

Book reviews

Principles of Population Genetics (3rd edn). Daniel L. Hartl and Andrew G. Clark. Sinauer Associates, Inc., Sunderland, Massachusetts. 1997. Pp. 542. Price £39.95, hardback. ISBN 0 87893 306 9.

There is demand for a more widespread understanding of population genetics. Many a 'health scare of the week' highlights the lack of public understanding of population processes. Areas ranging from law enforcement through agricultural and medical practice to biological conservation now require some expertise in population genetics. Does this book promise to satisfy the demand? Star qualities are immediately apparent: enthusiasm for the subject, a clear overview, and a universal style. Such qualities did not arise overnight. The two previous editions were considered to be the leading modern text for advanced undergraduates and beginning postgraduates. However, I feel that the presentation is too ambitious for most undergraduates, especially for those with no background. For such, Professor Hartl's *Primer in Population Genetics* (2nd edn) from the same publisher will provide a more accessible introduction.

To make life simpler, education tends towards telling a linear story. Population genetics on the other hand resembles a multidimensional jigsaw puzzle: its language is a colourful amalgam of physical mechanisms, mathematical models, and statistical descriptions. This text deals with the conflict by dividing the subject into its major processes and applications. Nonetheless, the authors try to emphasize connectedness: for example, between inbreeding and genetic drift. Another recurring theme is the current deficit in our understanding of the relationship between genetic and phenotypic variation.

The third edition introduces many changes in structure and content. The effect is to give a better flow from background concepts through processes to applications. The genetic system at the centre of attention is the classical gene in an outbreeding diploid. Nonetheless, glimpses are provided of other systems, such as selfing plants, transposable elements and bacterial chromosomes.

The first two chapters provide the genetic and statistical background. The resolution of the conflict between the biometrical and Mendelian views of inheritance by Sir Ronald Fisher is inserted to give the subject a historical perspective. Chapters three to seven form the core of the book, and describe the main influences on genetic variation, including the relationship between gene and genotype, population subdivision, inbreeding, mutation, recombination and migration. Chapter six provides a panorama of Darwinian selection, from single gene models, through the mutation-selection balance and interactions with genetic drift, to all the complexities of age-structured populations and epistasis. The long-standing debate about the relative roles of selection and drift in

adaptive evolution is referred to without the reader becoming enmeshed, and Kimura's neutral theory is accorded the role of universal null hypothesis in this context. The reader is given a taste of the diffusion theory which identified the equilibrium states of the classical literature, and which led to the latest coalescence models.

Chapters eight and nine deal with two major applications of population genetic theory: molecular evolution and quantitative genetics. The use of insights from the neutral theory to interpret protein and DNA sequence data is described, as are the methods for gene tree construction. Important applications of gene trees are described: for hypothesis tests of the direction of organismal trait evolution, for estimation of long-term migration rates, and for demonstrating selection at the gene level over evolutionary time scales. Quantitative genetics is given the standard presentation: the definition of heritability, and the estimation of components of genetic variance. The use of dense linkage maps for locating quantitative trait loci is presented as one way to elucidate the relationship between genetic and phenotypic variation. The book ends on this characteristically optimistic note. This book is essential reading for anyone requiring a firm foundation in modern population genetics.

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Arabidopsis Protocols (Methods in Molecular Biology 82). José M. Martínez-Zapater and Julio Salinas (eds). Humana Press, Totowa, New Jersey. 1998. Pp. 440. Price \$79.50, hardback. ISBN 0 89603391 0.

Arabidopsis Protocols represents a timely publication that is aimed to fill a niche within a market full of plant molecular biology-related titles. Interest in *Arabidopsis* as an experimental model for higher plants has increased exponentially since the mid-1980s and is set to rise even further with the impending completion of its genome project soon after the millennium.

