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Title

Techniques in Molecular Systematics and Evolution. Methods and Tools in Biosciences and Medicine

Permalink

<https://escholarship.org/uc/item/9kd1h2kz>

Journal

New Biological Boos - Book Review, 78

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Publication Date

2003

Review for the Quarterly Review of Biology

Techniques in Molecular Systematics and Evolution

Edited by: Rob DeSalle, Gonzalo Giribet and Ward Wheeler

Phylogenetic reconstruction techniques have revolutionized evolutionary thinking over the last thirty years. More recently, it is becoming indispensable in fields outside molecular systematics such as comparative genomics, environmental genomics, and evolution and development (evo-devo). Although several other books have been published in recent years that deal with various approaches to phylogenetic analyses, most of them are directed at an evolutionary audience. Therefore this compendium of articles brought together by DeSalle, Giribet and Wheeler is very timely. The chapters target a wider readership that is not familiar with concepts that are usually taken for granted by molecular systematists. The book is neatly divided into analytical methods and laboratory methods.

DeSalle et al. state in their introduction that one of their goals is to educate molecular biologists in how to analyze their data in an evolutionary context. However, the described approaches are almost exclusively based on maximum parsimony (i.e. cladistics) and, unfortunately, molecular biologists will have to look elsewhere for an appraisal of other methods. With a few exceptions, there is no comprehensive coverage of the various phylogenetic approaches from which one can choose. This may not be a problem for students in evolutionary biology who will eventually acquire a thorough understanding of the multiple methods in molecular systematics. However, this book may mislead readers into thinking that cladistic methods are the only ones appropriate or available.

The second section of the book is very useful for the intended audience. All the protocols included in the different chapters will certainly be helpful to shorten troubleshooting time when working with material of diverse origin. This section covers protocols including tissue preservation, DNA extraction, PCR, high-throughput sequencing and hybridization techniques used for gene expression studies, and all of these should be applicable to a broad taxonomic range.

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