and what is still in the pipeline and may turn out to be incorrect. So these chapters also leave us in the air. The real problem here is that, while there is quite an extensive list of references, it is not connected up with the numerous statements in the text, so that one does not know where to look for further information on such exciting topics as the use of somaclonal variation, plants with a built-in insecticide (does eating such plants do one any harm?), Calgene's 'Flavour Saver Gene' in tomatoes (since Calgene is an American company, this should surely have been spelt 'Flavor'), stealing a virus's clothes to make tomato and potato plants resistant to potato X and potato Y virus, and so on. For those of us – (geneticists, MPs, MEPs as well as the person in the street) worried about the speed of progress and possible dangers inherent in such projects, this book is not sufficiently helpful. Can we look forward to an expanded version, with a fuller list of references properly integrated into the text? This would of course be a major undertaking for one author, let alone a committee; and meanwhile knowledge, published and unpublished, accumulates at an awe-inspiring rate.

So, in my opinion, this book fails to fulfil the expectations of its title and is likely to be found frustrating by many of its readers. But it will at least give the reader many good talking points for parties and dinner tables, and the exciting prospects of which we are given a taste should help to line the empty coffers of some of our university research teams.

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Human Cytogenetics: A Practical Approach, Volume II: Malignancy and Acquired Abnormalities (second edition). Edited by D. E. ROONEY and B. H. CZEPULKOWSKI. IRL Press at Oxford University Press. 1992. 293 pages. Price Paper £22.50, ISBN 0 19963313 4. Spiralbound £30.00 ISBN 0 19 963290 1.

The second edition of this book (the first appeared in 1986) has undergone a form of mitosis resulting in two 'daughter' volumes of equal size but very different content.

The second of these volumes is entitled *Malignancy and Acquired Abnormalities*. Two-thirds of this volume deals with the cytogenetics of malignancies. As befits our current state of knowledge, five chapters are devoted to leukaemia cytogenetics followed by a chapter on solid tumour cytogenetics. The remainder of the book deals with Mutagen-induced Chromosome Damage; Breakage Syndromes; Somatic Cell Hybrids; Flow Sorting and Microdissection. Most of the contributors are UK cytogeneticists working in diagnostic laboratories, and all have a great deal of practical experience.

The section of the book which will probably be referred to most frequently by practising cytogeneticists is that on leukaemia cytogenetics. A useful overview chapter on methodology is followed by three largely descriptive chapters on the cytogenetics of myeloid, acute lymphoid and chronic lymphoid leukaemias. These chapters are well illustrated with pictures of chromosomes of varying quality: accurately reflecting what is seen down the microscope! These chapters also sensibly address the question of what approach to analysis should be adopted. References to the use of other techniques (see fluorescence in-situ hybridization) to confirm and support conventional cytogenetic findings could perhaps have been expanded. This section of the book is rounded off by a stimulating review of the role of cytogenetic findings in leukaemia. This chapter is particularly perspicacious in that it is written by a clinical haematologist. Anyone who remains to be convinced that the cytogenetics of leukaemia is little more than a glorified form of stamp collecting should read this chapter.

There is an adequate index and a useful glossary of haematological terms together with a list of reagent suppliers.

This volume and its 'sister' are aimed primarily at practising cytogeneticists as a technical *vade mecum*, and as such can be recommended. The nature of the information is such that it won't date too quickly, and at the asking price is well worth the investment.

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Introduction to Theoretical Population Genetics. By THOMAS NAGYLAKI. Spinger-Verlag. 1992. 369 pages. Price £35.00. DM. 98.00. ISBN 3 54 053344 3.

Mathematical models and methods have a long history in genetics, tracing back to Gregor Mendel, who used elementary mathematics to calculate the expected frequencies of the 'genes' in his experiments. In fact, he had studied mathematics and physics (at the University of Vienna), and this educational background may have influenced him to introduce the atomistic approach to heredity, and to formulate abstract models. Later, Hardy and Weinberg used simple mathematics to derive what is now called the Hardy–Weinberg law. Since the pioneering work of Fisher, Wright and Haldane, mathematical models and methods have become common in population genetics. Numerous good textbooks and monographs have been published, many of these treating probabilistic or statistical aspects of theoretical population genetics. Others, like those of Crow and Kimura, or Ewens, give a broader overview of mathematical models in population genetics.

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

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