The strongly nucleic acid-related theme within many chapters of the book reflects the array of techniques that are currently being employed by the international *Arabidopsis* community to map and clone their target genes. However, *Arabidopsis Protocols* does far more than provide solace for the loneliness of the long-distance chromosome walker. Initial chapters provide basic, yet important, information for new *Arabidopsis* researchers — how to grow this weed successfully! This section includes

useful chapters by Mary Anderson describing the control of *Arabidopsis* pests and diseases, plus Randy Scholl and colleagues detail how they preserve the longevity of *Arabidopsis* seed. In contrast, Part 2 proved disappointing. Whilst I commend the editors for including chapters describing the purification of *Arabidopsis* organelles and macromolecules, I was surprised to discover that *Arabidopsis* cells only contain mitochondrial and chloroplast organelles and that their macromolecules are totally nucleic acid-based! The inclusion of a chapter describing the subfractionation of *Arabidopsis* cellular membranes would have gone a long way towards balancing this section. Part 3 proved excellent reading, particularly the chapters on seed mutagenesis and genetic analysis which included useful introductory discussions, whilst Part 4 comprehensively describes PCR and RFLP-based techniques used to map *Arabidopsis* genes and mutations. Transient and stable *Arabidopsis* transformation techniques provide the theme for Part 5, including a description of vacuum-based *in planta*, *Agrobacterium*-mediated transformation by Bechtold and Pelletier. However, I was surprised to see no reference being made to detergent-based *in planta* transformation methodologies which are currently gaining favour amongst many *Arabidopsis* laboratories. Commendably, the treatment of gene cloning within Part 6 was well balanced, contrasting chromosome walking and landing strategies with transposon and T-DNA-based gene tagging approaches. The final section addresses techniques used to study *Arabidopsis* gene expression including a selection of chapters describing *in situ* hybridisation, reporter genes and, particularly enjoyable, *in vivo* footprinting. However, I was disappointed that the editors did not include a chapter on the localisation of those well known DNA by-products, proteins! This omission emphasises the overall nucleic acid-based theme within *Arabidopsis Protocols*. Whilst it is fair to say that the majority of *Arabidopsis* researchers are presently engrossed with nucleic acid-related topics, there is a growing interest in post-transcriptional processes.

In summary, *Arabidopsis Protocols* provides an excellent technical reference for molecular geneticists, old and new, and will represent a 'must-have' text for every *Arabidopsis* laboratory for the next decade.

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Principles of Genome Analysis (2nd edn). S. B. Primrose. Blackwell Science, Oxford. 1998. Pp 193. Price £19.50, paperback. ISBN 0 632 04983 9.

S. B. Primrose has authored or co-authored several books like this one: heavily illustrated texts of between 100 and 200 pages on subjects related to gene manipulation. Each is aimed at a broad market — students, lecturers or researchers interested in understanding, or considering entry to, the fields in question. All provide references to

both the original literature and to appropriate reviews (about 400 references are cited in this volume). The two most successful, *Introduction to Modern Virology* (latterly with Dimmock) and *Principles of Gene Manipulation* (with Old) are in their 4th and 5th editions, respectively, and have increased in size several fold (to about 400 pages). *Principles of Gene Manipulation* is used as a teaching text in this University.

Each of these books was last updated in 1994. *Principles of Genome Analysis*, subtitled *A Guide to Mapping and Sequencing DNA from Different Organisms* was first published in 1995 and has now been republished in revised, although not much lengthened, form. The subject of this volume is, of course, extremely timely. With public interest in human genome analysis reaching heights unprecedented for a problem in fundamental biological research, and with both large-scale commercial and government funding earmarked for the sequencing and analysis of the genomes of dozens of different species, the constituency of those interested in this volume should be both large and diverse.

The book is divided into seven chapters. Chapter 1 attempts both to explain the benefits of genome sequencing, from the lofty ('detailed understanding of the organism will only be achieved when every gene has been identified and its transcript and the timing of transcript synthesis known') to the practical (a more efficient way to find disease genes). It also lists sequencing projects which are underway, describes some techniques, and outlines the rest of the book. I found Chapter 2 on the organization and structure of genomes (with the lowest density of 'practical' information) the most interesting. As one more familiar with prokaryotes, the complexity and variability (even amongst related species) of eukaryotic DNA organization creates for me a bewildering picture: why does the cow have a genome which harbours 25% tandemly repeated DNA? Why is mammalian DNA heavily punctuated with functionally inactive interspersed repeats? Why do introns vary in size and frequency between species? Chapter 3 is a straightforward exposition of methods for subdividing chromosomes into minichromosomes and other vectors as a preliminary to sequencing and gene mapping. Chapter 4 offers a real challenge to the novice; it presents a veritable alphabet soup (fortunately there is an abbreviations list at the start of the book) of ingenious methods for assembling physical maps. I think, for the non-expert, it is more to be dipped into than assimilated. Chapter 5, on sequencing, began as a welcome relief but progressed to an explication of sequencing on microchips which defeated me. Chapter 6, on sequence analysis and new to this edition, is only 12 pages long and surprisingly, considering the subject matter of the rest of the book, concentrates primarily on bacterial genome sequences with heavy reference to the publications of Koonin and collaborators. Others are more circumspect than he at declaring pairs of genes homologous and the impression is perhaps given here that genes (and their functions) are more conserved between species

than may eventually prove to be the case. The final chapter deals with finding genes in the DNA-haystack of large genomes.

