Barry Polisky discusses replication control of ColE1-type plasmids and Robert Knowlton considers copy number and stability of yeast plasmids, in the next two chapters; and in both systems the implications for maximising expression of cloned genes are examined. These form important current areas of applied research and the authors examine the problems which each system presents.

Gary Stormo discusses translation initiation in both prokaryotes and eukaryotes. Some laboratories have begun to collect data on the efficiencies of particular initiation sites, and Stormo concentrates on the effects of mRNA sequence on translation efficiency. This, of course, brings up the very difficult problem of structural features of the mRNA, which are difficult to predict from its sequence but can have an important effect on initiation rate. The *E. coli* data lead to the following rules for maximizing the yield of a particular protein: (1) AUG is the best initiation codon; (2) A Shine-Dalgardo sequence of at least four nucleotides, taken from the sequence AGGAGG, should be used; longer may help some messages; (3) The optimum spacing between the S-D sequence and the initiator codon is about nine bases. Some additional rules are also given. Stormo finds that the requirements for efficient expression of eukaryotic proteins are quite different from those for prokaryotes, but only some less general proposals can be made for increasing gene expression.

In by far the longest chapter in the book, de Boer and Kastelein present data on biased codon usage, and show that genes coding for abundant proteins have a marked bias towards major tRNA species compared with poorly expressed genes, which make much more use of minor tRNA species. Data on translation time (amino acids per second) for strongly and poorly expressed genes are also given, and evolutionary aspects of biased codon usage are discussed.

In the last three chapters Goldberg & Goff describe the selective degradation of abnormal proteins in *E. coli* and the eight soluble proteases responsible; Dobner & Villa-Komaroff discuss the detection of proteins produced by recombinant DNA techniques; and Buell and Panayotatos consider how knowledge described in the previous chapters has been used for the overproduction of proteins, specifically in *E. coli* which has been the major source of information. Each chapter has a comprehensive list of references, and there is a detailed index.

Many of the studies presented in this book were no doubt motivated by practical or commercial aims, but they have often made novel and valuable contributions to basic molecular genetics, and this should make the book of considerable interest to a wide readership. The book, in spite of its sixteen contributors (thirteen from USA, two from Geneva and one from France), reads as a unified whole, and the two editors are to be congratulated. I have to give the book a very warm

recommendation, only mitigated by the high price, which will limit its siting to library rather than personal bookshelves.

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Molecular Evolutionary Genetics. By MASATOSHI NEI. New York: Columbia University Press. 1987. 512 pages. U.S. $50.00. ISBN 0 231 06320 2.

The rapid accumulation of data at the molecular genetic level, from protein and DNA sequencing, restriction enzyme analysis and electrophoretic variants have given us much information on the tempo and structure of the evolutionary process and on variability within populations. Major theoretical developments have ensued in order to interpret all the new data. It is now about a quarter of a century since Zuckerkandl and Pauling first drew attention to the steady molecular clock of protein evolution, over 20 years since Harris' and Lewontin and Hubby's demonstration of substantial polymorphism within species inferred from gel electrophoresis, and 20 years since Kimura's proposal of the neutral theory to explain these data. There have been other fundamental discoveries, such as of different rates of evolution at silent and coding sites and of concerted evolution of multiple genes, and developments in theory such as in measures of genetic distance, phylogenetic tree structure using molecular data and of models to describe evolution of gene families. As a consequence evolution and variation are now considered mainly by geneticists at the molecular level. Although this may seem to ignore the importance of adaptation and of an understanding of the evolution and maintenance of variation of continuous traits, this reductive stance does reflect the amount of new data coming forward and the power of molecular analysis.

Masatoshi Nei and his group at Houston have been major contributors and stimulators of this work, for example, on methods for distance measurement, for tests of neutral and alternative theories, and for synthesising theory and observations. It is not, therefore, surprising that his *Molecular Evolutionary Genetics* is a most useful book which brings together molecular data, methods for their analysis, and the theoretical basis of their interpretation. It will serve as a reference book on both methodology and results, and should be of value both to population geneticists and to those molecular geneticists prepared to extend their horizons to anything but the most superficial evolutionary interpretation of their data.

