Computational Methods In Phylogenetic Analysis

Phylogenetic Comparative Methods in RComputational Methods in Phylogenetic AnalysisPhylogenetic Analysis of DNA SequencesPhylogenies in EcologyBayesian PhylogeneticsPhylogenetic Methods and the Prehistory of LanguagesComparisons of Parsimony and Likelihood-based Methods in Phylogenetic AnalysisMolecular Evolution and PhylogeneticsAnalysis of Phylogenetics and Evolution with RPhylogenetic Methods and the Prehistory of LanguagesModern Phylogenetic Comparative Methods and Their Application in Evolutionary BiologyMaximum Likelihood Methods in Molecular PhylogeneticsEncyclopedia of Evolutionary BiologyRefining Phylogenetic AnalysesPhylogenetic Comparative MethodsStatistical Methods of Phylogenetic AnalysisFoundations of Phylogenetic SystematicsZoology Reprints and Separata, EtcComputational PhylogeneticsScience Liam J. Revell Arun K. Jagota Michael M. Miyamoto Marc W. Cadotte Ming-Hui Chen Peter Forster David Dale Masatoshi Nei Emmanuel Paradis Peter Forster László Zsolt Garamszegi Korbinian Sebastian Strimmer Pablo A. Goloboff Luke J. Harmon Peter J. Waddell Johann Wolfgang Wägele Tandy Warnow

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an authoritative introduction to the latest comparative methods in evolutionary biology phylogenetic comparative methods are a suite of statistical approaches that enable biologists to analyze and better understand the evolutionary tree of life and shed vital new light on patterns of divergence and common ancestry among all species on earth this textbook shows how to carry out phylogenetic comparative analyses in the r statistical computing environment liam revell and luke harmon provide an incisive conceptual overview of each method along with worked examples using real data and challenge problems that encourage students to learn by doing by working through this book students will gain a solid foundation in these methods and develop the skills they need to interpret patterns in the tree of life covers every major method of modern phylogenetic comparative analysis in rexplains the basics of r and discusses topics such as trait evolution diversification trait dependent diversification biogeography and visualizationfeatures a wealth of exercises and challenge problemsserves as an invaluable resource for students and researchers with applications in ecology evolution anthropology disease transmission conservation biology and a host of other areaswritten by two of today s leading developers of phylogenetic comparative methods

the aim of phylogenetic analysis is to reconstruct the phylogeny evolutionary history of a set of organisms or genes from present day data since this involves inferring past events from present day data this is a difficult endeavor even so it must be done for it is scientifically important and practically useful to do so phylogeneticists those who do this for a living are finding modern computational methods to be quite useful in this arduous task this short book presents the main computational methods in present use in this field as well as some on the cutting edge these methods are presented in the setting of building binary trees rooted or unrooted from molecular sequence data some of these methods are applicable to other types of data as well this book is written from the quantitative perspective the author has aimed to present the algorithms and ideas in sufficient depth and at a formal level for someone to be able to implement them or even adapt them to new situations this book may also be used in a graduate or upper division undergraduate course on the topic one in which the computational perspective is emphasized or as an adjunct in a course on bioinformatics towards this use there are a number of pictures and examples included to assist student readers in understanding the ideas there are also exercise questions included at the end of several chapters the first chapter is on substitution models stochastic processes and substitution matrices the second on distance based tree building methods the third on parsimony based tree building methods the fourth on probabilistic tree building methods and the fifth on finding consensus features in built trees the sixth and the seventh chapters present more cutting edge material on sequence graphs and aligning them and on using sequence graphs for building a phylogenetic tree from unaligned sequences the eighth chapter is on comparing and aligning trees the ninth chapter presents some other interesting computational problems in phylogenetic analysis for instance phylogenetic networks for handling convergent evolution

