Book Reviews

Automation Technologies for Genome Characterization. Edited by TONY J. BEUGELSDIJK. Wiley. 1997. 303 pages. Price £55. ISBN 0 471 12806 6

This volume made me feel like a traveller who jumps into a railway carriage only to find, too late, that he has boarded a local stopping train rather than the express. The book concentrates on large-scale genome sequencing and analysis using the existing technologies and systems through which, as is now clear, the human genome will be sequenced within a reasonable time-frame (4–7 years). On the other hand, the burgeoning field of functional genomics, and its associated technologies, is almost completely ignored. For instance, mass spectrometry is dealt with only in the context of DNA sequencing and not of proteome analysis. Whilst the chapter on hybridisation array technology starts with an excellent account of the theory and practice of hybridisation to short oligonucleotides, it then concentrates on the rather specialist area of flow-through devices for genotyping. There is nothing on expression analysis, nor on more conventional approaches to allele identification.

This multi-authored work is based on two very reasonable premises: that genome research is as much technology-driven as concepts-led, and that scientists and engineers have a lot to learn from one another in this area. Thus, it opens with a chapter about the development of automation systems for a genome centre. Whilst this account contains some important generalisations, it is rather anecdotal in its approach, and it is not clear who is the target readership. Setting up a genome centre is still far from being an everyday event, and those charged with such a responsibility are likely to have the resources to travel widely in order to obtain advice. The next chapter, on modular approaches to automation strategies, is far more helpful. It provides a reasoned and realistic evaluation of the presumed benefits of automation within the general context of genome research, and even shows an appreciation of such practical considerations as the advantages of small machines in crowded laboratories. However, in common with some other contributions, this chapter is virtually unreferenced. From this, you may gather that this volume is not only variable in quality, but also in style. It has been only loosely edited and contains a number of errors and inconsistencies.

The second section of the book contains two chapters on control systems. The first is far too specific in its coverage, but the second provides the reader with a good appreciation of how a central system controller works at its different levels. The next section is labelled 'Advanced Topics' and includes a chapter on capillary electrophoresis that provides a scholarly and well-referenced account, with explanation of the science behind the technology. The following chapter, on scanning probe microscopy, gives a good assessment of progress in this technology. However, in terms of practical applications, it seems to be firing at the wrong targets (eg restriction mapping) and fails to refer to successful rival technologies (such as optical mapping).

The final section contains two chapters and is entitled 'Analysis and Synthesis'. The first chapter is a rather formal account of how a formalism (the Petri net) may be used to model and, ultimately, control a 'genome factory'. This account is predicated upon some rather dated (and perhaps always mistaken) assumptions about how long it will take to sequence the human genome and how many centres (or 'factories') will be involved. Readers of *Genetical Research* may have met Petri nets before as a way of representing metabolic pathways in bioinformatics. The book's final chapter deals with the informatics aspects of genome sequencing projects. It sets out to cover the integration of data acquisition, analysis, and management. It provides a *very* general survey, but has some wise things to say about, for instance, the naming of things (such as clones), with emphasis on the fact that uniqueness is more important than descriptiveness. This book may be unique (I certainly can't think of an equivalent), but its descriptions of topics are of variable quality and relevance. It is certainly not the hoped-for 'express' and this traveller, at least, can only trust that there will be another (and better) one to come.

STEPHEN OLIVER
Department of Biomolecular Sciences
UMIST, PO Box 88
Sackville Street
Manchester M60 1QD
UK

Genetics Manual: Current Theory, Concepts, Terms. By GEORGE P. RÉDEI, Publishers World Scientific Publishing Co. 1998, 1141 pages, price £54.00, ISBN 981-02-2780-9.

This is an ambitious, one-author book which might alternatively have been called an encylopaedic dictionary. The author is a geneticist of some renown; one of the founders of *Arabidopsis* genetics, he edited the Stadler symposia for many years and is also the author of several Genetics textbooks.

The entries in the manual are in alphabetical order with some being very long. For example the entry on 'Introns' runs to six pages. The manual cannot, however, be recommended. It reminds me of the saying about the thirteenth stroke of the clock – not only incredible in itself, but casting doubt on all that has gone before – because when big mistakes are found in entries with which the reader is knowledgeable, confidence evaporates about other less familiar entries. The entry under 'Interference, Chromosome' reads 'One crossing over may either reduce (negative interference) or increase (positive interference) the occurrence of additional ones' which is exactly wrong! The definition of RIP [Repeat Induced Point mutations] is misleading on several counts; but by attributing ripping to a recombination event which ejects the duplicated DNA segment, the author misses the point of the acronym that RIP induces mutations in regions of duplicated DNA, and that this occurs premeiotically. Unfortunately these are two of many such errors.

