

have termed “phylophenetics” (examples of which abound in, for instance, the journal *Systematic Biology*). The book therefore reads as a restatement of the conceptual and epistemological independence of systematics, and a call to arms to get back to basic questions—to heed the character—a timely, very much needed message in my view.

*Foundations of Systematics and Biogeography* is organized into 13 chapters, almost all of which discuss or accentuate homology to some degree, even in the final chapter devoted to (historical) biogeographical relationships (area homology). After the introductory chapter, the book discusses important early contributors (Goethe, Haeckel, Bronn, Schleicher, and Owen, but note that relatively little homage is paid to Saint-Hilaire) and concepts (much space is devoted to the *archetype*, a precursor to homology). The volume brings to light a refreshing appraisal of usually overlooked late-19th and early-20th century pre-Hennigian German comparative biologists (e.g., Naef, Kálin, Remane, and Zimmermann) who contributed to the intellectual climate that helped foster Hennig’s own phylogenetic revolution. This book also discusses the spread and development of cladistics throughout Europe and North America from the late 1960s to the early 1990s, further highlighting classical but more contemporary papers on homology written by Nelson and Patterson, as well giving Brundin, Croizat, and the Swedish paleoichthyologist Stensiö, among others, their due credit. After these accounts, the authors dedicate considerable space to reflect upon the significance of data matrices, component analysis, Pattersonian congruence, three-item analysis, minimal trees, strict parsimony analysis, transformation (which they separate into material and logical), and explanatory power, among other topics.

The general approach throughout the book emphasizes *pattern over process, characters over optimization, relationship over transformation, and components over nodes*. In so doing, *Foundations of Systematics and Biogeography*, no doubt, will annoy and agitate many of its readers who will brand it as idiosyncratic, one-sided, and even too “pattern cladistic” (that metaphysical, ill-defined bugaboo that does not seem to go away, largely resurrected by Williams and Ebach themselves). But, as mentioned by one recent reviewer, this “is a book worth pondering”—what more can one ask from a volume?

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#### THE TIMETREE OF LIFE.

*Edited by S. Blair Hedges and Sudhir Kumar; foreword by James D. Watson. Oxford and New York: Oxford University Press. \$200.00. xxi + 551 p.; ill.; index. ISBN: 978-0-19-953503-3. 2009.*

The divergence patterns (phylogenetic trees) and divergence times are two major components of the evolutionary history of life. Together they constitute the timetree. The phylogeny is of fundamental importance to biological classification and comparative evolutionary analysis, while absolute divergence times allows biologists to relate the speciation events to the history of the planet, such as continental drifts and climate changes, thus gaining insights into processes of speciation and extinction. This book is the first ever compilation of the timetree of life.

The volume consists of approximately 81 chapters organized into two parts, and written by over 100 contributors. The first part consists of four introductory chapters. The first chapter (by the editors) provides a historical overview of molecular clock dating. They argue that molecular time estimates are more reliable than those inferred from the fossil record, but perhaps do not stress enough the fact that molecular clock dating is possible only with fossil calibrations. The second chapter (by Avise) documents the many wonderful things one can do if reliable time estimates are available. This is followed by a chapter by Gradstein and Ogg, with a review of the construction of the Geologic Time Scale. Chapter 4, by Benton et al., provides an updated list of fossil calibrations (hard minimum and soft maximum bounds) for a wide range of key species. Such information will be invaluable for future molecular dating analysis. The maximum bounds seem to me too confident (too young) if they are to be exceeded with only 2.5% of probability since they are often based on absence of fossil evidence taken as evidence for the absence of the species.

The second part of the book (more than 400 pages) consists of chapters that summarize the timetrees for various taxa at or above the family level, covering superkingdoms, protists, plants, fungi, animals, invertebrates, vertebrates, fishes, amphibians, amniotes, reptiles, birds, and mammals. They are all written by experts and have a consistent format, making it very easy to extract the key information quickly.

Divergence time estimation is often harder than phylogeny reconstruction, partly because time estimates will never become precise even if whole genomes are analyzed, as long as fossil calibrations involve uncertainties (and they always do). Such imprecise inference is easily influenced by a multitude of factors. Different studies have often been noted to produce quite different time estimates.