with increasing frequency systematic and evolutionary biologists have turned to the techniques of molecular biology to complement their traditional morphological and anatomical approaches to questions of the historical relationship and descent among groups of animals and plants in particular the comparative analysis of dna sequences is becoming a common and important focus of research attention today the objective of this volume is to survey the emerging field of molecular systematics of dna sequences and to appraise the strengths and limitations of the different approaches yielded by these techniques the contributors are an internationally recognized group of investigators from different schools and disciplines who critically address a diversity of crucial questions about dna systematics including dna sequence data acquisition phylogenetic inference congruence and consensus problems limitations of molecular data and the integration of molecular and morphological data sets the work will interest all botanists and zoologists involved in systematics taxonomy and evolution phylogenies in ecology is the first book to critically review the application of phylogenetic methods in ecology and it serves as a primer to working ecologists and students of ecology wishing to understand these methods this book demonstrates how phylogenetic information is transforming ecology by offering fresh ways to estimate the similarities and differences among species and by providing deeper evolutionary based insights on species distributions coexistence and niche partitioning marc cadotte and jonathan davies examine this emerging area s explosive growth allowing for this new body of hypotheses testing cadotte and davies systematically look at all the main areas of current ecophylogenetic methodology testing and inference each chapter of their book covers a unique topic emphasizes key assumptions and introduces the appropriate statistical methods and null models required for testing phylogenetically informed hypotheses the applications presented throughout are supported and connected by examples relying on real world data that have been analyzed using the open source programming language r showing how phylogenetic methods are shedding light on fundamental ecological questions related to species coexistence conservation and global change phylogenies in ecology will interest anyone who thinks that evolution might be important in their data

offering a rich diversity of models bayesian phylogenetics allows evolutionary biologists systematists ecologists and epidemiologists to obtain answers to very detailed phylogenetic questions suitable for graduate level researchers in statistics and biology bayesian phylogenetics methods algorithms and applications presents a snapshot of current trends in bayesian phylogenetic research encouraging interdisciplinary research this book introduces state of the art phylogenetics to the bayesian statistical community and likewise presents state of the art bayesian statistics to the phylogenetics community the book emphasizes model selection reflecting recent interest in accurately estimating marginal likelihoods it also discusses new approaches to improve mixing in bayesian phylogenetic analyses in which the tree topology varies in addition the book covers divergence time estimation biologically realistic models and the burgeoning interface between phylogenetics and population genetics

evolutionary phylogenetic trees were first used to infer lost histories nearly two centuries ago by manuscript scholars reconstructing original texts today computer methods are enabling phylogenetic trees to transform genetics historical linguistics and even the archaeological study of artefact shapes and styles but which phylogenetic methods are best suited to retracing the evolution of languages and which types of language data are most informative about deep prehistory in this book leading specialists engage with these key questions essential reading for linguists geneticists and archaeologists these studies demonstrate how phylogenetic tools are illuminating previously intractable questions about language prehistory this innovative volume arose from a conference of linguists geneticists and archaeologists held at cambridge in 2004

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 present various statistical methods that are easily accessible to general biologists as well as biochemists bioinformatists 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

as a result the inference of phylogenies often seems divorced from any connection to other methods of analysis of scientific data felsenstein once calculation became easy the statistician s energies could be voted to understanding his or her dataset venables ripley the study of the evolution of life on earth stands as one of the most complex fields in science it involves observations from very different sources and has implications far beyond the domain of basic science it is concerned with processes occurring on very long time spans and we now know that it is also important for our daily lives as shown by the rapid evolution of many pathogens as a field ecologist for a long time i was remotely interested in phylo netics and other approaches to evolution most of the work i accomplished during my doctoral studies involved field studies of small mammals and estimation of demographic parameters things changed in 1996 when my interest was attracted by the question of the effect of demographic parameters on bird diversification this was a new issue for me so i searched for relevant data analysis methods but i failed to find exactly what i needed i started to conduct my own research on this problem to propose some at least partial solutions this work made me realize that this kind of research critically pends on the available software and it was clear to me that what was offered to phylogeneticists at this time was inappropriate

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phylogenetic comparative approaches are powerful analytical tools for making evolutionary inferences from interspecific data and phylogenies the phylogenetic toolkit available to evolutionary biologists is currently growing at an incredible speed but most methodological papers are published in the specialized statistical literature and many are incomprehensible for the user community this textbook provides an overview of several newly developed phylogenetic comparative methods that allow to investigate a broad array of questions on how phenotypic characters evolve along the branches of phylogeny and how such mechanisms shape complex animal communities and interspecific interactions the individual chapters were written by the leading experts in the field and using a language that is accessible for practicing evolutionary biologists the authors carefully explain the philosophy behind different methodologies and provide pointers mostly using a dynamically developing online interface on how these methods can be implemented in practice these conceptual and practical materials are essential for expanding the qualification of both students and scientists but also offer a valuable resource for educators another value of the book are the accompanying online resources available at mpcm evolution com where the authors post and permanently update practical materials to help embed methods into practice

