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Review of Analysis of Phylogenetics and Evolution with R by Emmanuel Paradis

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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