of the papers in the first section deal with the activation of $p34^{cdc2}$ kinase and its cell cycle coupling with cyclin B. Other genes involved in this interaction are *cdc25*, *wee1* and *stf1*. Of interest is the paper by Pines and Hunter who examined cyclin A and cyclin B in HeLa cells. Although both have been shown to induce mitosis in frog oocytes, they are likely to have different cellular functions because, although they are obviously related, they are only 43% identical in the most highly conserved regions. Cyclin A can associate with two different cdc2-related protein kinases, $p34^{cdc2}$ and p33, and is active throughout S and G_2 phases; cyclin B only associates with $p34^{cdc2}$ and is tightly negatively regulated until the start of M-phase. The role of Cyclin A in *Drosophila* is discussed by Lehner *et al.* and although it is possible that the role may be a redundant one, curiously there is a lack of closely related cyclin genes. The localization of the $p34^{cdc2}$/$p63^{cdc13}$ complex is discussed by Alfa *et al.* and they show that there are two populations in cultures of *S. pombe*, one associated with the mitotic spindle pole and the other residing in the nucleolar matrix. This is an important observation since it suggests a role for the p34 kinase in fission yeast which does not have histone H1. Several papers then deal with the complicated question of the roles of cyclin in maturation of frog oocytes, in particular the role of Cyclin A. Maller *et al.* conclude that this cyclin alone can complex with $p34^{cdc2}$ and allow cells to enter mitosis and then, on being degraded, permit cells to exit from mitosis. The section on the control of mitosis ends with papers on the roles of *wee* and *cdc25* genes which are involved respectively in inactivating and activation of $p34^{cdc2}$. Hudson *et al.* describe a gene, *stf1*, that bypasses the requirement for *cdc25* in *S. pombe* and is postulated as being a new regulatory element of the mitotic initiation pathway acting on *cdc2* by a pathway independent of *cdc25* and *wee1*. Fantes *et al.* give an account of those genes that interact to control the entry into mitosis, paying particular attention to the response to the nutritional state of the cell.

Mitosis is the final section of the book and in this section papers deal with the organization of the mitotic machinery and progression through the process of mitosis. The section starts with a useful overview by McIntosh of the structural changes that accompany preparation for division. Kinoshita *et al.* describe the role of protein dephosphorylation in sister chromatid separation in fission yeast and have isolated five genes involved in serine/threonine phosphorylation. Goldman *et al.* discuss intermediate filaments whose subunits are substrates for a variety of kinases and which may have a role to play in signal transduction. A detailed description of the work of Kellog *et al.* into the centrosome is highly enlightening, particularly as this is an obscure organelle; they have identified MAP proteins (microtubule associated proteins) that associate with the centrosome as a multiprotein complex and whose locations vary dramatically during the cell cycle possibly as a result of their association with cyclins. Sikorski *et al.* describe their isolation of a new protein family, TRP proteins, that are characterized by a repeating amino acid motif and which play a role in mitotic segregation. Further papers in this section explore the roles of the centromere and the spindle pole body in dividing nuclei. Glover *et al.* suggest distinct roles for Cyclins A and B during development of the *Drosophila* embryo, Cyclin A being largely cytoplasmic in its location and increasing in amount at a time corresponding to cellularization; Cyclin B on the other hand is associated with the centrosome and its microtubules, suggesting that it has a role in targeting $p34^{cdc2}$ kinase to the astral microtubules. Meiosis is the subject of only one paper in this volume and the subject is dealt with at length and very clearly by Kleckener *et al.* An elegant study of chromosome movement is given by Hyman and Mitchison who show that there are two different proteins that can move in opposite directions and whose activities are regulated by phosphorylation.

Since the 1991 Symposium and the publishing of this book, there has been continued progress in the unravelling of the elements of mitotic control. Much more has been learned about the structure of the different cyclins and how their destruction is brought about and indeed, a variety of new cyclins have been discovered. However, this book is invaluable as a statement of more or less current knowledge of the control of cell division and related events and, although it will fairly rapidly represent where the field has been, it should still prove a useful addition to the bookshelf of the serious cell cycle researcher.

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Regional Physical Mapping: Genome Analysis, vol. 5. Edited by K. E. DAVIES and S. M. TILGHMAN. Cold Spring Harbor Laboratory Press. 1993. 140 pages. Cloth. $49.00. ISBN 0 87969 413 0.

The mention of physical mapping usually sends some of my colleagues into a state of apoplexy – 'boring, only a means to an end, not biological' I hear them say. If they could be persuaded to peruse this volume I hope that it might cause them to modulate their views. Regional physical mapping is volume 5 of the Genome Analysis series edited by Kay Davies and Shirley Tilghman. Other volumes in this series have covered physical mapping strategies, gene expression and genotypes and phenotypes. This volume concentrates on the detailed physical restriction maps of four regions of the human genome and, on a rather different level, the long-range sequence analysis of 100 kb of DNA from the T cell receptor loci. Each of

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.

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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