the chapters is straight from the horse's mouth, written by those who really got their hands dirty (or at least directed others to) trying to build maps of their respective part of the genome. Hence, there is a wealth of practical advice in this book for those who are ready or who intend to follow suit. Most importantly, each chapter also gives intriguing observations on genome structure and evolution that have been thrown up by the various mapping exercises.

For me, the most enjoyable chapter was the first one. Written by Duncan Campbell, it describes the long-range map of the human MHC complex at human 6p21.3, surely one of the most extensively mapped regions of the human genome, extending over 4000 kb of DNA and now completely cloned in cosmids and YACs. Work on this region of the genome has been one of the paradigms for showing the value of using CpG islands, localized on restriction maps, as a way of locating new genes. At least 80 genes have been localized within this 4000 kb of DNA, including genes with diverse patterns of gene expression, and genes which seem to play no obvious role in the function of the immune system. The map has highlighted regions where a small physical distance relates to a high level of meiotic recombination and conversely regions where there is no or very little recombination. Comparative maps made from different haplotypes show that deletions or insertions of DNA have occurred in this region of the genome on different chromosomes.

In a similar vein, the study of the terminal region of human chromosome 16p by Peter Harris and Doug Higgs highlights the high level of male recombination and the corresponding relatively low level of female recombination, seen at the ends of this, and several of the other, human chromosomes. The biological basis for these sex differences in recombination behaviour is not understood. Again akin to the MHC story, polymorphisms in the maps generated from different chromosomes are seen, this time in the length of the subterminal region of the chromosome so that the α-globin locus can be as little as 170 kb or as much as 430 kb from the end of the chromosome. Understanding these changes in structure will help elucidate some aspects of human telomere biology.

In contrast to the gene-rich MHC and 4p16 regions, Monaco *et al.* describe the characteristics of the physical map around the dystrophin gene on Xp21, where genes seem relatively scarce. The map around the APC gene on chromosome 5 appears to share some of these characteristics.

The natural progression from detailed long-range physical maps is to sequencing of long contiguous stretches of the genome. The case for this is made out by Leroy Hood and his colleagues, using the three T-cell receptor gene families of mouse and man. It has highlighted our general ignorance about how to interpret the role of DNA sequences that do not immediately suggest that they are coding regions. The conservation of some of these regions between mouse and man suggests that they are under some selective pressure, but what is this?

Overall, I think this volume is probably beyond the scope of most undergraduate genetics or biochemistry courses. It is, however, a very worthwhile read for anyone interested in genome structure and evolution and a great pocket-sized book of tips and hints for anyone who is battling their way through constructing a long-range restriction map of their own.

WENDY BICKMORE
MRC Human Genetics Unit,
Western General Hospital,
Edinburgh EH4 2XU

Genetics of Cellular, Individual, Family and Population Variability. Edited by CHARLES F. SING and CRAIG L. HANIS. Oxford University Press, Oxford. 1993. 305 pages. ISBN 0 19 506625 1.

This volume was brought together as a tribute to W. J. (Jack) Schull with chapters by colleagues and friends. This recognizes his major contributions to human genetics and his leadership of research at the University of Michigan in Ann Arbor and the University of Texas in Houston. The title of the book, a span of genetic variability at all possible levels, is most ambitious, so it is not surprising that with just 18 chapters, the coverage is patchy. It is also apparent that some authors put much more work into their chapters than others. The main strengths of the book are in medical genetics and human population genetics and evolution, and it is likely to be of most interest to those wishing to get a reasonably up-to-date introduction to and review of the methods and some current opinions in this field. As so much work and resources are put into the study of the genetics of man, much new knowledge and understanding of the genetics of basic systems of disease and of populations comes from its study. Well-known examples are the analysis of globin variants, of short repeat sequences in Huntington's disease genes, and of population structure.

The book is in four sections, as suggested by the title, but they are unequal in size. I did not find much solid information in that on Cellular Variability. In that on Individual Variability, there are nice reviews on the analyses undertaken in Japan on the mutational effects of the atomic bombs and on the effects of inbreeding. On the latter, J. V. Neel speculates as to why inbreeding effects in man are so small, reviewing modern knowledge on gene structure in relation to mutation effects. Inbreeding effects are not negligible, however; cumulative mortality to 7 years of age is increased by 17% of its mean by cousin marriage.

