

instruments, as well as the computer software designed to process the data. The most important role of the cell biologist or biochemist is to ensure that the biological specimen is in the best possible state. This group of chapters is particularly valuable for the tips on specimen preparation and preservation, with some explanation of why the steps involved are of such crucial importance.

Volume 2 (Cell Function) is more specialised, focusing on more complex cellular specimens and the processes carried out in them. The organelles dealt with include chromosomes, intact nuclei, mitochondria, vesicles derived from endoplasmic reticulum, late endosomes and chloroplasts. Other chapters cover processes taking place in whole cells (cell cycle control, receptor biology, signal transduction). The range of protocols is huge. The uses of fluorescence, for example, extend from the location by light microscopy of specimens labelled by immunofluorescence or by GFP, to measurement of mitochondrial membrane potentials. These sections all fit in nicely with the general advice in Volume 1 on the choice of fluorophores for particular purposes. The only technique that seems conspicuously absent is the use of siRNA; however, details of this popular new tool are fairly easy to find in recent literature, unlike older techniques that have been gradually improved over many years.

Each chapter is written by expert practitioners who are able to include up-to-date tips on how to take advantage of reagents and pieces of equipment that are currently available. For example, in the chapter on gel electrophoresis, in addition to a nice combination of background theory and practical details of the very varied uses of electrophoresis, there is useful information about commercially available precast gels, whose use is becoming increasingly widespread for routine assays. Also, now that success so often depends on using the right 'kit'

More than just a tasty snack:

Crustacean Issues 15: Evolutionary Developmental Biology of Crustacea (2004). Gerhard Scholtz, ed. A. A. Balkema Publishers, Lisse, The Netherlands 285 pp. Hardback £80.00 ISBN 90 5809 637 8

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The *Crustacean Issues* series was founded by Frederick Schram in 1983, and since then has provided roughly biennial volumes of comprehensive reviews on a wide range of topics from crustacean phylogeny and systematics to biogeography and physiology. The current issue, however, is perhaps the issue most accessible to developmental biologists, and the

for the job, the list of suppliers, including their website addresses, is a useful feature, especially as the addresses of agents in Europe are given wherever possible.

I have to say that the chapter on enzyme kinetics at the beginning of Volume 2 does not quite fit into the general context. I expected to find protocols describing how to assay enzyme substrates or products of common interest to cell biologists. Instead there is a detailed theoretical treatment of enzyme kinetics and ways of plotting the data to distinguish between different classes of inhibitors. Assays of some particular enzymes are described in detail in later chapters. In most chapters, I would like to have been provided with a few more illustrations; cell biology is, after all, a very visual area of research. Also, I feel that the index could be more comprehensive, since it provides very little cross-referencing between different chapters. In fact, this whole series seems to be ideal material for publication on-line (next edition?), where extensive cross-referencing can be readily accomplished. But for the reader of the present printed books, it is probably not too great a hardship to read through several chapters, comparing related sections, before choosing the most appropriate protocol or fluorescent tag etc.

In summary, with these easily-affordable books in your laboratory you should no longer have any excuse or indeed lack the confidence to tackle an unfamiliar experiment that might provide the vital supporting evidence to back up your main results. At the very least, you will have a much better understanding of other kinds of experiments that impact on your own field.

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first to include a large body of data derived from molecular developmental genetics approaches.

For scientists interested in the developmental evolution of crustaceans and of arthropods generally, the classic reference book to date has been Donald T. Anderson's *Embryology and Phylogeny in Annelids and Arthropods*, published in 1973.⁽¹⁾ Those of us hoping for a second edition, updated to reflect the advent of molecular approaches to understanding embryonic development, as well as significant changes in arthropod phylogeny, have had to wait for 30 years. Our patience was rewarded in 2003 with the publication of Bruce Heming's *Insect Development and Evolution*,⁽²⁾ and this year editor Gerhard Scholtz has brought us a volume on the *Evolutionary Developmental Biology of Crustacea*.

In his preface, Scholtz points out that "The rise of the molecular approach towards the development of non-model organisms [has] led to numerous important new insights and perspectives of crustacean development and the development of arthropods in general." With this in mind, the purpose

of the volume is to “review the more recent literature on crustacean development”, and to “show that the new developments have to be associated with more traditional approaches in order to make a complete story.” These aims are thoroughly achieved, and most of the essays feature an introduction general enough to convey the interest and complexity of the field to biologists from a wide range of disciplines. The usual audience of crustacean biologists will certainly be aware of this latest addition to the *Issues* series, but many of its reviews discuss topics also of interest to the broader community of developmental biologists, such as Hox genes, nervous system and limb development.

