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 Mazumder'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.