The section on Family Variability deals with linkage analysis, an exampie of how a topic in classical genetics has had a major recent stimulus as large

numbers of molecular markers have become available, on diseases with genetical but not simple inheritance, and on pedigree analysis in animal models. The topic I considered most surprising, albeit through ignorance, was the use of populations of baboons for the latter.

Analysis of population variability takes up half the chapters. Although most of the work is not new, that which I found most interesting was the summary of human population diversity and discussion of the lack of evidence for population bottlenecks by Nei, Li and colleagues. Other papers in this section deal with theoretical problems, including a novel, but somewhat out-of-place, theoretical analysis of occupancy problems by Chakraborty.

Most geneticists will find both useful and interesting material in this volume because of its great breadth and the quality of the authors. As with other collected volumes, however, some of the material is being regurgitated and some is yet undigested.

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

Clonal Forestry I: Genetics and Biotechnology. Edited by M. R. AHUJA and W. J. LIBBY. Springer-Verlag, Berlin and Heidelberg. 1993. 277 pages; 32 figures (including photographs). Price DM. 198.00. ISBN 3 540 52501 7.

Clonal Forestry II: Conservation and Application. Edited by M. R. AHUJA and W. J. LIBBY. Springer-Verlag, Berlin and Heidelberg. 1993. 240 pages; 34 figures (including photographs). Price DM. 198.00. ISBN 3 540 55714 8.

These two volumes on clonal forestry are edited by two eminent researchers and writers in the field. The first volume sets out to give an insight into the theory and science underpinning clonal forestry and the second volume surveys the applications of clonal forestry for various purposes and settings around the world. The editors suggest in their preface that they set out to recruit authors from amongst younger scientists across a number of countries to foster a diversity of thought and experience. When the editors recruited established authors, they were asked to write on recent advances or on different topics from their previously published work.

The editors introduce Volume I with an overview of the current situation, linking together the fields of genetics, biotechnology and clonal forestry. This is followed by a series of more or less linked chapters that take the reader through the genetics of clones, maturation, the population biology of clonal deployment and the selection and breeding of extreme genotypes.

The reader is then taken into areas in which he or she is faced with all the problems that have to be answered before clonal material, from whatever source, can be introduced into the forest. Are regenerants from tissue culture systems genetically stable, how do you identify the ramets of a clone and how do you field test the clonal material? The various techniques for vegetative propagation are then described and the techniques discussed from a commercial viewpoint. This commercial point of view suggests that no vegetative propagation system established to date has made a steady return on the investment, let alone made a profit.

The problem of maturation and the possibilities of rejuvenation of mature genotypes are discussed. There is a classical Catch 22 in forestry in that when trees have expressed their desirable characteristics, they are too old to propagate vegetatively and when they can be propagated successfully, they are too young to be tested. The authors suggest possible ways to get around this problem but it must be said that this might prove difficult to do on a commercial scale.

The remaining chapters in Volume I include an in-depth survey of the current status of somatic embryogenesis in conifers and a description of the structure and organization of the nuclear, chloroplast and mitochondrial genome. The volume is concluded by an overview of DNA transfer in conifers, outlining the techniques and possibilities.

The emphasis in Volume II is very much the practice of 'full' clonal forestry rather than the techniques involved in the successful cloning of forest trees. Volume II can therefore be seen as a logical development from the methodology presented in I. Once it has proved possible to propagate a species vegetatively and obtain substantial genetic gain as measured in clonal trials, managers need to decide if there is a need to alter certain silvicultural practices. For example, should clones be laid out in monoclonal blocks or in intimate mixture? As genetic diversity of the nearest neighbour decreases, what is the effect on competition and mensuration of the crop? Is there an advantage in selecting specific clones for specific site-types? Should other management practices vary with specific clones? And, of course, what is the correct balance between genetic gain and risk in terms of number of clones deployed?

Most of the above questions are addressed, although, admittedly not all are answered in the 13 chapters which constitute this volume. Nine of the chapters involve detailed accounts of the experiences of different authors as they approach full clonal forestry with a variety of different tropical and temperate species. This is one of the strengths of the book in that any tree breeder or manager interested in learning how other organizations have moved towards full clonal forestry ought to be able to find a species related to his own. Experiences with radiata pine, Norway spruce, willows, poplars, teak, Eucalyptus and others are all presented.

The remainder of the chapters cover the advantages and disadvantages of clonal forestry with a bias