The greater part of the text deals with the kind of molecular data which has been collected: initially protein and subsequently DNA sequences between species, on electrophoretic, DNA sequence and restriction fragment length variation within species and how

each can be analysed and interpreted. Thus there is extensive discussion on measures of distance, and their various pros and cons, on measurement of and inferences from polymorphism, and on tree construction. Throughout, the underlying uniform rate molecular clock theory gives a reference point for the measures and their comparisons, and the results are related to the evolution by neutral substitution interpretation. Subsequently there is a rather brief review of population genetics theory. In these and previous chapters formulae are usually stated, perhaps with verbal argument, and the reader is referred to the original papers for derivation. Sometimes this is rather frustrating, in that the reader can not readily see what is the basis of the conclusions, but usually it is more than sufficient and the book is therefore not cluttered up with formulae. The final chapter is essentially an essay in which Nei discusses how the molecular data square with models of evolution, and in which he puts forward his own synthesis.

The book is clearly written and, as far as I detected, with few errors. (I think, however, that if Nei actually tries multiplying the matrices defined on page 355 he will find some transposition necessary.)

This is a quite different book from Kimura's *Neutral Theory of Molecular Evolution*. Nei's text deals more with methods of analysis rather than with either developing a thesis or with mathematical population genetics. Although Nei is clearly a confirmed neutralist, he uses it rather as a framework for describing and interpreting data. As such it should become a standard reference.

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Phycomyces. Edited by E. CERDA-OLMEDO and E. D. LIPSON. New York: Cold Spring Harbor Laboratory. 1987. 430 pages. $88.00. ISBN 0-87969-199-9.

This book is dedicated to the memory of Max Delbrück who was the source and inspiration behind many projects, including the exploitation of Phycomyces as a system for studying several diverse biological phenomena. The volume, consisting of 11 chapters and 8 appendices, is a fitting testimony to his influence.

The book's primary virtue is its comprehensiveness; not only are a large number of unanswered questions discussed in depth, but the literature underpinning each of them is thoroughly documented. In addition, a comprehensive, 38 page bibliography is included at the end of the book to make it an indispensible reference source of Phycomyces literature.

The most widely studied aspects of Phycomyces biology are the tropic growth responses, of which phototropism has been investigated most extensively, but the avoidance of physical barriers – fugotropism

– is one of the more mysterious. A Phycomyces sporangiophore, for example, will grow away from a physical barrier placed close to its growing zone, but neither the mediator nor the receptor of this growth response has been identified. In geotropism too the receptor for the gravity stimulus is unknown. Phycomyces sporangiophores also exhibit a growth response when exposed to a laminar wind. The extent of this positive anemotropism depends on the humidity of the wind to which the sporangiophore is exposed. This observation suggests an effect of humidity on cell wall extension and this latter topic is the subject of another chapter. It is generally envisaged that fungal hyphae grow at their tips by a process of 'softening' the rigid enclosing wall, through the action of lytic enzymes, followed by the incorporation of 're-inforcing' material into the expanded cell wall. The kinetics and control of these two antagonistic reactions, either in tropic growth response or in normal cell wall extension, has still to be satisfactorily quantified, but several models of cell wall growth are extensively and critically discussed.

As one might expect, mutants which lack one or more tropic growth responses have been isolated but the contribution of genetics towards unravelling the problems in sensory physiology has been disappointing. Classical genetic analysis faces considerable problems in Phycomyces. The multinucleate nature of the cell cycle, the uncertainty over the time of nuclear fusion and meiosis, the complex tetrad analysis which follows zygospore germination, and the long dormancy period are just a few of the complicating factors which have hindered the genetic contribution.

Another surprising feature which is apparent from reviewing this book is the slight contribution which has been made up to now by genetic manipulation technology. I write 'surprising' because the possibility of a major contribution certainly exists, especially in the areas of differentiation and regeneration, and sexual morphogenesis. The book contains chapters covering the physiology and cytology of these topics, but here I was struck by the potential for breakthrough using the techniques of molecular biology. For example, experiments on regeneration from segments of sporangiophores have shown the existence of a polarity of morphogenetic information which is thought to be stored in the cell surface and cell membrane in the form of a gradient. The isolation of membrane mutants should be feasible and the molecular analysis of these together with existing mutants which are defective in sporangiophore development, should yield greater insight into differentiation and regeneration. Similarly in sexual morphogenesis the analysis of differential gene activity associated with pheromone-induced changes should allow the molecular basis of hormone action to be described.

In this review I have tried to convey some of the stimulation which I obtained from reading this book. I can recommend it as a valuable library purchase. It