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Pentastomida, and Ostracoda + Cirripedia. Section V gains special importance by advancing questions concerning the deep phylogenetic divisions of the Arthropoda. Nevertheless, it is clear that different data sets can lead to different results. This conflict suggests that support for the different clades is still not very strong, which is also noticeable in relatively low statistical support for most of the critical branches in all of the phylogenetic trees. Presumably, the data set of Giribet et al. deserves most credibility, because it encompasses mitochondrial and nuclear markers that are treated separately by Babbitt and Patel and Carapelli et al. At least a consensus seems to exist in the finding that Hexapoda and Crustacea represent sister taxa. However, additional data will be needed to determine phylogenetic relationships between and within these two taxa.

Section VI looks into phylogenetic divisions that predate these within the Arthropoda. The single contribution by Ronald Jenner and Gerhard Scholtz reviews available morphological evidence to place the Arthropoda within the Metazoa, where the opposing concepts of the Articulata versus the Ecdysozoa are discussed and compared by testing the robustness of published morphological datasets. The authors conclude that the Articulata gain support, if problematic characters are excluded and scoring errors are corrected, but the likeli-

hood of support for either concept depends on the phylogenetic philosophy adopted by the respective scientists.

The bottom-line message of this book is thus that more conclusive information is still needed to accurately place the Arthropoda within the phylogeny of the Metazoa, and also to understand early divisions in the evolution of the Arthropoda that would allow an unequivocal classification into monophyletic subunits. In years to come, with corresponding advances in scientific insight and the promulgation of new hypotheses, this book will doubtless still be considered a benchmark in the field, regardless of debate and controversy that will certainly follow: "it has been put forward and it is there to use". Fred Schram, as well as the many researchers honouring him with this volume, have markedly advanced our present understanding of arthropod phylogeny, while also providing a template for testing of arthropod relationships as the field advances in years to come.

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Biogeography, third edition.—Mark V. Lomolino, Brett R. Riddle, and James H. Brown. 2005. Sinauer Associates, Sunderland, MA. 752 pp, 447 illustrations. ISBN: 0-87893-062-0. \$92.95 (hardback).

Placing populations and their attributes into a geographic context is currently the thing to do. Partly this may be because mapping has been revolutionized by geographic information systems (GIS) technology and the increasing power of desktop computers. Also, molecular data now allow inference of monophyla that are worth mapping; and for population-level analyses, there is phylogeography (Avice, 2000), a statistically rigorous way of overlaying geography onto an estimated gene tree to measure the strength of geography/phylogeny associations. Age estimation from molecular sequences has emerged as another powerful new tool. With access to absolute times, evolution can be linked to geological events and, for the first time, the most recent arrival of a lineage in an area can be estimated, which is different from the information gained from fossils. Inferring the historical assembly of ecological communities via the comparison of multiple dated phylogenies is a recent outgrowth of this ability (Webb et al., 2002; Pennington et al., 2004). Lastly, the geographic mosaic theory of coevolution

(Thompson, 2005), although hardly full-fledged (Herre, 2006), may have added further to the excitement about the geographic context of evolution and adaptation.

This new edition of *Biogeography* by Mark V. Lomolino, Brett R. Riddle, and James H. Brown thus comes at an opportune time. The first edition of *Biogeography* by Brown and Arthur C. Gibson was published in 1983, the second edition, by Brown and Lomolino, 15 years later in 1998, and the third a mere 6 years later in 2005. This is not just a textbook—it is the most comprehensive text and general reference book in the field, now with a 50-page long bibliography that cites over 1000 sources published between 1820 and 2004. There are 18 chapters, grouped into six units, and 447 black-and-white illustrations, mostly graphs and maps, but also a few wonderful photos of people and landscapes.

Unit 1, focusing on the history of biogeography, has hardly changed from the previous editions, and ends with the role of null hypotheses in studies of community assembly. Unit 2 includes chapters on the physical setting (solar radiation, winds, rainfall, soils, aquatic environments, oceans), the factors covering distributions of single species and those that may govern the geography of communities. As expected, there are brief descriptions of all major biomes.

