Recombinant DNA Technology and Population Genetics. The intended target readership for this package is not made clear but, in my opinion, it is pitched somewhere between A-level and first year undergraduate. For the purposes of this review, it seems appropriate to consider the book and the CD-ROM separately and then to see how well they interact to deliver the stated aim.

The workbook is not attractively presented. It is flimsy, has an awkward fastening and, after the CD-ROM has been removed from the front cover, looks and feels a bit of a mess. There is no colour, no introduction and no instructions for use. What you get are short summaries with little detailed information (2 pages) followed by a series of questions and answers (around 26) for each topic. Apart from the number of questions, there is nothing here that you can not get in a typical textbook, although the questions were different to those compiled on the CD-ROM.

What, then, of the CD-ROM? In these days of 'all-singing, all-dancing' multimedia software this had a very limited feel. The image size was not adjustable and on my 17' monitor the available window was small enough to make diagrams and text difficult to read. Secondly, there was no 'undo' function and this rapidly became infuriating; clicking a wrong button meant having to go back through a series of pages. Finally, I had problems with the search facility. This failed to find hits for 'PCR' or 'sex-determination' despite the fact that I had read the appropriate entries! When these deficiencies are coupled with the lag-time at each click, I think students will find their patience tested.

As for content, the CD-ROM covers the same topics as the workbook but the format does not offer sufficient advantages to compensate for the lack of detail. There are a limited number of animations and simple videos that do help to explain certain topics (for example chromosome segregation) but they were not particularly gripping and were backed by a very uninspiring voice over. The topic reviews contain only marginally more information than the topic summaries in the workbook and students in all but the most basic of genetics courses will have to consult a textbook to fill in the many gaps. There are also deficiencies in the content. I was, for example, very disappointed with the coverage of population genetics. It is over simplified and makes no attempt to integrate the subject with the modern era. The review has just seven paragraphs (allele frequencies, H–W equilibrium, selection, heterozygous advantage and mutation–selection equilibrium) forming a random selection with little coherence or structure and not even any whizzy multimedia by way of justification. The CD-ROM presents sex determination in *Drosophila* as a simple XY system and makes no attempt to explain the importance of X:autosome balance. Curiously, this topic is correctly presented in the workbook! Finally, there are some aspects of the software that are simply quirky. The description of non-disjunction in *Drosophila* has diagrams of insects which vibrate their wings noisily and fly away just as you are trying to take in the information. This was amusing the first time, but irritating and unhelpful subsequently.

Are there any advantages? Once again, some students might appreciate the 'self-tests' which can be taken in any or all of the topics. The CD-ROM format presents little interaction here although there are some on-screen hints. One or two of the questions are awkwardly phrased, as if they were designed to trick the student. Anyway, that is my excuse for scoring only 60% on the test that I did! All in all, I found the package disappointing and, although I might use some of the questions, I can see little scope for its inclusion in my courses as a teaching aid. I suspect that students would rather spend their £20 on a comprehensive and colourful textbook.

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DNA and Protein Sequence Analysis — A Practical Approach M. J. Bishop and C. J. Rawlings (eds). IRL Press (Oxford University Press), Oxford. 1997. Pp 374. Price £29.95, paperback. ISBN 0 19 963463 7.

The quantity of DNA and protein sequence data generated by the research community continues to expand at an ever increasing rate. The availability of automated DNA sequencing technology has led to the determination of the complete genome sequences of several unicellular organisms, and the *C. elegans* and human genomes are likely to be characterized within a few years. This has resulted in the accumulation of a large number of sequence databases and the increasing use of computers both to store and analyse sequence data. However, the establishment of many independent databases has led to a lack of standardisation that complicates the retrieval of information, whilst the vast choice of software for a given application can often be confusing.

This volume, from the Practical Approach Series, provides clear and critical guidance on the analysis of DNA and protein sequence data from experts in all areas of the field. The book begins with an excellent overview of the sequence databases currently available, including methods for depositing, identifying and retrieving data and the potential problems associated with disparity between databases. Later chapters include appraisals of software for sequence analysis, covering the uses, advantages and disadvantages of individual programs. There are excellent reviews of DNA sequencing methodology, including many clear and helpful protocols, and of methods for gene identification. Other topics covered include: the analysis of simple and repetitive sequences; methods for sequence alignment — with an overview of the advantages and disadvantages of the many algorithms available; and the use of programs for sequence alignment and structure prediction as a means of forecasting protein

function. The volume is concluded by detailed reviews of methodologies for phylogenetic estimation and the determination of evolutionary relationships between proteins on the basis of sequence and structure comparison. Taken together this should allow the researcher to progress from the generation of DNA sequence data to the identification of genes and prediction of the sequence, structure and function of the proteins they encode.

All the chapters in this book are well written and cross-referenced with very little redundancy. The rapid development of the field and the huge volume of software available precludes the provision of specific protocols in many cases, and these have been replaced by critical summaries of the different methodologies available and their capabilities and uses. The majority of this volume is written in a way that should be understandable by those with little prior knowledge of the topics covered. Most chapters include an extensive and up-to-date bibliography and a particularly useful feature is the provision, throughout this book, of addresses for E-mail, ftp and World Wide Web servers from which the software described, as well as additional information, can be obtained.

This book will be a valuable resource for researchers in molecular biology as well as those interested in bioinformatics.

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