horse, and gene nomenclature for protein coding loci in fish. They should help authors of papers on the genetics and cytology of these organisms, and the editors of *Genetical Research* would appreciate their use.

(1) *ISCNDA 1989: International System for Cytogenetic Nomenclature for Domestic Animals (1989)*. Reprinted from *Cytogenetics and Cell Genetics*, 53 (2–3), 65–79 (1990). Reprints available from Dr Helene Hayes, INRA, Centre de Recherches de Jouy-en-Josas, Domaine de Vilvert, 78350 Jouy-en-Josas, France.

This report of the Second International Conference on Standardization of Domestic Animal Karyotypes gives photographs of standard GTG-banded, QFQ-banded, RBA- and RBG-banded cattle karyotypes, and diagrammatic comparisons of their G- and R-bands, RBA- and RBG-bands of sheep and goats, and a combined haploid karyotype of RBG-banded chromosomes of goat, sheep and cattle, together with comments on various bands, and also tabulates the confirmed similarities between G-banding patterns of

sheep and cattle chromosomes. The above conference proposes that papers on these species should only be accepted if they follow the recommendations and standards of ISCNDA 1989.

(2) *Standard karyotype of the domestic horse (Equus caballus)*. By C. L. Richer, M. M. Power, L. R. Klunder, R. A. McFeely and M. G. Kent. *Hereditas* **112**, 289–293 (1990). This paper gives a photograph comparing unbanded (Giemsa-stained), C-banded and GTG-banded horse chromosomes at the level of 400 bands, and a photograph of the RBG-banded horse karyotype at the level of 550 bands, which shows the active and inactive X chromosome.

(3) *Gene Nomenclature for Protein-Coding Loci in Fish*. By James B. Shaklee, Fred W. Allendorf, Donald C. Morizot and Gregory S. Whitt. *Transactions of the American Fisheries Society* **119**, 2–15 (1990).

The authors constitute the Fish Genetics Nomenclature Committee of the Fish Genetics Section, American Fisheries Society, and reprints are available from Dr James B. Shaklee, Washington Department of Fisheries, 115 General Administration Building, Olympia, Washington 98504, USA. The above paper contained some errors in Table 1 due to typographical misplacing of prefixes of enzyme abbreviations for guanylate kinase through alpha-mannosidase, so

authors should make sure that they have the correct Table 1. This paper is important in providing guidelines for gene and locus symbols as well as the proteins they code for, and an attempt has been made to make the fish system as similar as possible to the human gene system. It is proposed to use capital letters for both gene and protein symbols, italics distinguishing the former from the latter. Locus symbols, it is strongly recommended, should be immediately followed by, and allele symbols immediately preceded by, an asterisk; and detailed instructions are given for expressing a variety of complex gene/protein formulae. These have not yet been universally accepted, and the editors of *Genetical Research* would not at present necessarily insist on complete adherence to this system. Gene symbols and names are far from being consistent between organisms and there is no likelihood of their being made so. Those with an interest in gene symbols should read the 3-page appendix at the end of the Fish Nomenclature paper, which discusses the varied opinions of twenty-five reviewers of the proposals in an earlier draft.

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