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March 2013; The Quarterly
Review of Biology 88(1):47-48;
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Phylogeny--Data processing.

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The Phylogenetic Trees Made
Easy Website 9 Chapter 2 □

Tutorial: Estimate a Tree 11 Why
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Sequences Related to Your
Sequence 13 Decide Which

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The increasing availability of molecular and genetic databases coupled with the growing power of computers gives biologists opportunities to address new issues, such as the patterns of molecular evolution, and re-assess old ones, such as the role of adaptation in species diversification. In the second edition, the book continues to integrate a wide variety of data analysis methods into a single and flexible interface: the R language. This open source language is available for a wide range of computer systems and has been adopted as a computational environment by many authors of statistical software. Adopting R as a main

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Easy A Phylogenetic Analyses will ease the workflow in biologists' data analyses, ensure greater scientific repeatability, and enhance the exchange of ideas and methodological developments. The second edition is completed updated, covering the full gamut of R packages for this area that have been introduced to the market since its previous publication five years ago. There is also a new chapter on the simulation of evolutionary data. Graduate students and researchers in evolutionary biology can use this book as a reference for data analyses, whereas researchers in bioinformatics interested in evolutionary analyses will learn how to implement these methods

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The book starts with a presentation of different R packages and gives a short introduction to R for phylogeneticists unfamiliar with this language. The basic phylogenetic topics are covered: manipulation of phylogenetic data, phylogeny estimation, tree drawing, phylogenetic comparative methods, and estimation of ancestral characters. The chapter on tree drawing uses R's powerful graphical environment. A section deals with the analysis of diversification with phylogenies, one of the author's favorite research topics. The last chapter is devoted to the development of phylogenetic methods with R and interfaces with other languages (C

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Baum and Smith, both professors evolutionary biology and researchers in the field of systematics, present this highly accessible introduction to phylogenetics and its importance in modern biology. Ever since Darwin, the evolutionary histories of organisms have been portrayed in the form of branching trees or "phylogenies." However, the broad significance of the phylogenetic trees has come to be appreciated only quite recently. Phylogenetics has myriad applications in biology, from discovering the features present in ancestral organisms, to finding the sources of invasive

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species and infectious diseases,
to identifying our closest living
(and extinct) hominid relatives.

Taking a conceptual approach,
Tree Thinking introduces readers
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During the last ten years remarkable progress has occurred in the study of molecular

evolution. Among the most important factors that are responsible for this progress are the development of new statistical methods and advances in computational technology. In particular, phylogenetic analysis of DNA or protein sequences has become a powerful tool for studying molecular evolution.

Along with this developing technology, the application of the new statistical and computational methods has become more complicated and there is no comprehensive volume that treats these methods in depth.

Molecular Evolution and Phylogenetics fills this gap and

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present various statistical methods that are easily accessible to general biologists as well as biochemists, bioinformaticists and graduate students. The text covers measurement of sequence divergence, construction of phylogenetic trees, statistical tests for detection of positive Darwinian selection, inference of ancestral amino acid sequences, construction of linearized trees, and analysis of allele frequency data. Emphasis is given to practical methods of data analysis, and methods can be learned by working through numerical examples using the computer program MEGA2 that is provided.

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Phylogenetics is a topical and growing area of research.

Phylogenies (phylogenetic trees and networks) allow biologists to study and graph evolutionary relationships between different species. These are also used to investigate other evolutionary processes?for example, how languages developed or how different strains of a virus (such as HIV or influenza) are related to each other. This self-contained book addresses the underlying mathematical theory behind the reconstruction and analysis of phylogenies. The theory is grounded in classical concepts from discrete mathematics and probability theory as well as techniques from other branches of mathematics (algebra,

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The biological relevance of the results is highlighted throughout.

The author supplies proofs of key classical theorems and includes results not covered in existing books, emphasizes relevant mathematical results derived over the past 20 years, and provides numerous exercises, examples, and figures.

DNA can be extracted and sequenced from a diverse range of biological samples, providing a vast amount of information about evolution and ecology. The analysis of DNA sequences contributes to evolutionary biology at all levels, from dating the origin of the biological kingdoms to untangling family

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Relationships. An Introduction to Molecular Evolution and Phylogenetics presents the fundamental concepts and intellectual tools you need to understand how the genome records information about evolutionary past and processes, how that information can be "read", and what kinds of questions we can use that information to answer. Starting with evolutionary principles, and illustrated throughout with biological examples, it is the perfect starting point on the journey to an understanding of the way molecular data is used in modern biology. Online Resource Centre The Online Resource Centre features: For registered adopters of the book: - Class

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plans for one-hour hands-on sessions associated with each chapter - Figures from the textbook to view and download

What are the models used in phylogenetic analysis and what exactly is involved in Bayesian evolutionary analysis using Markov chain Monte Carlo (MCMC) methods? How can you choose and apply these models, which parameterisations and priors make sense, and how can you diagnose Bayesian MCMC when things go wrong? These are just a few of the questions answered in this comprehensive overview of Bayesian approaches to phylogenetics. This practical guide: □ Addresses the theoretical aspects of the field □ Advises on

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how to prepare and perform phylogenetic analysis □ Helps with interpreting analyses and visualisation of phylogenies □ Describes the software architecture □ Helps developing BEAST 2.2 extensions to allow these models to be extended further. With an accompanying website providing example files and tutorials (<http://beast2.org/>), this one-stop reference to applying the latest phylogenetic models in BEAST 2 will provide essential guidance for all users – from those using phylogenetic tools, to computational biologists and Bayesian statisticians.

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