

Book reviews

Adaptive Evolution of Genes and Genomes. Austin L. Hughes. Oxford University Press, New York. 1999. Pp. 270. Price £45.00, hardback. ISBN 0 19 511626 7.

The author doesn't waste any time in letting the reader know that the account of adaptation and molecular evolution spun in his book will be a highly personal and opinionated one. In fact, the author admits up front that the majority of the examples in the book come from his own work on a large range of molecular evolutionary subjects. As the book is about adaptation, the author also quickly lets the reader know that one of the more influential papers of the 1970s on this subject — Gould and Lewontin's spandrels classic — is nothing more than non-adaptationist story telling. According to Hughes, adaptationism thrives today because of an even more important paper from the 1970s by Maxam and Gilbert, that shepherded the DNA sequence age into evolutionary biology. This book, therefore, is about this 'so-called' adaptationist triumph from a molecular or genomic perspective.

Accordingly, the book is organised to firstly establish the prevalence of adaptation at the molecular level and its importance in modern evolutionary biology. Hughes then describes the methodology used to examine adaptation at the molecular level and how the neutral theory fits into the picture. These introductory chapters are followed by five chapters on specific molecular evolutionary systems, that address balancing selection, directional selection, evolution of new protein function and genome evolution. Along the way specific analytical approaches are explained and used, and specific genes or gene families are chosen as examples of the principles being discussed. The author concludes with a chapter that places modern molecular evolutionary studies in the context of Neo-Darwinism and characterises evolutionary biology as 'a boat that we continually repair while remaining afloat in it' (after Otto Neurath, p. 234). The implication is that all we have learned in the past four decades from molecular evolutionary studies can be completely understood in the context of the Neo-Darwinian paradigm.

The author had to know that a phylogenetic systematist (cladist) would review the book sooner or later and in this respect I have reservations concerning the approach he has settled upon. Of the 36 phylogenetic trees in the book, 34 are Neighbor Joining trees and there is no real explanation of that method, how it works or of its philosophical basis. I do not really want to discuss here the foundations of the various means of phylogenetic analysis, but rather wish to take issue with Hughes' suggestion that 'some systematists have continued to view the field from the perspective of old controversies that are no longer relevant' (p. 34) and that new molecular data have 'made many old controversies obsolete' (p. 34). The special nature of molecular data that Hughes implies should make them immune from controversy, simply does not exist in

my opinion and his dismissal of problems with data analysis and embracing of phenetics is less than convincing to this phylogenetic systematist. An unconvincing discussion of maximum likelihood is also part of this chapter. Hughes characterises likelihood as 'less frequently used because it takes a great deal of computer time' (p. 37). The operational utility of an approach should never be used as an argument against its use, simply for the reason that the operation of techniques almost always get better and better with time. I suppose that, to Hughes, I am simply promulgating these old controversies, but in the opinion of many non-morphological systematists, these controversies are at the core of what we do as molecular systematists. My comments about tree building methods would, in my view, be a damning criticism of the book were it not for the fact that much of what Hughes has to say about adaptation at the molecular level can be said independent of phylogenetic trees. In this respect, the utility of statistical methods developed around silent and replacement substitution theory is evident in many places in this book and these methods are clearly the methods of choice for assessing the relevance of the important topics of balancing selection, directional selection and adaptation.

A final, positive, aspect of the book is that the descriptions of the biological systems examined are incredibly clear and easy to read. The MHC system, perhaps one of the most difficult genetic systems to explain, is clearly described with concise text and informative figures. This facet of the book should not go unnoticed as it really makes digging into what is important about the author's approach much easier. Instead of wasting time trying to figure out the biology of the systems in the book, the reader can concentrate on the scientific methods used. Whether you agree or disagree with the analytical approaches taken by Hughes, you will not be confused by the molecular systems that he takes as examples.

ROB DESALLE

*Molecular Laboratories
American Museum of Natural History
79th Street at Central Park West
New York, NY 10024
U.S.A.*

Methods for Risk Assessment of Transgenic Plants. Klaus Ammann, Yolande Jacot, Vibeke Simonsen and Gösta Kjellson (eds). Birkhäuser Verlag, Basel. 1999. Pp. 272. Price sFr. 128 (DM 148), hardback. ISBN 3 7643 5917 X.

If I had been asked to invent imaginary titles of the world's most boring books a few years ago, I might well have included a volume on the risk assessment of some technical procedure, perhaps along with the complete encyclopaedia of soap operas and juggling for beginners. It is a strange world though and I