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Book Reviews

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Analysis of Genes and Genomes. R. J. Reece. John Wiley & Sons Ltd. 2004. 469 pages. ISBN 0 470 84380 2. Price £34.95 (paperback).

It is almost exactly thirty years since the start of the revolution that changed the way we do, and think about, research in biology. The union of nucleic acid and protein biochemistry with bacterial genetics which occurred then gave us methods which allow us to not just speculate about what genes and genomes might be like, and how they might work, but to actually get stuck in and find out. In the ten years or so which followed many books were published explaining these techniques to readers at all levels, from first year undergraduate to bench scientists. The pace with which the technology changed meant that new books, or new editions of old books, had to appear frequently to keep pace, but as the methodology has matured and has become incorporated into the toolkit of nearly every biologist, so the frequency with which new texts have appeared has declined. The technology has continued to evolve, however, and older texts no longer provide satisfactory support for teaching while general texts go into insufficient detail. I am pleased to say that 'Analysis of Genes and Genomes' looks like filling the gap.

More or less the full range of topics one would wish to see in such a book are covered, from a brief introduction to DNA, proteins and genes probably not necessary for anyone likely to use the book but difficult to exclude, through standard methods for cloning in bacteria, yeast and mammalian cells, including PCR, *in vitro* mutagenesis and protein expression and on to genome sequencing and the manipulation of the genomes of plants and animals. Nothing is covered in great depth but the information provided is commendably up to date and there is a welcome chapter on post genomics including microarray analysis. The text is generally easy to read and the book is thoroughly illustrated and well referenced, including mention of at least one paper published in 2003.

Inevitably there are some oddities. It is not clear why the particular examples of single-gene human genetic disorders were chosen for Table 13.2 or the tissue specific promoters for Table 13.1, the inclusion of a Table illustrating Chargaff's rules (Table 1.1) seems quaintly out of place, and, a more significant point, the omission of any reference to transposable elements in the discussion of genetic manipulation of plants and animals is surprising given their use for transformation of many species and their possible role in gene therapy. On the other hand there is some information that anyone would be glad to find in one place such as the properties, including error rates, of different thermostable DNA polymerases (Table 4.2), and the sequences and origins of different epitope tags (Table 8.1). For those wanting to delve more deeply into techniques it might have been helpful to have guided them to more detailed sources, such as the three volumes of Sambrook and Russell's 'Molecular Cloning' (Cold Spring Harbor Press).

When I was sent this book I expected to find in it a detailed discussion of genes and genomes. This is not what it is about, and 'Techniques for the Analysis of Genes and Genomes', or something similar, might have been a better title. Hopefully those wanting to learn about modern cloning technology will find it nonetheless. I certainly welcome the book, and shall make use of it to support my teaching.

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A Genetic Switch, Third Edition, Phage Lambda Revisited. M. Ptashne. Cold Spring Harbor Laboratory Press. 2004. 154 pages. ISBN 0 87969 716 4. Price $39 (paperback).

A Genetic Switch, as published first in 1986, was a celebration and tribute to the biological dissection of the amazingly complex genetic regulation within bacteriophage Lambda. The original book was a joy to read for both novices and established academics. For students trying to grasp the intricacies of biological decision-making, the clear and concise construction of A Genetic Switch took them by the

hand and guided them to an enlightened view of a system that superficially looked daunting. This description was true for the second edition published in 1991, but is it still applicable for the third edition and 21st century students?

The purpose of A Genetic Switch is to take the reader through the complexities of Lambda's regulatory network that dictates whether the phage undergoes lysogeny or the lysis. The elegant use of repressors and activators to distinguish between these two ''life styles'' is a tour de force of developmental biology. The book is well written and the diagrams clear and concise. The third edition of this book has been subtitled ''Phage Lambda Revisited'', one would therefore suspect that the book had been updated since it's inception 18 years ago. Here lies the dilemma. The first four chapters of the book are identical to the 1986 version while some additional new material has been added at the end as a fifth chapter. The outcome from this construction is a book that reveals its antiquity and then tries to patch-up the shortcomings with some more recent research. From a teaching point of view this is an unacceptable approach. By their very nature, text books are out of date by the time they reach the bookshelves, however, one should not accept a text that is 18 years out-of-date. This book is aimed at intermediate level biology students – an assumption based on the fact that the Introduction starts with a simplistic description of DNA. Why would teachers recommend a text marred by inaccuracies which then makes a limited and late attempt to provide the correct information? Why not simply rewrite the book with the correct information? How are students expected to differentiate between pertinent ideas and those that haven't stood the test of time? Perhaps the author and the publishers haven't realised that students tend to be dogmatic – if it's in a book, it's fact!

