

Book reviews

Genetics of Populations (2nd edn). Philip W. Hedrick. Jones and Bartlett Publishers, Sudbury, MA. 2000. Pp. 553. Price £26.99, hardback. ISBN 0 7637 1076 8.

Some years ago, population genetics was an esoteric discipline, apparently relevant only to those interested in developing a rigorous theory of how evolution occurred. Most biologists were happy to work within an evolutionary framework dominated by verbal descriptions of neo-Darwinism and Natural Selection. The molecular revolution of the past 20 years has had at least two consequences relevant here: firstly, all of biology has now become a subset of genetics, with the majority of disciplines using molecular genetics techniques to test hypotheses; secondly, many of these disciplines are explicitly or implicitly using methods or assumptions rooted in population genetics theory as standard techniques within their work. There is thus a great need for population genetics texts that are accessible to all biologists who wish to understand the background to the methodology they use.

This book is a new edition, which has been revised to incorporate some of the recent ideas emerging from the molecular revolution, while still providing the traditional theory underpinning the techniques. The major topics covered include; measures of diversity, selection theory, inbreeding, genetic drift, effective population size, gene flow, population structure and metapopulations, mutation, molecular population genetics (including phylogenetic tree building), multiple gene models and linkage disequilibrium, and quantitative genetics (including modern QTL techniques).

It is probably rare to read this sort of book from cover to cover, as a reviewer is expected to do. At the end of the introductory chapter, which is intended to provide an overview of the text, I was irritated by minor errors and simplifications and was beginning to form a negative image of the book, and framing a negative review. As I read further, I revised my initial opinion, and was increasingly impressed. The book covers a wide scope and marches through the various topics at a good pace. I might have given greater emphasis to some topics and queried the arrangement of others (for instance why is the discussion of self-incompatibility alleles not included with that of frequency dependent selection?) but that is a matter of taste and judgement. What is good is the mix of mathematics and example. Sufficient theory is included to provide rigour and the theoretical basis of the subject. This theory is developed at a level which should be accessible to the average numerate biologist. The theory is flashed out by a series of examples, separated from the text in boxes, which use real data to illustrate techniques or principles. These examples are generally interesting and well chosen. The weakest part of the book is probably the treatment of quantitative genetics, which neither is sufficiently detailed to provide a good

grounding in the traditional analysis of heritability, nor sufficiently introduces the principles and limitations of quantitative trait locus (QTL) mapping.

So who will buy this book? The preface suggests that it is designed for graduate students and advanced undergraduates 'who have had a course in genetics or evolution *and* have an aptitude for quantitative thinking' (my italics). I think this is an accurate descriptor. I could not use this as a standard undergraduate text in Britain because the level of algebra required would be beyond the competence of the average Biology student. As a library resource, it is excellent. I could certainly imagine using it as a core text for a postgraduate (MSc or PhD) taught course: I fear these are too rare to make the fortunes of author or publisher.

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The Triple Helix — Gene, Organism and Environment. Richard Lewontin. Harvard University Press, Cambridge, MA. 2000. Pp. 136. Price £14.50, hardback. ISBN 0 674 00159 1.

Back in the 1960s, Richard Lewontin was one of the first to use the technique of protein gel electrophoresis for assessing levels of genetic variation in natural populations. It was nothing short of a revolution in population genetics. Yet writing some 30 years later, Lewontin has a less rosy view. 'The result [of protein electrophoresis] was an almost universal abandonment of the research in all aspects of evolutionary genetics other than the characterization of genetic diversity. A single easily acquired technique changed and pauperized ... an entire field of study'.

This book is Lewontin's attempt to tell us what evolutionary biology has been lacking all these years. The message is simple and inescapable: only by looking at the context in which biological traits are expressed can we fully understand the complexity of evolution. Put another way, biology is messy, but it is the mess that is important. This is not a new idea, or even a plea for a new methodology, just an eloquent and dogged iteration of a biological truth. The question is, is it a useful truth? Lewontin is very keen to tell us about the limitations of a reductionist approach and cites plenty of examples where a blinkered gene-by-gene paradigm cannot make sense of biology. But, he is less good at telling us just how we should alter our perspective. About the closest he gets