the breadth and complexity of the subject. The three following, on the control of metabolism and of gene activity, are designed to aid the cell biologist in comprehending the molecular basis of the events he studies. There then follows a chapter dealing with the changes that take place at the morphological and biochemical level in selected tissues during development; the examples, which include erythrocytes, liver cells, lens tissue, muscle, mammary gland and pancreas, have been chosen with care and will stimulate the interest of the reader. The book ends with a discursive chapter which draws conclusions and considers several models proposed to account for the differential expression of genetic information during development.

The overall effect has in some measure been spoilt by a lapse in organisation possibly in the pursuit of readability as well as a few omissions and errors. It is unfortunate that more care was not taken in chapter 3 (Regulation of Cellular Activity) to distinguish clearly between control achieved by the regulation of enzyme synthesis and that accomplished by a modulation of the activity of preformed enzyme. In addition, the attribution to enzyme specificity of a role in regulation is to stretch the concept of control beyond reasonable limits. The simple bacterial model for the regulation of gene expression certainly deserved mention but it is to be regretted that a consideration of other bacterial mechanisms for the control of gene expression have not been discussed in the context of differentiation; for example, during sporulation and bacteriophage infection, changes in the transcription machinery influence gene expression in a qualitative manner superficially reminiscent of differentiation. There is conflict between the definition of the operon implied in figure 28 and that given in the text and the glossary; the regulator gene is not usually regarded as a component of this unit of regulation. The diagram of the key steps in carbohydrate metabolism (figure 8) is spoilt by errors (hexokinase is not reversible whereas phosphoglycomutase is) and omissions (pyruvate kinase is not included in the diagram though it is assumed in the text, page 24). It is unlikely that the reader will gain much insight into changes in the RNA complement of the cell from figures 15 and 16 without more assistance from the text; in fact, little would have been lost had they been omitted altogether.

At a fraction under 2p per page of text, this publication would appear on the costly side. Nevertheless, it is easy to read and frequent reference to relevant reviews encourages the reader whose appetite has been whetted to dig deeper into the literature. It is a useful introductory book to stimulate interest in a specialised field which is and will continue to be of great importance in current research.

A. J. SMITH

*Department of Biochemistry and Agricultural Biochemistry,
University College of Wales, Aberystwyth*

COMPUTER SIMULATION IN GENETICS. Jack L. Crosby. John Wiley & Sons Ltd., London and New York. Pp. xiii + 477 + 69 text-figures. £9.

I realised too late that I should not have agreed to review this book. I have run many genetic computer simulation programs and I have always found it very difficult to borrow bits of other people's programs or even to understand my own a year later.

The author writes from the point of view of one who is basically non-mathematical but who wishes to use the computer to gain more insight into genetical problems. He immediately comes up against the problem of computer languages—that if he writes the computer programs in the book in one of the known languages, then a proportion of his readers will not be able to understand them. This he solves by writing them all in a new language which he calls Mendol. The uninitiated will therefore have to master this language before learning a second with which to communicate to their own machine. I suspect, therefore, that the book will have a comparatively limited readership. But my basic disagreement with the author is that I think that the real advances in this field have been made by those who are mathematically competent.

