Book reviews

Human Gene Evolution. David N. Cooper. BIOS Scientific Publishers, Oxford. 1999. Pp. 490. Price £75.00, hardback. ISBN 1 859961 51 7.

This is a wonderful book, but it made me wonder about books. What are they for nowadays? It would be very straightforward to argue that all the information collected in this book might just as well be put on a website, with the great advantage that updates could be made without posting any paper to anyone. I suspect that the pragmatic answer is that books are still a lot easier to sell, and for this kind of book many people will still prefer a physical book with an index rather than a searchable website. What kind of book is it? Essentially it is a work of reference, but with the facts accompanied by lucid and critical explanation. It is especially timely in providing a comprehensive and scholarly review of the state of knowledge on human gene evolution at the end of the 'pregenomic era'. It distils a huge amount of dispersed primary literature into an accessible reference source, and for me (and probably many others) it will be most valuable as a source of examples of all the rich and strange inhabitants of the genome: overlapping genes, semiprocessed pseudogenes, genes with 4 bp exons, genes with 3' UTRs of -2 bp, and genes involved in fusion splicing and exon scrambling.

As one would want from such a source, the text is well integrated by cross-referencing and the index is excellent and the depth of resource it represents can be illustrated by the fact that of the 490 pages you get for £75, more than 150 are occupied by references or index. This book is not, however, simply a catalogue, and at all points care is taken to integrate the examples with explanation of the principles at stake. If I have to find minor imperfections, there are one or two references appended to the wrong chapters, and a figure curiously distant from the text describing it, but there is little to compromise the impact of the whole.

Overall, I simply have to admire the thorough and scholarly approach to the subject. It must have involved a huge amount of work, and the author can rest assured that the product will not simply be rendered redundant by the production of the genome sequence. On the contrary, this book will serve as a starting point for making sense of the avalanche of 'information' that venture will produce.

John Armour

Institute of Genetics, University of Nottingham Queen's Medical Centre Nottingham NG7 2UH U.K.

Migration and Colonization in Human Microevolution. Alan G. Fix. Cambridge University Press, Cambridge. 1999. Pp. 236. Price £40.00, hardback. ISBN 0 521 59206 2.

During the twentieth century various biological disciplines tried to reconstruct and understand the origin and past history of modern humans. For anthropologists and human geneticists the study of microevolution, i.e. the factors affecting the variation of gene frequency patterns, has been the major field of investigation. In the early thirties, Fisher developed a systematic theory of evolution by natural selection and predicted that in a large population even slight selective differentials could replace a less advantageous twentieth with a more favoured one. At the same time Wright also developed a general theory of evolution and his argument was based on the fact that a species is composed of many small and nearly isolated subpopulations and within most there exist some boundaries to breeding. The size of these isolates is very important in the evolutionary process and assuming the population is randomly mating and there is no selection or mutation, such subdivisions will show genetic differentiation as a result of chance processes. When the isolation is partial the rate of divergence will depend on the amount of migration or gene flow. Gene flow between subpopulations retards the process of genetic differentiation. It is obvious therefore that in addition to conventional genetic factors, an understanding of demography, ecology, environment of the natural habitat, social behaviours and all other factors which promote migration and colonization are very important for understanding present day population structure. Since extensive information was available from historical records of the social and demographic structure of the human population, this led to the development of many classical models of population structure. More recently computerintensive simulation methods have been developed which allow the study of migration and its effects through time, during the microevolution of humans.

The other vital achievement of the late 1900s was a revolution in the development of methodologies for genome analysis. There was a sudden explosion of new molecular markers, which helped in the reconstruction of the history of human migration and in testing explanations for demic diffusion. The spread of Homo sapiens sapiens to occupy the New World, colonization of Oceania and expansion through Europe via demic diffusion of agriculture were initially investigated using classical markers (blood groups, enzymes and proteins, human leucocyte antigens and immunoglobulin allotypes), but later confirmed by the study of autosomal (STRs) and sex-related mitochondrial and Y chromosome markers. With all these new inventions and the sequential expansion of population genetics in mind, Alan Fix has attempted to trace the role of migration in human populations by taking examples of well investigated populations which vary extensively in population density, land occupied and social integration.

The book includes six chapters. In the first migration is examined through causal models based on the overlapping interest in migration among different biological disciplines. As