

assignment is considered firm then the catalogue number is preceded by an asterisk. For example, traits thought to be homologous to haemophilia A in man (MIM number 30670) are listed as '*30356 Coagulation factor VIII (Haemophilia A; classical haemophilia; F8C) [30670]' and descriptions and references are given for homologues found in cat, cattle, dog, horse and mouse. Similarly, homologues for human testicular feminization (MIM number 31370) are listed as '*30494 Dihydrotestosterone receptor (testicular feminization; androgen receptor deficiency; DHTR) [31370]' and entries are for chimpanzee, cattle, horse, mouse, pig and rat.

The widespread use of molecular techniques has revived interest in comparative genetic mapping. Although this inevitably means that lists of genetic loci are likely to be out of date before they are published, such lists are, nevertheless valuable sources of information. This catalogue is an important initiative and, as more data becomes available, I hope it will be updated and expanded to include DNA sequence data from different species and more comparative maps to supplement those of man and mouse that are included in the Introduction. This book is modestly priced and will be a useful reference work for mammalian geneticists who have a special interest in the X chromosome or comparative mapping and may also be a valuable resource for researchers who are looking for animal models of human X-linked conditions. It should be available in all academic libraries that encompass animal or human genetics.

References

- Ohno, S. (1967). *Sex Chromosomes and Sex-linked Genes*, ch. 4, pp. 46–73. Berlin: Springer-Verlag.
- Green, M. C. (1981). *Genetic Variants and Strains of Laboratory Mice*. Stuttgart: Gustav-Fischer-Verlag.
- Lyon, M. F. & Searle, A. G. (1989). *Genetic Variants and Strains of the Laboratory Mouse*. Oxford University Press.
- McKusick, V. A. (1986). *Mendelian Inheritance in Man: Catalogs of Autosomal Dominant, Autosomal Recessive, and X-linked Phenotypes*, 7th edn. Baltimore: Johns Hopkins University Press.

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Advances in statistical methods for genetic improvement of livestock. Edited by D. GIANOLA and K. HAMMOND. Advanced Series in Agricultural Sciences 18. Springer Verlag. 1990. 538 pages. DM 138. ISBN 3 540 50809 0.

This book is a collection of papers presented at an international symposium held in Armidale, Australia

in February 1987 and was organized by the editors. Despite the three-year delay in publication this volume represents an excellent summary of the last 20 years of research in statistical methods used in animal breeding, as well as highlighting the areas of controversy and needs for future research. The book comprises 23 chapters in 7 sections (although the allocation of chapters to sections is sometimes arbitrary). There is probably a slightly greater bias (6 out of 23 chapters) towards Bayesian methods (not surprising, given prior information on one of the two organizer/editors) than the last 20 years of research (or genetic evaluation on real data) merit, but the side-by-side comparison of frequentist and Bayesian approaches in a single volume is useful and perhaps represents the emphasis for the next 20 years of research.

The symposium was elite, with 12 invited authors/speakers, each presenting two (nearly) papers on general topics for which they are internationally renowned. The calibre of the authors is sufficient to assure that this is a 'must' for all statistically orientated animal breeders.

The first section entitled 'General' introduces overviews of three main themes of the symposium, namely mixed model methodology from the frequentist (Henderson) and Bayesian (Gianola, Im, Fernando and Foulley) perspectives and methods for differentiating between alternative genetic models of inheritance (Elston). The paper of the late Charles Henderson is a brief historical overview of statistical methods in animal breeding, with insight through his personal views, and culminating in his own pioneering work of the last 40 years in the development of BLUP (Best Linear Unbiased Prediction) which forms the basis of many subsequent chapters of the book. From this historical account one might, however, be misguided into thinking that advances in statistical methods have occurred solely in North America!

The second section on design of experiments and breeding programmes begins with a paper by Hill which reviews optimal use of experimental resources in the design of breeding programmes to estimate genetic parameters. In particular, the author summarizes his own numerous contributions to this area in combination with more recent work. Next, Kennedy reviews mixed model methodology and its use in analyses of experimental records and in so doing helps remind mixed modellers about genetics. Fernando and Gianola investigate optimum designs for sire evaluation schemes, demonstrating through simple examples how to maximise genetic progress, but in another chapter, Dempfle, again using simple examples, warns that designs which maximize short-term progress are not necessarily the same as designs which maximize long-term progress.