There are several ways in which computers may be used in genetics. The first is an aid in teaching. To help in the understanding of quantitative genetics, simulation programs are now available whereby the student can “improve” random numbers as though they were real animals. At a slightly higher but perhaps still trivial level, they can be used to give a check, and an illustration for the uninitiated, of the results obtained by sophisticated mathematical methods. Kimura and his school have made much use of them in this respect. But I would regard their real advantage to be that they allow us to understand the behaviour of complex genetic systems—in which we know the general structure (the way in which the different parts are combined) and the rules for the operation of each part, but we cannot predict the properties of the whole system. This understanding may be at two levels. It may be purely qualitative in the sense that it tells us very generally how the system behaves without allowing us to quantify this in any way. I suspect that many of the earlier papers in this field were of this kind—they really did not tell us anything new. Occasionally a completely new phenomenon turned up as, for instance, in the paper by Lewontin and Franklin on the importance of linkage in populations when heterozygotes are at an advantage. It was unexpected that structure within chromosomes could persist even when there was segregation at very many loci. But this, I think, is not what we usually mean when we say that we understand a complex system. Understanding means essentially to be able to describe it in comparatively simple terms so that we can then predict its behaviour without complicated mathematics. We must use a computer to show us how to think about the system without needing to use a computer. We are then searching for a new conceptual viewpoint and the tactics used become almost those of the practical experimentalist—to probe the system to see how it behaves, first of all in a very crude manner, but always in the hope of finding as simple a possible final description as we can. It is to me fundamental that this description has to be quantitative. It need not be complete in the sense that it gives accurate results in all circumstances. It is satisfactory if it is 90 per cent accurate provided it is simple. I would then regard it as essential to use algebra where ever possible—not only in the carrying out of the simulation, but in the analysis of simplified special cases. It very often happens that we can deal with these with direct algebra so that the shape of the answers and the way in which the different variables are combined can give a clue to the messier cases. There is perhaps one final level of use in which one never runs the program at all. To give an example from my own work, it became clear in dealing with linkage in selection for

quantitative characters that, provided the total amount of genetic variation controlled by a particular chromosome remained constant, it did not greatly matter how many loci this was due to, provided this number was reasonably large. If enough loci were involved the whole process could be described by three combinations of variables rather than the five. Thus as the number of loci increased one moved into a limiting situation. One might then be tempted to seek for an algebraic solution in this situation. Not being able to do this, I tried to write a program in which the loci were not considered as individual units but merely as an infinite number of sources of genetic variation, smeared uniformly along the chromosome. After a great deal of labour, I succeeded and then realised that this was enough, that it was in fact equivalent to an algebraic treatment of the problem. The program proved to be exceptionally slow to run and it was always faster to run programs with 50 identified loci. But I had demonstrated that there was a limiting case even if I had never run the program.

This book is essentially a description of the author's own adventures and makes no attempt to provide a general approach or a complete description of what other workers have done. Nevertheless, some of the sections are very stimulating to read. After a chapter in which the problems of linkage is discussed and various intriguing and comparatively sophisticated solutions are suggested, it comes as rather a surprise to read that "the author has never actually introduced linkage into a simulation experiment".

Is there a need for a book like this? I feel inclined to answer—no! Though there are some problems which are very general, I think it probable that each research worker has to work out his own salvation. In other words, once he had mastered the problems of programming in one particular language, it is comparatively simple to translate his own specific genetic problems into it.

ALAN ROBERTON

Institute of Animal Genetics, Edinburgh

THE GENETIC STRUCTURE OF POPULATIONS. A. Jacquard. Springer-Verlag, Berlin, Heidelberg, New York, 1974. Pp. xviii+569. DM96, \$37 (Biomathematics Vol. 5).

The very first volume in the series, called *Biomathematics*, was a collection of articles on population genetics. It was reviewed in this journal by W. Bodmer (*Heredity*, 1972, 28, 413-414). That book was published in 1970 and in the same year Jacquard's "Structures génétiques des populations" was published in Paris. We now have a translation by D. and B. Charlesworth of Jacquard's work, with some amendments, additions and corrections. R. C. Lewontin, a general editor of the series, explains that the objective was to make "the lucidity and elegance of (Jacquard's) presentation" more widely accessible; in particular "the fusion of demographic and genetical concepts" deserved a wider audience.

The first part of the book, "Basic facts and concepts" consists of two chapters, of which the first, on the foundations of genetics, may be of use to mathematicians. The second, dealing with probability and with genetic structures, deserves careful study to help the reader to understand the rest of the book. It is most unfortunate that in defining the matrix representing