BOOK REVIEWS

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The Genetical Analysis of Quantitative Traits. Michael J Kearsey, Harpal S Pooni. (Pp 381; £27.50.) UK: Chapman & Hall. 1996. ISBN 0-412-60980-0.

This soft back textbook will satisfy the curiosity of students and investigators who wish to understand both the biology and associated statistical approaches that are necessary to study quantitative inherited traits in experimental organisms. The authors have built on years of teaching plant and animal genetics to students at the School of Biological Sciences, Birmingham, and this experience has influenced the style and organisation of the text. The book includes features and details that will encourage the reader to persist with the difficult subject matter; chapters are well organised, there are plenty of informative diagrams as well as one or two photographs, key points are summarised at the end of each chapter, and test questions and solutions are tucked away at the very end of the book. The balance between prose and algebra seems perfectly judged to me. It is an inviting book to dip into; I found the chapter entitled "Predicting the response to selection" particularly enlightening, which will stand me in good stead if I am ever asked to advise Sheikh Mohammed Maktoum on his plans to breed potential classic flat racing winners.

I try to keep an eye out for new methods for analysing quantitative data in experimental organisms, as they occasionally provide good ideas that can be implemented on human data. From this perspective, I have noted a few curious omissions. For example, there is a detailed description of RFLPs but just a mention of RAPDs and microsatellites which predominate contemporary mapping efforts. I was unable to find any reference to selective genotyping, an important concept with far reaching implications that was proposed by

Eric Lander and David Botstein to reduce the burden of genotyping during genome wide search for QTLs. Rodent models of hypertension and other such phenotypes have been intensively studied in recent years but regrettably they do not seem to be specifically covered.

The authors rarely explore the human field, but where they do the balance and choice of topic for discussion strike me as whimsical and might perplex the casual reader. The short section on "Studies of human populations" opens with a discussion of heritability of intelligence and personality, political correctness, and scientific fraud (the "Burt" affair); a latter section discussing selective evolutionary pressures in human populations returns to IQ as its theme. Surely there must be more pertinent examples for discussion?

I do not see that this book will become a mainstream text for human geneticists preparing to undertake studies of quantitative data. Human data consist of diverse family structures and experimental designs that have led to specialised statistical approaches, such as mixed model segregation analysis, measured genotype analysis, and combined linkage/segregation analysis; these topics are beyond the scope of Kearsey and Pooni's book. It does, however, provide a clear explanation of basic concepts, comprehension of which is necessary in order to interpret more complex tests. Geneticists undertaking quantitative analysis of plant or animal data will want to have their own copy ready to hand. For those studying human data, a library copy will suffice.

MARTIN FARRALL

Variation in the Human Genome. Editors D Chadwick, G Cardew. (Pp 329; £52.50.) Chichester: John Wiley. 1996. ISBN 0-471-96152-3.

Good books on variation in the human genome are thin on the ground and usually patchy or superficial in their coverage of the area. This book is an exception. Based upon a Symposium entitled *Variation in the Human Genome* held in London in June 1995, this volume in the Ciba Foundation Symposium series is commendably broad in its scope. The book is divided into four sections: Chapters 1-3 cover variation in human populations, its origins and its evolution, chapters 4-7 discuss variation in mendelian disorders, chapters 8-12 focus on genetic variation and causation in complex traits, while chapters 13 and 14 cover evolutionary principles and methods for aetiological inference. Chapter 15 is an overview by David Weatherall on selective forces and the prevalence of specific genetic diseases. Each chapter is followed by a (usually brief) participant discussion section.

Although perhaps a little forced in places, and despite a tendency for some discussants to contribute disproportionately, these exchanges are on the whole both stimulating and thought provoking.

Chapters on specific diseases (phenylketonuria, cystic fibrosis, β thalassaemia, and fragile X syndrome) provide numerous examples of how the frequency of disease alleles is influenced, or even determined by, such factors as selection, population migration, expansion, and contraction, genetic drift, the founder effect, and mutation, both recurrent and dynamic. The authors and discussants alike raise the issue of ascertainment bias, illustrating the point that raw mutational spectrum data need to be carefully scrutinised before conclusions are drawn.

It became very clear reading this volume that the traditional view of pathological mutations being quite distinct from neutral polymorphisms has now broken down irretrievably. Also blurred is the distinction between the so called single locus disorders and multifactorial diseases owing to the phenotypic expression of the former often being affected by the existence of modifier loci. Discussion of multifactorial disease, specifically cancer, hypercholesterolaemia, coronary artery disease, and HLA-disease associations highlighted the difficulties inherent in trying to identify common alleles at loci with weak effect. Particularly noteworthy is a chapter by Charles Sing and coworkers on the "genetic architecture of common multifactorial diseases". Although perhaps rather contentious, these authors challenge us to think in new ways about possible approaches to the identification of common alleles with weak effect that, at least on a population wide basis, may make a more important contribution to the disease phenotype than rarer alleles with much stronger effects.

Inevitably in any volume with a broad remit, there will be important omissions. Mismatch repair genes causing non-polyposis colorectal cancer are scarcely mentioned. This is a serious omission since polymorphic variation at these "mutator gene" loci could in principle serve to modulate mutation rates on a genome wide basis. Perhaps more surprising is that, apart from a single chapter on microsatellites, little attention is paid either to the origins of genetic variation and mechanisms of mutation or to the evident similarities between the processes of mutational change in evolution and those in pathology. The volume is nevertheless a very worthwhile collection of essays on different aspects of variation in the human genome and one which both the specialist and the novice will find very useful.

DAVID N COOPER