Book reviews

Molecular Evolution: Producing the Biochemical Data. Methods in Enzymology (Vol. 224). E. A. Zimmer, T. J. White, R. L. Cann and A. C. Wilson (eds). Academic Press (Harcourt Brace), London. 1993. Pp. 725. Price £63.00, hardback. ISBN 0 12 182125 0.

The recent growth of interest in molecular evolution can be measured in various ways: the number of new specialist journals being launched such as *Molecular Phylogenetics and Evolution*; the number of requests for exotic strains and species received by culture collections and museums; the number of registered users of computer programs such as PAUP; perhaps even the numbers of thermocyclers sold. Another milestone in the transformation of molecular evolution from a curiosity into a discipline has been reached with the publication of this dedicated volume of *Methods of Enzymology*, which forms a companion to Volume 183 (*Molecular Evolution: Computer Analysis of Protein and Nucleic Acid Sequences*). That volume, edited by Russell Doolittle and published in 1990, dealt exclusively with 'dry lab' computer analysis of finished sequences. Zimmer *et al.*'s volume is all about wet labs and even wet feet, reflecting the newfound ability of evolutionary biologists to go out and generate experimental data, largely thanks to PCR.

The early chapters introduce us to collecting specimens in the field and getting the all-important nucleic acids out of them. For anybody planning to bag some vital taxon in some far-flung country and export it back to the lab for analysis, permits and licences will constitute a major problem. Kenneth Sytsma and colleagues tell us how it can take up to a year to get the seven different permits needed to use a helicopter to collect plants from the tepuis of southern Venezuela, and even then we could spend a further week in Caracas negotiating with the authorities. For shipping the critters home, Rebecca Cann suggests looking for dry ice locally at hospitals, meat packers, ice cream wholesalers or gas dealers. Her suggestion that we label the parcel 'Biomedical Samples for Scientific Research', might indeed work better at the post office than the more accurate 'Dead Birds for Cladistic Research'. When all else fails, Sytsma suggests stuffing a leaf sample into an envelope, along with the necessary permits, and mailing it back to the lab.

The importance of collaboration with expert systematists surfaces throughout the volume. Meredith Blackwell and Russell Chapman comment that it is a sad irony that, even as interest in applying molecular techniques to the systematics of every species under the sun is booming, there are fewer and fewer experts who can accurately identify those species. They go on to argue for the inclusion of 'alpha-level' taxonomists at all stages of the design and execution of molecular systematics projects. Many of the new breed of molecular

biologists-turned taxonomists have a cavalier attitude towards vouchering specimens and otherwise making their work repeatable. Mathew Dick and colleagues point out that, given the amount of effort required to obtain a DNA sequence, it behoves the researcher to identify the sample with something a little more detailed than *Genus* sp.!

The numerous chapters dealing with aspects of nucleic acid isolation and sequence analysis are in general very informative and readable (despite the awful format that *Methods in Enzymology* uses for references). One of the highlights for this reader is an excellent guide to the animal mitochondrial genome by Rob DeSalle and colleagues, who discuss the appropriateness of different regions of mtDNA for phylogenetic analysis at different depths. Their data should enable those designing future studies to strike an optimal balance between experimental effort expended and evolutionary information gained. It is surprising, though, that the use of the rapidly-evolving mitochondrial D-loop region for within-species studies is not mentioned in DeSalle's or any of the other chapters, particularly since the pioneering work in this field was carried out in Allan Wilson's laboratory.

There is, however, more to molecular evolution than PCR and DNA sequencing. The real eye-opener in this book is the diversity of methods by which DNA and proteins can be used for phylogenetic analysis without actually sequencing the molecules. While sequences offer an unparalleled degree of resolution of character states, some other methods have the advantage of being able to survey the whole genome (or at least hundreds of genes) simultaneously, albeit at lower resolution. Liz Zimmer and her co-editors deserve great credit for inviting articles from authors who are not (entirely) on the PCR bandwagon. The methods covered include DNA-DNA reannealing kinetics (M. S. Springer and R. J. Britten; C. P. Kurtzman), two-dimensional protein gel electrophoresis (D. Goldman and S. J. O'Brien), immunological distances (E. M. Prager and A. C. Wilson) and denaturing gradient gel electrophoresis (E. P. Lessa). Grouped at the end of the volume under the catch-all heading 'Comparing Macromolecules: Exploring Evolutionary Pattern and Process' is a mixed bag of topics that defy classification but nonetheless fit under the umbrella of molecular evolution. These include biochemical methods for identifying self-splicing group I introns (B. Reinhold-Hurek and D. Shub), gene recruitment in crystallins (G. Wistow), and a fascinating essay by Andrew Ellington on how to test theories about the RNA world.