The text is well illustrated with mostly useful diagrams (some borrowed from *Principles of Gene Manipulation*), although some were hard to understand, and with a lesser number of tables (I would have liked more). There are a number of proof-reading errors, omissions (several references are absent from the reference lists) difficult or inadequate figure captions and the occasional misstatement, but these do not seriously detract from the usefulness of the book. Although I suspect that private purchases may be limited, this is certainly a volume with a place in every comprehensive biology library.

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Genetic Structure and Local Adaptation in Natural Insect Populations. Susan Mopper and Sharon Y. Strauss (eds). Chapman and Hall, New York. 1997. Pp. 449. Price £65.00, hardback. ISBN 041208031 1.

Some 30 years ago, three seminal papers were published that have steered subsequent work on insect/plant interactions. First, Hairston, Smith & Slobodkin (now known as HSS, 1960) published a short note based on the observation that 'the world is green' and that the nature of population regulation depends on the trophic level examined. This work sparked research and controversy eventually leading to debates on the role of competition vs. other forces in structuring ecological communities. Following HSS, Ehrlich & Raven (1964) made the case for reciprocal coevolution between plants and insects, prompting investigations into the role of phytochemistry in insect/plant interactions, as well as phylogenetic tests of macro-evolutionary cospeciation between insects and plants. Finally, Bush (1969) stirred the pot with evidence from plant associated flies of sympatric speciation, a topic that remains controversial to this day. Now, 30 years later, we are wondering where this field stands.

For the past decade, Denno & McClure's (1983) *Variable Plants and Herbivores in Natural and Managed Systems* and Strong, Lawton & Southwood's (1984) *Insects on Plants* provided the backbone for this discipline. In this volume, Mopper and Strauss have offered a much-needed update to these well-worn bibles of insect/plant interactions. It is an impressive collection of well-edited papers that focus on the genetic issues at the heart of insect/plant interactions, and in particular the importance of demic adaptation. In the past third of a century, the field has matured, not coincidentally as a result of more sophisticated genetic techniques as well as methods of analysis.

So, what's new? Several themes emerge. As Boecklen & Mopper (Ch. 4) point out, the proper designs to test for local adaptation are now recognized, and the relevant

data are pulled together here for the first time. Picture insects feeding on plants. First, selection for adaptation to host plants can be strong enough to overcome most scenarios of gene flow (Strauss & Karban, Ch. 8), and, as a result, local adaptation can occur at several possible scales, for example, individual plants, plant species, and sites (Mopper, Ch. 7). Local adaptation can lead to the formation of demes (Alstad, Ch. 1; Stiling & Rossi, Ch. 2), but not always (Cobb & Whitham, Ch. 3; Boecklen & Mopper, Ch. 4; Hanks & Denno, Ch. 11). Dispersal, or lack thereof, is critical in permitting local adaptation (Mopper, Ch. 7; Strauss & Karban, Ch. 8, Hanks & Denno, Ch. 11; Thomas & Singer, Ch. 14). Feeding style (Stiling & Rossi, Ch. 2), inherited environmental effects (Rossiter, Ch. 6), social behaviour and other intrademic structure (McCauley & Goff, Ch. 9; Costa, Ch. 10), life history patterns (Peterson & Denno, Ch. 12), and many sorts of habitat heterogeneity (Gandon *et al.*, Ch. 13), all influence the magnitude of gene flow if not the likelihood of local adaptation. Finally, host fidelity can act as a reproductive barrier to gene flow either partially (Thomas & Singer, Ch. 14; Itami *et al.*, Ch. 15) or nearly completely (Feder *et al.*, Ch. 16).

