methods which will be necessary for some potential medical applications. These are aspects of the technique that will surely be important in the next few years. Alternative technical books would be *In situ Hybridisation. Applications to Neurobiology* – (edited by K. L. Valentino *et al.* (1987), Oxford University Press), or *In situ Hybridisation. Principles and Practice.*' (edited by J. M. Polak and J. O. D. McGee (1990) Oxford University Press). As a compendium of scientific reviews, the book will probably be more useful in the library than on your own bookshelf since much of the data described will be irrelevant to a single user. In this sense, the strength of *in situ* hybridization, its diversity of application, is the book's Achilles' heel.

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X-linked Traits; A Catalog of Loci in Nonhuman Mammals. By JAMES R. MILLER. 1990. Cambridge University Press, 198 pages. £25 ($39.50) hardback. ISBN 0 521 37389 1.

The mammalian X chromosome has long been a subject of fascination for geneticists both from the view of X-linked inheritance and the mechanism of dosage compensation by X chromosome inactivation. Susumu Ohno (1967) postulated that 'there should be extensive homology of the X-linked genes among placental mammals'. Evidence supporting this postulate, now widely accepted and known as Ohno's Law, has continued to accumulate since 1967 and no exceptions are known for placental mammals. The situation for marsupials and monotremes is less clear cut. Although some of the genetic loci that are X-linked in placental mammals are also X-linked in non-placental mammals, others have been shown to be autosomal.

This book is a catalogue of X-linked genetic traits in non-human mammals and includes entries for a monotreme (platypus), several marsupials (dasyurids, kangaroos, wallabies and Virginia opossum) as well as about 30 species of placental mammals (including African green monkey, American mink, baboon, black rhinoceros, capouchin monkey, cat, chimpanzee, chinese hamster, cattle, deer mouse, dog, donkey, gibbon, gorilla, hare, horse, Indian mole rat, Indian muntjac, mouse, mouse lemur, orangutan, owl monkey, pig, rabbit, rat, red fox, rhesus monkey, sheep, Syrian hamster, vole and wood lemming). The main catalogue follows 22 pages of Introduction with references, two Appendices with references ('X-linked DNA segments in the mouse' and 'the mammalian Y chromosome') and a few pages of explanatory notes on using the catalogue. The Introduction includes several tables of X-linked loci in different species, emphasising the possible homologies, and a diagram comparing the map positions of homologous X-linked loci in mouse and man. After the catalogue, there is an author index and a subject index, which provides an alphabetical list of over 150 names and synonyms of X-linked genetic traits but does not list the various mammalian species alphabetically. Tables 2 and 4 in the Introduction give some idea of the extent of the available data. Table 4 illustrates that the four genetic loci that encode the enzymes glucose-6-phosphate dehydrogenase, α-galactosidase, phosphoglycerate kinase and hypoxanthine guanine phosphoribosyl transferase have been linked to the X-chromosome in a large number of species (25, 20, 19, 18 species respectively). Table 2 lists the number of known (plus suspected) X-linked loci for man and 17 non-human species. This number is high for man (130 known + 164 suspected loci) and mouse (66 + 5) but very much lower for all the others. After man and mouse, the three entries with the highest number of X-linked traits are dog (12 + 3), a group of several species of non-human primates (total of 10 + 1 for all species) and cattle (9 + 3). Moreover, as Professor Miller points out, if the data on the above four enzyme loci are omitted only two non-human species have more than five loci available to compare.

Linkage data and descriptions of X-linked traits in the mouse are readily available elsewhere and have been compiled in two editions (Green, 1981; Lyon & Searle, 1989). However, the real value of Professor Miller's catalogue is the descriptions of the X-linked traits of the other non-mammalian species and the putative homologies between traits in different species. This information is not so readily available and the catalogue provides a wealth of comparative information that has been gathered together, after painstaking research, into a well-organized and useful reference work for comparative geneticists. Professor Miller has carefully organized his catalogue so that it can be used as a companion volume to McKusick's (1986) well-known catalogue of human genetic traits. The MIM numbering system is used and helpfully, these numbers are included in both the author index and the subject index. The main catalogue, documenting just over 100 X-linked traits, starts on page 47 with a description of trait 30006 (absent pinnae in the black rhinoceros) and ends on page 173 with trait 31499 (yellow mottling in the mouse). The number of species sharing a homologous trait varies from one (as in the above two examples) to about 20 (the four enzymes mentioned above). Each trait is listed by number and name, followed by synonyms or abbreviations and MIM number (if different from the assigned catalogue number). Names sometimes differ from those used in MIM because they have been chosen to describe the gene product or primary effect of the locus rather than the name of a particular mutation. If a condition is homologous to a human condition and the same name has been used, the catalogue number is the same as the MIM number. If the

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 (Hemophilia A; classical hemophilia; 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.

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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