ferent outcomes of hybridization and/or horizontal gene transfer. Despite these concerns, *Evolution Through Genetic Exchange* represents a compelling argument for a paradigm shift in evolutionary biology, in which the "Tree of Life" is replaced conceptually by a "Web of Life" that connects all living organisms and their genomes.

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Annual Review of Genomics and Human Genetics. *Volume 7: 2006.*

> *Edited by Aravinda Chakravarti and Eric Green. Palo Alto (California): Annual Reviews.* $80.00. xii + 486 p; ill.; subject index and cumulative indexes (contributing authors and chapter titles, Volumes 1–7). ISBN: 0-8243-3707-7. 2006.

Conservation and the Genetics of Populations.

> *By Fred W Allendorf and Gordon Luikart; illustrated by Agostinho Antunes. Malden (Massachusetts): Blackwell Publishing.* $69.95 (paper). xix + 642 p; ill.; index. ISBN: 1-4051-2145-9. 2007.

The authors got the title of their publication right: conservation comes first in their presentation of population genetic concepts and applications. The first chapter briefly introduces genetics and conservation before asking: What should we conserve? How should we conserve biodiversity? This emphasis on practical applications to real conservation issues makes this book both interesting to and appropriate for readers who are curious about conservation biology and have a basic understanding of genetics.

This volume has its roots in course lecture notes and is written as a textbook. The chapters are arranged in three major parts. The first two parts contain topics found in any population genetics textbook, including genetic variation from phenotypes to DNA and mechanisms of evolutionary change. Even here the focus is on conservation applications in the text and examples, as well as in the guest boxes provided by researchers in conservation genetics. The third part is, however, where this volume really stands out. Here, the concepts previously described are applied in the chapters, including Demography and Extinction, Units of Conservation, and Conservation Breeding and Restoration. This large collection of conservation-focused chapters (eight in total) sets this publication apart from other population genetics textbooks, and makes it especially useful for conservation biologists and ecologists.

This volume is appropriate for advanced students and practicing resource managers with appropriate backgrounds. My experience is that many introductory genetic courses cover little, if any, population genetics. Considerable time may be needed just to establish population genetic principles. Fortunately, many of the examples and problem sets in the early chapters are a prelude to the types of issues and applications addressed in the third part of the book. On the other extreme, it is not designed for a traditional population genetics course for someone who wants a high level of expertise. Many of the complex models and derivations are intentionally omitted to focus on the conclusions and applications of the models. This volume may not make someone an expert in population genetics, but it will help them take the next step from introductory genetics to applying genetic principles to conservation issues.

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Evolutionary Genetics: Concepts and Case Studies.

> *Edited by Charles W Fox and Jason B Wolf. Oxford and New York: Oxford University Press.* $109.50 (hardcover); $59.50 (paper). xvi + 592 p; ill.; index. ISBN: 0-19-516817-8 (hc); 0-19-516818-6 (pb). 2006.

The editors of this volume cunningly recruited—and boldly edited—a dream team of contributors. Each of the 32 chapters features a concise overview, reasonable discussions of "future prospects," and helpful suggestions for "further reading." The first six foundational chapters—a historical précis plus summaries of genetic variation, the process of mutation and selection, and the roles of stochasticity and substructure in population genetics—are invigorating rather than remedial. Anyone preparing for qualifying exams should read them. In the subsequent five parts, consecutive chapters frequently overlap in focus (e.g., genetic variation and mutation; reproductive isolation and the genetics of speciation; genetic architecture and variance-covariance structure), but the material is minimally repetitive and amply cross-referenced. A nice glossary precedes a volume-wide reference list and a unified index. Literature from the past decade is emphasized; papers and books as recent as 2004 are cited. Finally, whole-genome approaches are maturely discussed across many chapters rather than segregated in an "-omics" section.