Section III, on estimation of genetic parameters, begins with an excellent summary of likelihood based methods for variance component estimation, concentrating particularly on computational algorithms

(Newton–Raphson, Fisher’s Scoring, EM). The section concludes with two chapters on variance component estimation for more specialized situations, namely binary response data (Knuiman and Laird) and nonlinear models (Smith). Section IV, on prediction and estimation of genetic merit, begins with two chapters (Gianola, Im and Macedo; Harville) on the general Bayesian framework for prediction of breeding values, but the repetition is not a bad thing for the uninformed. Harville’s paper is particularly useful in its systematic comparison of Bayesian and frequentist approaches. The final chapter in this section is a comprehensive examination of the important, but little researched, area of connectedness (Foulley, Bouix, Goffinet and Elsen).

Section V covers prediction and estimation in nonlinear models and begins with a general review of methods (Thompson) followed by contributions on specific topics: growth models (Laird), censored observations (Smith), and discrete polygenic traits (Foulley, Gianola, and Im). Section VI on selection and non-random mating again begins with the frequentist (Henderson) and Bayesian (Fernando and Gianola) viewpoints, the frequentists’ aim being to ensure that the property of unbiasedness is maintained despite selection or non-random mating, whilst the Bayesians are happy to sacrifice unbiasedness to achieve faster genetic progress, although a generalised solution is elusive. In the final chapter, Dempfle examines the use of the relationship matrix and highlights problems arising from a genetic viewpoint which perhaps both the frequentists and Bayesians are likely to forget. His use of simple examples in this case however is somewhat misleading.

The final section on statistics and new technology begins with a review of methods (Hill and Knott) and a general linkage method (Elston) for the detection of major genes. This is an area where perhaps most advances have been made between the symposium in 1987 and the publication of the book. The final chapter by Kennedy and Schaeffer considers how records of animals, resulting from new reproductive technologies (embryo transfer, sexing, cloning, etc.) can be included in genetic evaluation procedures.

Each section concludes with a summary of the discussion following the oral presentation of the papers. At first sight, these summaries appear superfluous but they can highlight the areas of controversy to the uninformed or can provide entertaining reading as one speculates as to which ‘member of the audience’ raised a particular point.

This book will serve as an excellent reference for many years to animal breeders, quantitative geneticists and statisticians working in this area; a book I am sure they will want on their own bookshelf rather than just in the library. There is a considerable void of advanced textbooks for graduate students in this field and the review chapters of this volume in particular

could provide essential reading material for graduate courses.

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Genes in Populations. By ELIOT B. SPIESS, 2nd edn. New York, USA: John Wiley & Sons. 1989. 774 pages. Cloth price £59.00. ISBN 0 471 84973 1.

This textbook deals with conventional population genetics topics, containing both theory and experimental results as well as exercises at the end of the chapters and an extensive statistical and mathematical Appendix.

The dust cover claims that ‘The presentation... is at a level readily accessible to those with a background in basic genetics and mathematics.’ However, beginning students in population genetics are likely to find this text very hard going, as it is difficult to read and long winded. It is much more difficult to follow than Falconer’s highly acclaimed *Introduction to Quantitative Genetics*.

Is this book suitable for graduate students and professionals? It certainly has more the flavour of a comprehensive literature review than a beginning textbook. It provides a fine historical review of population genetics, albeit with a North American bias. References as recent as 1988 are included, but only about 30% are 1980 and later compared to over one-half in Maynard Smith’s *Evolutionary Genetics*.

The scope of population and evolutionary genetics has expanded markedly since the appearance of the first edition, with molecular evolutionary genetics (multigene families, unequal crossing over, gene conversion, transposons, DNA sequence studies, DNA fingerprinting, mitochondrial DNA, etc.), evolution in age structured populations, evolutionary stable strategies, work on prokaryotes, evolution of life, speciation, punctuated equilibrium, etc. assuming a much greater importance. While the dustcover makes much of revision to emphasise developments since the first edition, particularly those in molecular genetics, the flavour of the book reflects the issues current when the first edition was published in 1977. Chapter headings in the two editions are the same, as is much of the text. New developments are predominantly treated as minor additions, rather than as topics of prominence. This contrasts starkly with Maynard Smith’s *Evolutionary Genetics* where much of the text is concerned with consideration of these newer topics.

In a few places the contents of the book are uncritical or misleading, especially in sections dealing with quantitative genetics. The comments on Yoo’s long-term selection studies in *Drosophila* (p. 190) fail to mention that mutations arising in long-term selection lines made significant contributions to genetic variation and selection response in those lines.