Unit 3, "Earth History and Fundamental Biogeographic Processes," has a chapter on dispersal (focusing on autecology and with only 19 post-1998 references), and one on speciation and extinction. The latter includes discussions of species concepts, micro- and macroevolution, and modes of speciation. This year's astonishing discovery of a case of sympatric speciation in palms on an oceanic island (Savolainen et al., 2006) unfortunately could not yet be included. In an idiosyncratic choice, Unit 3 has the geological time scale, continental drift, and Pleistocene glaciations (Chapters 8 and 9) following speciation and extinction (Chapter 7). Many of the paleo-distribution maps are new, and the text of all four chapters has been much updated. For teaching purposes, the Northern Hemisphere responses to the Pleistocene climatic cycles are the ideal basis for a discussion of global warming, and the book's bias towards its largest market is nowhere more evident than in this chapter, which contains a single figure illustrating Pleistocene changes outside the Americas (p. 290, 9.13).

Unit 4, "Evolutionary History of Lineages and Biotas," comprises chapters on endemism and biogeographic regions, on reconstructing the history of lineages and that of biotas. The last two are the contribution of the new coauthor of *Biogeography*, Brett Riddle, whose research focuses on the phylogeography of Great Basin montane island biota and molecular systematics of North American rodents. He has done an excellent job of explaining the relevant basic concepts, such as phylogenetic inference, properties of molecular characters, construction and interpretation of haplotype networks, and molecular clocks. The sections explaining the role of fossils in biogeography are all new, and very good. By comparison with another recently revised text, Cox and Moore's *Biogeography* (cf. the review by Sanmartín, 2006), Lomolino et al. provide much more information about methods, such as reconciling trees, dispersal-vicariance analysis and Brooks parsimony analysis, always pointing the reader to appropriate original literature.

Unit 5 turns to ecological biogeography, and comprises two chapters on island biogeography—Brown and Lomolino are important contributors to the current nonequilibrium view of island biota—and a chapter on diversity gradients and macroecology from the keyboard of Brown. This chapter pays tribute to historical explanations of diversity, even if the exposition is strangely ahistorical. For example, the tropical conservatism hypothesis (that the tropics on average are larger and older than other biomes and regions, and that speciation rates there are higher and extinction rates lower so that species over time accumulated in the tropics), which is beautifully set out in Herbert Baker's (1970) classic review "Evolution in the Tropics" and also detailed by Farrell and Mitter (1993) and other authors in the Ricklefs and Schluter book on species diversity, is attributed to a 2004 paper in *Trends in Ecology and Evolution* (Wiens and Donoghue, 2004). Those people who are interested in explanations of diversity disparities up to 1980, of course, can turn to *Foundations of Biogeography: Classic Papers with Commentaries*, a fascinating compendium

by Lomolino et al. (2004). *Foundations* and *Frontiers* (Lomolino and Heaney, 2004) have been produced by the young and fit International Biogeography Society, whose cofounder and first president was Lomolino. (Brown and Riddle also are cofounders and past and present presidents of the 6-year-old society.)

The final unit (6), "Conservation Biogeography and New Frontiers," comprises chapters on the biodiversity crisis, invasive species, conservation biogeography, and the biogeography of humans. The book ends with a chapter on the frontiers of biogeography, excerpted from *Frontiers*.

The only omission in this book seems to be a section on GIS methods of mapping and model-based analyses of species ranges. GIS is mentioned in the Introduction and on the very last pages (pp. 722, 747; these mentions are not in the index), but the capabilities and use of widely available packages, such as Domain, BIOCLIM, and GARP, and their role in element distribution modeling, is something that the next generation of biogeographers, to be taught with this book, really needs to know about. Nowhere in the index does one find predictive distribution modeling, predictive range mapping, species distribution mapping, habitat distribution mapping, or ecological niche modeling.