Here are two examples that reflect the lack of modernisation and would adversely affect student learning outcomes. First, the SOS response. Exposure of *E. coli* to ultra-violet light was central to the demonstration of lytic induction of an integrated Lambda prophage that ultimately led Jacob and Monod to postulate the existence of gene regulators. Both chapters 1 and 3 give brief descriptions of the SOS response and how it relates to cleavage of the Lambda repressor. Both chapters refer to the activated form of RecA protein (RecA*) as a protease – which it is not. Work from the Little laboratory in the late 1980's demonstrated that RecA* is a co-protease that assists with the auto-catalytic cleavage of proteins such as LexA and the cI repressor. Students reading the description of the SOS response in A Genetic Switch will be given the incorrect version in the first 3 chapters and will then have to read chapter 5 before being informed of the reality. Perhaps publishers should note that students don't always finish books. The second example involves a number of assertions that state nothing is known about the structure of RNA polymerase. Obviously in 1986 nothing was known about the structure of RNAP, however, a student reading such as statement today would be justifiably confused considering the excitement over the crytal structure of core RNAP from *Thermus aquaticus* in 1999.

So who is this book for? Two groups of academics spring to mind: those that have a limited knowledge of Lambda and want to skip the first 4 chapters to read some new stuff; or those that left their original cherished copy on a train or in an airport. Students beware (unless you're specifically interested in a historical lesson on Lambda)!

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Design and Analysis of DNA Microarray Investigations. R. M. Simon, E. L. Korn, L. M. McShane, M. D. Radmacher, G. W. Wright & Y. Zhao. Springer-Verlag. 2003. 200 pages. ISBN 0 387 00135 2. Price $59.95 (hardback).

While the applications of gene-expression studies in biological and medical research are filling major proportions of scientific journals, there is still a lot of debate on the design and analysis of microarray studies. A textbook on the design and analysis of microarrays is not only very timely, but also very brave, given that the field is still moving rapidly and new methods of design and analysis are published weekly.

The book provides a very good overview of the issues and techniques, suitable for a non-specialist readership that would be interested to embark on microarray studies. Throughout, the authors discuss both spotted cDNA arrays and oligonucleotide arrays (i.e. Affymetrix chips), which adds further merit to this book.

Following a brief introduction in Chapter 1 (a summary of gene expression biology is provided as Appendix A), Chapter 2 describes the technology underpinning microarrays. Chapter 3 deals with the design of microarray experiments, including a number of designs for two-colour arrays and statistical power calculations.

The following chapters deal with different aspects of microarray analyses. The first step, image analysis, is discussed in Chapter 4, while Chapter 5 describes quality control strategies including some data imputation approaches. Chapter 6 is dedicated to array normalization providing a concise but clear overview of current approaches.

The remainder of the book deals with the different applications of gene expression data. Chapter 7 describes the methods for class comparisons, including several permutation approaches to deal with the multiple testing problems that are an integral part of microarray studies. While Chapter 7 describes the tools to detect (groups of) differentially expressed genes between different classes, Chapter 8 focuses on the selection and analyses of subsets of genes to assign samples to different classes (class prediction). Chapter 9 describes various analyses for discovering clusters of co-regulated genes. The Appendices deal with a general overview of gene expression biology (Appendix A), a description of the example data (Appendix B), and a description of the software that is developed by the authors (Appendix C).

A great asset of this book is that all the example data are freely available for analysis, along with the BRB-ArrayTools software (http://linus.nci.nih.gov/BRB-ArrayTools.html). The full-colour pictures are instructive, but the fact that they are inserted in the centre of the book reduces their utility somewhat.

The authors have their roots in cancer research and all examples are in this area. This provides a somewhat skewed view of the potential applications of gene expression arrays with little or no attention for new applications like genetic control of gene expression or their merit for systems biology.

The authors have made significant contributions to the methodology in the areas of design and analysis and this sometimes affects the choice and depth of the methods that are presented in the book. For instance, in Chapter 3 the authors state that, for two-colour arrays, reference designs are generally preferable and dye-swaps are not necessary (citing mostly their own work). The methods for gene expression analyses are subsequently detailed mainly for this type of design, although lip service is paid to alternative methods. Keeping this in mind, the book provides an excellent introduction to all aspects of microarray analyses and its modest 200 pages make it a very good read for anyone interested in the subject.

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