Given that the book is a solid and important contribution to the field, is anything missing? The mechanisms underlying adaptation have received little attention by the contributors and are 'conspicuous by their absence' (Berenbaum & Zangerl, Ch. 5). This criticism may be valid—reciprocal transplant studies used to detect local adaptation often make it difficult to distinguish among various selective mechanisms. However, this is a criticism of the field rather than the book. One promising area that was overlooked in the book is the use of phylogenetics or genealogies to understand the evolution of host associations, although Itami *et al.* (Ch. 15) come close.

With regards to organization, I have four reservations about the volume. First, the collection of papers is dominated by North American schools of insect/plant studies – 15 of 16 papers; the 16th, Gandon *et al.*, is out of France. Second, the authors missed an opportunity to comment on the chapters — the four sections would have benefited from both synthesis and perspective. Third, the index is thin at seven pages, compared to 37 pages in Denno & McClure (albeit a larger volume) and 20 pages in Strong, Lawton & Southwood (a smaller volume) which included a very useful author index, an unfortunate omission here. Fourth, and this one is for the publishers, £65.00 is beyond the grasp of most graduate students worldwide. Does it really cost this much to produce an edited volume of 16 papers when academics write these chapters for free?

That said, who will want to read the book? I would recommend the book as required reading for anyone interested in insect/plant interactions. Perhaps more importantly, it is an outstanding source of ideas. The perfect target would be students in a seminar setting, or a grant-starved professor submitting another proposal on insect/plant interactions (thank you!), or a beginning PhD

student looking for a project. But, for those of you whose daily encounters with entomofauna is a splat on the windshield and the millennium bug, there is still a lot here — genetic differentiation, selection, adaptation, specialization, life-history variation, speciation, and biodiversity. There is no doubt this field is evolving quickly, so read the book and keep up with the Red Queen!

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Melanism: Evolution in Action. Michael E. N. Majerus. Oxford University Press, Oxford. 1998. Pp. 338. Price £23.95, paperback. ISBN 0 19 854982 2.

The classical example of natural selection at work concerns melanism (the occurrence of dark forms). Probably all biologists have heard about ‘the peppered moth story’, first published by Kettlewell in *Heredity*. The simple version of the story is that once upon a time there were two forms of the peppered moth (*Biston betularia*), a common white one and a rare black one. When pollution made tree trunks black, more whites than blacks were eaten by birds, and since then most peppered moths in industrial areas are black. If you suspect that the reality is not as simple as that you are right. The moths, for example, do not normally rest on tree trunks, and intermediate forms exist. Michael Majerus dissects the story in his book on melanism and shows that it is more complex and fascinating than most biologists will have realized.

The book starts with general principles. First what melanism is and its possible causes, then principles of genetics and finally those of evolutionary processes. Readers of *Heredity* can skip the genetic part, unless they want to have a clearly written text that explains genetics at the very basic level. Likewise the evolutionary part: it is basic, but might be suitable in a course for first year students. The remainder of the book is on melanism in specific groups of organisms. First two chapters on the peppered moth, then two on other moths, and finally a large chapter on ladybirds. The reason for the choice of organisms is not that melanism is restricted to them, but simply that the author happens to work on them. Is the book therefore only of interest to those who work on moths and ladybirds? Surely not! By ignoring the book workers on other organisms would make the same mistake that Majerus did, missing interesting and important work outside their own realm.

The author states in the preface that one of his original goals was to ‘update Kettlewell’ but that this was not achievable in one book. Instead he has ‘used only those examples known to me to illustrate the points I have tried to make’. His real aim then was to engender renewed interest in melanism. But he could have done a better job in this respect. By sticking to his ‘own organisms’ he missed the opportunity to highlight several important topics related to melanism. There is, for example, nice work on plasticity in melanism, and on the relationship between the darkness of wings and mate locating behaviour in butterflies. The author apparently also missed the fact that the forms of the scarlet tiger moth (*Panaxia dominula*) are mainly determined by temperature, thereby making it useless as an illustration of balanced polymorphism. The book is almost exclusively on cases of melanism with discrete forms determined by a few alleles. Heritabilities are hardly mentioned, although there exists work dealing with continuous variation, even in ‘his own’ ladybirds. I found the last section on ‘the future of research into melanism’ disappointing. I think that the most exciting opportunities arise by integrating different biological disciplines. What, for example, is the developmental basis of the spots in ladybirds, is it the same in the different forms, and in different species? By combining such questions with a phylogenetic approach we would really learn something new about the evolution of melanism. The book is, however, very readable — something which cannot be said of many books containing so much interesting scientific material.

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