Meanwhile, dating methods have been under active development recently, especially those that accommodate uncertainties in calibrations. The time estimates discussed in this book are not always obtained from the most trustworthy methods. Nevertheless, this volume summarizes a wealth of information, which will be extremely useful for an overview of divergence times in major taxa.

The entire book is freely available online. An excellent online resource, to be constantly updated, allows one to retrieve divergence time estimates between any two species, with links to references. The volume and the online resource will prove invaluable to researchers interested in the phylogeny and divergence times of particular species groups, and indeed to anyone interested in evolutionary biology.

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#### THE NEW FOUNDATIONS OF EVOLUTION: ON THE TREE OF LIFE.

By Jan Sapp. *Oxford and New York: Oxford University Press.* \$99.00 (hardcover); \$39.95 (paper). xix + 425 p.; ill.; index. ISBN: 978-0-19-538849-7 (hc); 978-0-19-538850-3 (pb). 2009.

This book recounts in a very thoughtful and accessible way the historical making of a tripartite relationship, that of microbiology, biological classification, and evolution, and how this triangle is still evolving to generate a more holistic vision of evolutionary biology. In the beginning chapters, Sapp summarizes, in a very balanced and insightful way, the key steps in the discovery of microbial life and the problems and conceptual issues that its classification posed. Were microbes plants, animals, or something else? Classification schemes changed as technological improvement and knowledge accumulated. Well into the 20th century, microbiology had established a certain know-how, yet the issue of prokaryotic classification was far from solved. Should taxonomy reflect phylogeny or should it not? And if so, how? Sapp explains the theoretical background of this dilemma and how the transition toward a natural classification of microorganisms and, concomitantly, of all terrestrial life, occurred. The author moves to more contemporary history, recalling how Carl R. Woese came up with the use of ribosomal RNA as a universal phylogenetic marker and how he discovered the archaea. Sapp provides a wealth of interesting and sometimes moving details from letters and interviews about how Woese, in complicity with Otto Kandler and his German school, fought the skepticism of a large part of the scientific community, posed new evolutionary questions, and overcame part of them. Finally, when the concept of the

three domains of life (Archaea, Bacteria, and Eukarya) appeared settled down and a phylogenetic classification of life seemed possible, Sapp discusses new problems that are shaking the foundations of evolutionary thinking these days. High-throughput genome sequencing reveals that extensive horizontal gene transfer is the rule and not the exception, and symbiosis has an increasingly recognized role in evolution. With an unavoidable higher dose of subjectivity in the final chapters, the author has the merit of making history of very contemporary, unsettled, conceptual issues in evolutionary biology, leaving the road open for future answers.

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#### THE EVOLUTIONARY BIOLOGY OF HUMAN FEMALE SEXUALITY.

By Randy Thornhill and Steven W. Gangestad. *Oxford and New York: Oxford University Press.* \$125.00 (hardcover); \$49.95 (paper). x + 411 p.; ill.; index. ISBN: 978-0-19-534098-3 (hc); 978-0-19-534099-0 (pb). 2008.

The human animal has long been considered exceptional, or even unique, because female libido and sexual behavior apparently vary little over the ovarian cycle. If you have accepted the proposition that a crucial event in human social evolution was the "loss of estrus," then read this book. Recent discoveries about ovarian cycle stage effects on women's psychology and behavior abound (many but by no means all of them are provided by the authors), and these discoveries demand a thorough rethinking of the evolution of human sexuality.

Thornhill and Gangestad argue that women possess two distinct evolved sexualities. One is the "extended sexuality" that women engage in when conception is impossible; the other they call "estrous" sexuality. The former functions to elicit "material benefits" from males, the latter to acquire "good genes" for offspring, and in keeping with these distinct functions, candidate male partners are evaluated on distinct criteria in the two contexts. In making the case for these views, the authors provide an impressively up-to-date, thorough, and evenhanded review not only of recent work on human sexuality in relation to ovarian cycle stage, but also of relevant research on other taxa and of the latest theoretical and empirical work on sexual selection and antagonistic coevolution of the sexes. The result is a tour de force, and those who wish to refute it will have to come to grips with its forceful argumentation and impressive breadth of information.