The book’s introductory review by Scholtz is one of the best pieces in the volume, and I would encourage readers to refrain from rushing straight to their chapter of interest, and to first spend some time on this introduction. It provides an excellent and thoughtful overview of the conceptual framework within which the data must be considered. Scholtz points out some of the potential problems involved with concepts of body plans and phyla, stresses the importance of following the logic of phylogenetic systematics when interpreting developmental data, and suggests that only the study of development of homologous characters will provide information on evolutionary relationships. The introduction makes clear why such a diverse collection of reviews has been gathered into one volume, and is likely to persuade specialist readers who had intended to read only the chapter(s) directly relevant to their field, to explore other chapters as well.

The book is divided into three main sections: (1) Genes and body organisation, (2) Cells and segments, and (3) Morphology and phylogeny. The first section is almost entirely dedicated to the contributions of the study of Hox genes to our understanding of crustacean body plan evolution. This section presents a lot of recent data in great detail, but does not offer many new approaches to data synthesis or interpretation. Jean Deutsch and colleagues present an historical introduction to the many attempts that scientists have made to understand cirripede (barnacle) development and evolution. They present largely their own recent data on Hox genes, but the lack of functional genetic analysis (presumably impossible for technical reasons) leads them to the disappointingly general conclusion that “the evolution of the Cirripedia. . . seems to have been accompanied by multiple changes in the genetic basis of their development”. This article is followed by Arhat Abzhanov and Thomas Kaufman’s review of recent data on malacostracan (crabs, shrimp, wood lice, beach hoppers and krill) Hox genes, again principally their own work. This essay essentially recaps the existing literature, rather than presenting new hypotheses or predictions. The section finishes with an article by Fred Schram and Stefan Koenemann, which uses gene expression patterns and morphological characters to propose a new set of definitions for crustacean body regions, suggest a hypothesis of segmentation and make

predictions about the role of the Hox gene *Abdominal-B* in arthropod segmental development and evolution. Unfortunately, the overlap of the subject matter of the three essays in this section results in a certain amount of repetition in the introductory paragraphs of the articles. Although this makes reading them sequentially rather tedious, it also makes them more accessible to readers who may want to read only one of them.

The second section of the book contains three essays that are much more varied in scope than those of the first section. Wolfgang Dohle and colleagues review the literature on crustacean cell lineage and development. They examine issues such as malacostracan germ band formation, development of segmental ectoderm and mesoderm by teloblasts and asymmetric cell division in the ectoderm and the nervous system. The historical, mainly histological data is nicely incorporated into and complemented, but not replaced, by more recent analysis of gene expression patterns. Paul Whittington’s essay on crustacean nervous system development is presented as an example of “a comparative approach to developmental biology to address fundamental problems in evolution”. While this clearly written article illustrates the usefulness of extending classical “single system” developmental biology to comparative developmental biology, the reasoning behind his introductory claim that nervous system development, presumably more than other aspects of development, has “a convenient balance of evolutionary conservation versus diversity” is not made clear in the text. The final essay in this section is Terri William’s analysis of crustacean limb homologies. This essay makes the valuable point that “it can be easier to discover RNA or protein expression [in a limb] than to describe [limb] morphogenesis”, an observation pertinent not only to studies of crustacean evolution and development, but to the whole field of modern evo-devo. Correspondingly, an explanation of the contribution of morphology to the understanding of leg homologies precedes her summary of gene expression data, both new and previously published.

The final section of the book comprises two studies that use morphological analysis to try to solve particular problems in crustacean phylogeny. The first paper, by Jens Høeg and colleagues, describes a series of characteristics of Cirripede larvae, using these characteristics to assess the monophyly of the Cirripedia. This paper’s introduction emphasises that “the monophyly of this taxon is by no means straightforward,” and that “molecular data have failed to support that the three cirripede orders (Acrothotacida, Thoracica and Rhizocephala) form a monophylum.” This statement is at odds with affirmations within the contribution of Deutsch et al., where the reader is given the impression that Cirripede monophyly is currently a non-issue, that it is “generally accepted [that] the Rhizocephala are true cirripedes,” and that cirripede monophyly “is supported both by morphological arguments and molecular data.” The book’s final essay also concerns larval

morphology and phylogeny: Jørgen Olesen integrates new data on larval characters into existing Branchiopod (fairy shrimp, clam shrimp, tadpole shrimp, and water fleas) phylogenies.