The manual is also littered with trivial typographical errors which could so easily have been rectified by more careful proof reading. Worse, in places the entries are badly phrased or ungrammatical. Under 'Mutation, beneficial' for example I read the sentence, 'In simple words, approximately 35 times must a mutation, with 0·01 selection coefficient, to occur to be ultimately accepted and fixed'. Sometimes this poor phrasing is combined with surprises of a different sort. The entry under 'Siamese Cat' reads: 'Displays dark color at the extremities because of [sic] a temperature sensitive gene slows down circulation and more pigment develops at specific locations of the body.' Besides the grammar, I wasn't sure whether it was my understanding or the explanation in the manual which was wrong. I was unaware that the gene responsible affected blood circulation of the cat and had always ascribed the phenotype to lower temperature of the extremities, which would occur in all cats, and a temperature-sensitive enzyme. Other types of error are also common. Cross-referencing is essential if the reader is to be able to use the manual but this often leads nowhere. Under 'Cell fusion' the reader is referred to 'Somatic hybridization' for more information; and 'cosmid, library' cross-refers to 'Cosmids, mapping'; neither of these references exists. On occasions the cross-referencing is circular or leads down a blind alley. Bach, Sebastian gets an entry [there are many intriguing entries of this sort] 'One of the greatest geniuses of classical music. … This family tree indicates that musical ability may be controlled by relatively few genes, and the cultural environment also may have a major role.' which doesn't seem to get us very far. Then 'Recent studies demonstrated that musical talent is correlated with stronger development of the planum temporale, increased leftward symmetry of the brain cortex. (See dysmelodia)'. Under dysmelodia 'An apparently autosomal dominant gene with low penetrance causes reduced musical ability. There is also another dominant gene (perfect pitch) enabling the individual to remember and play a tune. (See Bach)' All very frustrating because nothing in the Bach entry refers to a gene for perfect pitch and none of this is referenced. This is one of the major defects of the manual. Individual entries are not referenced and the reader can take an entry no further without a literature search.

The manual contains intriguing entries some of which might not be expected in a Genetics Manual – 'Oil spills' for example – and consequently there is an entry to catch the eye on almost every page. I was surprised too at some of the definitions. Recombination is defined only in terms of crossing over of linked genes. Independent assortment, which is recombination of genes too, falls outside this definition. You may interpret this as a personal quirk on my part, but I object to the narrowing of the definition of recombination in a way that puts the definition at variance with the majority of dictionaries. There is a need for a term that is neutral with respect to mechanism and 'recombination' fills that need. Mendel's Laws are stated in an unusual way. What we are used to calling his First Law of segregation becomes his second law; his Second Law of independent assortment becomes his third. 'Affinity' is defined as: 'Unlinked genes segregate to the same gamete more frequently (quasi-linkage) or less frequently (reverse linkage) than expected on the basis of randomness.' Which is all very well, but I would have expected some reference to the difficulty in establishing that the phenomenon is real. The definition of 'Coding strand' is another example where the definition fails to confront important issues. Dictionaries of genetics give either of two, mutually exclusive, definitions of which of the DNA chains is called the coding strand. For some it is the DNA chain which encodes the mRNA, while for others it is the DNA which has the same base sequence as the mRNA. It is the latter definition which is favoured in the manual but no reference is made to this dichotomy of usage, though the author draws attention to the difficulty caused by

the fact that in some cases both DNA chains may be transcribed into message.

There are some good features, including a Section of General References which is subdivided by subject, but the good points are, I'm afraid, outweighed by the overwhelming sense that too much is unreliable. It is a shame that such an ambitious effort should be marred by serious defects.

JEFF BOND
Institute of Cell & Molecular Biology
University of Edinburgh

The Genetics of the Pig. Edited by M. F. Rothschild and A. Ruvinsky. CAB International. 1998. 640 pages. Price £85/$160. ISBN 0 85199 229 3.

Until quite recently, there was little study of the genetics of the pig other than of the quantitative traits of growth, carcass and reproduction which are important in animal production. Perhaps the species did not sufficiently attract the attention of fanciers, interested in the inheritance of colour and conformation, even though its high reproductive rate makes it more amenable than cattle to such study. Now that genome mapping has become feasible, opening up the opportunity to map quantitative trait loci (QTL), formal pig genetics has become an active and fashionable discipline. Whilst this means that some reviews rapidly become out of date, it is nevertheless useful to have a comprehensive survey available. This multi-authored volume, one of a series being published by CAB International on the major domestic species, largely fulfils this need. Rothschild and Ruvinsky have brought together a well balanced set of reviews.

The coverage is broad indeed. It includes the evolution and domestication of the pig, the (mainly) Mendelian genetics of colour, enzyme variants and the immune system, molecular genetics, physical and linkage mapping, the (mainly) quantitative genetics of the commercial traits of reproduction, growth and carcass, and the inheritance of morphology and other inherited disorders which have discrete expression but not simple inheritance patterns. There are discussions of genetic improvement programmes and of conservation.

I found the quality of the articles generally very high, not surprisingly as most were written by leading international figures in pig genetics and breeding. Whilst one can find much of the material elsewhere, much of it by these same authors, this volume brings them into one place. There are some lapses in the general quality: notably the description and analyses of what should be an interesting subject, that of domestication and breed origins, left me wanting something more incisive and up to date.

Although the pig has not been a favourite animal for the demonstration of Mendelian genetics, it has probably been the most used of any mammal for the study of the inheritance of quantitative traits relating to carcass quality and organoleptic properties. It will be interesting to see, now there is the major investment in QTL mapping, how rapidly we learn more about the production traits of the pig, and how useful this information will be. There is no doubt, for example, that identification of the molecular lesion leading to halothane and stress sensitivity had a major impact on breeding practice. Time will tell whether other genes with such large effects will have such an impact, or whether pig improvement will continue to come largely from application of intense selection using phenotypic records.

The pig breeder or geneticist should find this well balanced and comprehensive book an important reference.

WILLIAM G. HILL
Institute of Cell, Animal and Population Biology
The University of Edinburgh