Since the volume does not promote any single approach to critiquing evolutionary science, it is odd that the title refers to "case studies." Many good examples are offered. Another imperfection: the numerous "boxes" that present material relevant to, but not exactly about, evolutionary genet-

ics. Some boxes are worthwhile (e.g., a minireview of species concepts, a short summary of phylogenetic controversies, and two clarifying explanations of molecular clocks), but others seem tangential and even distracting. This more than 500-page book is affordable thanks to tiny type and double-column formatting, but these features also make a complete reading somewhat arduous. Yearlong graduate courses can easily finish the volume, but semester-long seminars will need to cull from the four central sections (six chapters on molecular evolution, five on genotype-phenotype mapping, six on quantitative genetics, and five on speciation) as well as the final "applied" section. Choose those assignments and get reading soon. This volume will probably result in the further acceleration of this already fast-moving field.

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Annual Review of Genetics. *Volume 40: 2006.*

Edited by Allan Campbell, Wyatt W Anderson, and Elizabeth W Jones. Palo Alto (California): Annual Reviews. $80.00. xii + 509 p; ill.; no index. ISBN: 0-8243-1240-6. 2006.

Analysis of Phylogenetics and Evolution with R. *Use R!*

By Emmanuel Paradis. New York: Springer. $49.95 (paper). xii + 211 p; ill.; index. ISBN: 0-387-32914-5. 2006.

Statistical inference and the use of phylogenies is frequently divided among a variety of only partially interoperable computer programs. This is not only unwieldy, but can prevent us from combining analyses in creative and potentially informative ways. For those who would like to integrate the analysis of phylogenetic data into their normal statistical practice, what is needed is a software package with statistical methods that can be modified and extended by workers who develop phylogenetic methods. The software package R (freely downloadable from http://www.r-project.org) is widely used for statistical analyses, and users can develop packages that extend the functionality of the software. Paradis is also the author of a package (APE) that includes a number of phylogenetic and evolutionary methods.

This slim volume begins with a brief introduction to using R. The heart of the book is a how-to guide to using this software for phylogenetic inference, plotting phylogenies, comparative methods, estimation of ancestral character states, and analysis of diversification rates. The book concludes with a brief section on programming new methods in R.

This volume will be most helpful for those who have already used R for other forms of statistical analysis and are familiar with the phylogenetic methods that are discussed. My suspicion is that the brief introduction at the beginning will not be enough for most biologists to be comfortable working with the software. The program's command line interface allows a great deal of power and flexibility, but this comes at the cost of having a rather steep learning curve. New users will probably need to make extensive reference to freely available manuals or to one of a number of books that introduce the software. This volume will also not be sufficient for anyone interested in understanding the theory behind the analyses, as the focus is instead on how to perform the analyses. To really understand the methods, readers will need to consult a good book on phylogenetic inference or molecular evolution, or go back to the original papers.

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Compositional Evolution: The Impact of Sex, Symbiosis, and Modularity on the Gradualist Framework of Evolution. *The Vienna Series in Theoretical Biology.*

By Richard A Watson. A Bradford Book. Cambridge (Massachusetts): MIT Press. $50.00. xix + 324 p; ill.; index. ISBN: 0-262-23243-X. 2006.

Evolutionary computation and evolutionary biology are related disciplines with surprisingly little cross-pollination. The current volume stands at the intersection of these two perspectives. This is an expansion of Watson's PhD thesis work with Jordan Pollack's Dynamical and Evolutionary Machine Organization group. Although Watson is a computer scientist, his postdoctoral training in John Wakeley's population genetics laboratory has infused his thinking with a healthy dose of biology. Readers familiar with the work of Sewall Wright, Stuart Kauffman, and John Holland will benefit from reading this thought-provoking book.

Compositional evolution refers to evolutionary change via the combination of preadapted modules. This stands in contrast to gradual evolution. Two mechanisms of compositional evolution are sexual recombination and symbiotic encapsulation, each of which is given equal attention. The central idea is that a set of problems exists that can be solved by compositional evolution, yet is unsolvable by gradual evolution. Although gradual evolution involves hill-climbing algorithms, compositional evolution proceeds via bottom-up, divide-and-conquer algorithms. A compelling bridge between disciplines involves the metaphor of a fitness landscape and the Boolean operator if-and-only-if. Watson demonstrates that if-and-only-if statements possess the