All in all, *Molecular Evolution: Producing the Biochemical Data* is excellent and deserves a place in your library. One criticism that might be levelled at it is that readers (particularly those new to the field or considering new techniques) could have benefitted from a little more overview. Faced

with a smörgasbord of alternative methods for addressing a phylogenetic question, how does one choose the 'best' approach? The authors of the 47 separate chapters tend to assume that readers will *want* to use the techniques they describe, and so provide little or no justification for their choice of approach or comparison with other methods. In some chapters the authors do not even describe any results obtained using their methods. Once in a while it would help if the authors could step back from their gel rigs and tell us *why* they prefer sequencing mitochondrial DNA over isoelectric focusing, or *vice versa*. This is *Methods in Enzymology* after all, but a little less methodology and a little more ideology would not have gone amiss.

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Footprinting of Nucleic Acid-Protein Complexes. Arnold Revzin (ed.). Academic Press (Harcourt Brace), London. 1993. Pp. 193. Price £33.00, spiral bound. ISBN 0 12 586500 7.

This book is the first in a series 'Separation, Detection, and Characterization of Biological Macromolecules' and the series as a whole is also edited by Revzin. The aim of the series is to be inclusive (though not excessively so) and user-friendly (hence the spiral binding) as well as to expand the user's horizons. This volume begins with a short introduction by the editor, followed by accounts of: quantitative DNase I fingerprinting, by M. Brenowitz, D. Senear, and colleagues; footprinting of DNA-protein and RNA-ligand interactions with 1,10-phenanthroline-copper, by A. Mazumber, who earlier worked with D. S. Sigman, a pioneer of the use of this compound; hydroxyl radical footprinting, by T. D. Tullius (with J. S. Bashkin); permanganate probing, by J. D. Gralla and colleagues; DNA photofootprinting *in vitro* and *in vivo*, by M. M. Becker (with G. Grossmann); and exonuclease III digestion and interference and missing contact footprinting, by A. Revzin (with J.-L. Cao). The authors (all located in the USA) are largely either the developers of a technique or those who have worked directly with them, and the articles are therefore reasonably authoritative.

Each chapter starts with an introduction describing the basis of the particular footprinting method, goes on to provide extensive protocols, and finally – at a length that differs in the various contributions – gives examples of the use of the technique. The introductions are in general sufficiently detailed and chemically precise to be worth forcing on impatient research workers anxious to put the methodology into action merely as cookery. The protocols were judged by members of my research group to be clear and genuinely useful. Only the chapters by Revzin and by Gralla *et al.* have sections explicitly on troubleshooting, and my colleagues felt that more attention to this might have been helpful.

DNase I footprinting, in its qualitative form, is probably still the most widely used footprinting technique. The Brenowitz/Senear *et al.* article devotes the first third of its 41 pages to useful coverage of this aspect, the remainder being a suitably detailed description of the thermodynamic analysis of quantitative footprinting data. The latter is in two parts, densitometric analysis and mathematical analysis of the resulting site-binding isotherms. The densitometry primarily relates to use of a two-dimensional optical scanner for digitization; this is perhaps unfortunate since phosphor storage screens (mentioned here briefly) are becoming increasingly common. Densitometry and the use of phosphor storage screens are also described in the chapter by Bashkin and Tullius.

Protein-nucleic acid interactions are frequent objects of experimentation among those interested in the control of gene expression and mechanisms of drug action on virus assembly, in both pro- and eukaryotes. This book puts together the most widely used current techniques in a useful but adequately detailed form, and I would certainly recommend it as likely to be found helpful in laboratories of many kinds. In such a fast-moving area, it is inevitable that existing methods will be improved and new ones invented, and a new edition of this book will become necessary before long. It will probably then be found that much more attention will have to be given to protein-RNA interactions, a topic which finds its way only into Mazumber's contribution here.

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Evolution. Mark Ridley. Blackwell Science Ltd, Oxford. 1993. Pp. viii + 670. Paperback, £19.50, ISBN 0 632 033481 5; hardback, £39.50, ISBN 0 86542 226 5.

This is a very useful, reasonably priced, well-written evolution textbook. It is a strong competitor to previous texts like Douglas J. Futuyma's *Evolutionary Biology* (1986), John Maynard Smith's *Evolutionary Genetics* (1989) and Strickberger's *Evolution* (1989). For obscure reasons, my students found Futuyma's book, which is much more expensive, rather complicated. For the lecturer, Maynard Smith's book came as a breath of fresh air with its novel approaches to molecular evolution and other topics. However, my enthusiasm was not shared by students who found the abbreviated mathematics very hard going. Ridley's approach, which is similar to Maynard Smith's in some chapters (compare especially Ridley's 'Two-locus and multilocus population genetics' to Maynard Smith's 'Evolution at more than one locus') has greatly expanded verbiage at the expense of mathematical rigour. Ridley has also added chapters on biogeography, phylogeny, and macroevolution, to make a more complete evolution text. Students liked it, so I have adopted it for the second year course in evolutionary genetics at University College London.