The authors of *Biogeography* hold that little in evolution, and for that matter ecology, paleontology, conservation biology, and human evolution, makes sense unless viewed in a geographic context. The new edition of their book strongly supports this contention, and the very personal, sometimes chatty, sometimes missionary style in which it is written conveys a feeling that one is close to people who have seen the action. This is an empirically and conceptually rich text (as Andy Sinauer stated about the second edition), whose third edition confirms its status as an indispensable classic.

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Statistical Methods in Molecular Evolution.—Rasmus Nielsen (editor). 2005. Springer Verlag, New York. 508 pp. ISBN 0-387-22333-9. \$89.95 (£61.50) (hardback).

Molecular evolution and its sister disciplines of phylogenetics, molecular systematics, and comparative genomics are progressing rapidly. Of particular importance has been the creation of powerful statistical tools, which have enabled biologists to coax increasingly more information from biological data. *Statistical Methods in Molecular Evolution* seeks to provide an introduction to these tools and the mathematical theory that underpins them.

Before discussing the contents of the book, it is useful to linger for a moment on its definition of the phrase “molecular evolution”: only the evolution of biological sequences or things that can be simply inferred from them, such as gene order or microsatellite length, are covered in the book. There is little to no discussion about the evolution of protein structures, alternative splicing, domain shuffling, or the currently fashionable topic of network evolution. This is not a criticism—a book can only cover a limited number of topics—but potential readers should be aware of its limitations. The target audience includes scientists with mathematical or biological backgrounds, with the intention of being accessible to most numerically minded biology research students. This is a difficult task to manage and there are inevitably chapters that many biologists will struggle with, because some ideas are presented in a relatively formal statistical way, or both deal with particularly difficult conceptual issues. The majority of authors, however, do try and guide less technically minded readers through some quite difficult subject matter, and in general they succeed, making the book a pleasant and informative read.

In terms of structure, the book consists of a collection of peer-reviewed chapters from significant innovators in their respective fields, tied together by the editorial hand of Rasmus Nielsen. The individual chapters feel distinct, and each reads as a review in its own right, which leads to the book’s main strengths and weaknesses. The weaknesses are typical of books with a large number of authors. There is redundancy of material, with

some basic topics being covered multiple times, particularly regarding the definition of some popular evolutionary models. There is also a frustrating inconsistency with nomenclature, with different symbols being used for the same term in different chapters. A glaring example of this is the commonly used parameter κ in nucleotide models, which is defined in the usual way as the transition/transversion rate ratio in all but one chapter, where the authors have atypically defined it as the transversion/transition rate ratio. Of more concern is that some topics are only sketchily covered, and some escape being covered at all. This tends to be particularly true for the justification of modeling choices, which occasionally have gaps in the logical progression building from their biological foundations. This will be a particular problem for statisticians using the book as an entry point into molecular evolution. There is also occasional patchiness in quality both within and between chapters. Although the overall quality is high, with some notably concise and informative expositions of difficult subjects, some chapters feel in places that they are drifting.

Dwelling on the negatives too long would be an injustice and, to some extent, miss the point. By pulling together the thoughts and opinions of leading researchers, and letting them write in-depth about their preferred topics, this book has managed a rare thing: to become more than the sum of its parts. It provides an introduction to a lot of the most exciting research going on in molecular evolution, describing it from different perspectives and providing readers with a key to explore different aspects of the literature. This is illustrated by the discussion of models of protein evolution, where chapters introduce perspectives and opinions from structural biology, phylogenetic inference, and statistics. The eclectic mix of topics also invites the reader to think of molecular evolution at different temporal and spatial levels, and to spot difficulties with our current approaches. For example, one chapter discusses evolution over short timescales and how population structure affects natural selection, whereas the next describes recent attempts to draw inferences about selection from more distant evolutionary relationships. The comprehensive coverage of both topics serves to highlight the similarities between