With the caveat that perhaps more could have been done to decrease repetition and improve cohesion by cross-referencing some of the essays, *Evolutionary Developmental Biology of Crustacea* is a very worthwhile collection of papers; not only is it essential reading for crustacean biologists, it also contains useful insights for all those interested in the practicalities of integrating developmental biology with phylogeny and evolution. These papers admirably summarise the existing modern

Finding genes in the Web

Bioinformatics for Geneticists. (2004). Edited by Michael R. Barnes and Ian C. Gray. John Wiley & Sons Inc. Price £45. ISBN: 0-470-84394-2.

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Fast Internet connections have led to many of the biological data and analysis tools becoming available on-line and readily accessible through a web-browser. *Bioinformatics for Geneticists* is the first book solely focusing on the use of web-portals for genomic databases and web-based applications for the analysis of this information. Being mostly written by bioinformaticians supporting bench scientists, not the actual developers of these methods, the book takes a practical approach and provides hands-on instructions for the application of modern bioinformatics methods in a genetics study.

One should, however, remember that 'bioinformatics' and 'genetics' are very broad definitions and do not necessarily mean the same thing to all of us. The first of the words seems to cover any research that somehow combines biology and a computer, and as it is one of those lucrative terms meaning something 'new-fashioned', it gets included in every grant application or in a book title. In a broad sense, the databases and web-applications discussed in the book may be considered to be 'bioinformatics', but they do not provide a full picture of the field, even of the research relevant to geneticists; the book may work as an introduction to genetics analysis for bioinformatics developers and statisticians, but describes the theoretical basis of applied methods too thinly to serve as a complete reference to the computational analysis. The word 'genetics' has got, if possible, an even narrower definition and, in this book, it denotes the process of identifying the target gene, or more precisely, the cause for a given phenotype, in the human genome. This clearly reflects the editors' background in the pharmaceutical industry where organisms other

literature on crustacean development, and provide new syntheses and hypotheses that should stimulate further experiments and discussion in the field.

References

1. Anderson DT. 1973. Embryology and Phylogeny in Annelids and Arthropods. Oxford: Pergamon.
2. Heming BS. 2003. Insect Development and Evolution. Ithaca: Cornell University Press.

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human only have supporting roles in the task of understanding the underlying process in *the* species. Naturally, most of the described methods can be applied to other organisms, especially now that the main portals provide an easy access to several genomes, but a reader should not assume that non-mammalian model organisms, such as *Drosophila melanogaster* or *Caenorhabditis elegans*, get mentioned more than a couple of times.

In the post-genomic era, the quest for the hidden genes is easier than it was five years ago, but it is still far from trivial. A standard procedure is to use variable nucleotide sites and linkage/association analysis to roughly delimit the chromosome region of interest, and then start fishing, more or less randomly, across the candidate region until the target gets hit close enough. As the study area can be thousands of kilobases in size and contain tens of genes, using the brain is generally preferred over the brute force method, and the hunt is focused on the biologically or statistically most promising genes or chromosome regions. The authors loosely follow this scheme, and start their book by describing the databases of human genetic variation and the usage of different portals to the genome information (Ensembl and UCSC Human Genome Browser in the greatest detail). The chapter on rodent genome informatics is clearly a sidestep, and the story quickly returns to human genetic maps and, the main point of the book, the genetic analysis of a candidate region defined by a linkage study. As the necessary tool set for the analysis has been described, this chapter is written in the form of case studies, each specifying a problem and giving a procedure of resolution. Obviously six examples will not satisfy everyone's needs but they do demonstrate how the theory is put into practice and real-life problems are solved.

The following two chapters describe the SNP discovery and PCR assay design for laboratory experiments, and the statistical methods used for the genetic analysis of these data. The odd order of presenting the methods for linkage/association studies *after* the analysis of the candidate region that they were supposed to define is justified by the great complexity of the former. Here the authors have also been forced to make an exception to their web-based approach as easy 'click-and-go'