encyclopedia of evolutionary biology four volume set is the definitive go to reference in the field of evolutionary biology it provides a fully comprehensive review of the field in an easy to search structure under the collective leadership of fifteen distinguished section editors it is comprised of articles written by leading experts in the field providing a full review of the current status of each topic the articles are up to date and fully illustrated with in text references that allow readers to easily access primary literature while all entries are authoritative and valuable to those with advanced understanding of evolutionary biology they are also intended to be accessible to both advanced undergraduate and graduate students broad topics include the history of evolutionary biology population genetics quantitative genetics speciation life history evolution evolution of sex and mating systems evolutionary biogeography evolutionary developmental biology molecular and genome evolution coevolution phylogenetic methods microbial evolution diversification of plants and fungi diversification of animals and applied evolution presents fully comprehensive content allowing easy access to fundamental information and links to primary research contains concise articles by leading experts in the field that ensures current coverage of each topic provides ancillary learning tools like tables illustrations and multimedia features to assist with the comprehension process

this volume discusses the aspects of a phylogenetic analysis that go beyond basic calculation of most parsimonious trees practical application of all principles discussed is illustrated by reference to tnt a freely available software package that can perform all the steps needed in a phylogenetic analysis the first problem considered is how to summarize and compare multiple trees including identification and handling wildcard taxa evaluation of the strength of support for groups another critical component of any phylogenetic analysis is given careful consideration the different interpretations of measures of support are discussed and connected with alternative implementations the book reviews rationales for estimating character reliability on the basis of homoplasy with particular attention to morphological characters the main methods for character weighting and their practical implementation several of them unique to tnt are discussed ad libitum also unique to tnt is the ability to directly analyze morphometric data including landmarks on the same footing as discrete characters finally the scripting language of tnt is introduced with scripting it is possible to program tnt to create personalized routines and automate complex calculations taking analyses to the next level and allowing exploration of new methods and ideas key features discusses the treatment of ambiguity in phylogenetic analyses in depth for summarizing results or comparing trees reviews literature on arguments and methods for weighting morphological characters and their practical application describes theory and application of methods for evaluating strength of group support based on either resampling or comparisons with suboptimal trees discusses the use of morphometric characters in phylogenetic analysis presents extensive information on commands and options of the tnt computer program including the use and creation of scripts

an introduction to statistical analyses of phylogenetic trees using comparative methods

phylogeny inference and the classification of organisms are indispensable for all fields of biology on the basis of a well corroborated tree of life it is possible to understand the evolution of structure and function of genomes of gene families of cascades of developmental genes and the origin of genes of medical importance ecologists need a stable classification of organisms to identify organisms to find their correct names and thus further information on relevant species this book offers an introduction to the theory of phylogenetic systematics and is a companion for all biologists who want to analyze morphological or molecular data with classical methods or with modern computer programs the first part of the book explains the epistemological basis that is independent of the type of method used to construct phylogenetic trees unlike other empirical sciences the estimation of data quality in phylogenetics is still little developed and very often neglected here a theoretical basis is presented that enables the systematist to assess critically and objectively the quality of different data sets and to make statements on the plausibility of results this requires a conception of the notions of information content probability of homology probability of cognition probability of events the principle of parsimony the differentiation of phenomenological and modelling methods willi hennig s original method is compared with modern numerical systematics and an updated hennigian procedure of data analysis is discussed the difference between phenetic and phylogenetic cladistics is explained popular tools for data evaluation implemented in computer programs are explained including their axiomatic assumptions sources of error and possible applications for the more common tools the mathematical background is explained in a simple easy to understand way johann wolfgang wagele was until recently head of the department for animal systematics lehrstuhl fur spezielle zoologie at the university of bochum and is now director of the museum alexander koenig in bonn germany his main research interests are the taxonomy phylogeny and biodiversity of isopoda which implies observations of life history biogeography and ecology in combination with phylogeny inference further subjects include arthropod phylogeny and tools for explorative data analyses the author is president of the gesellschaft fur biologische systematik a central european society of systematists and he is actively promoting biodiversity research

a comprehensive account of both basic and advanced material in phylogeny estimation focusing on computational and statistical issues no background in biology or computer science is assumed and there is minimal use of mathematical formulas meaning that students from many disciplines including biology computer science statistics and applied mathematics will find the text accessible the mathematical and statistical foundations of phylogeny estimation are presented rigorously following which more advanced material is covered this includes substantial chapters on multi locus phylogeny estimation supertree methods multiple sequence alignment techniques and designing methods for large scale phylogeny estimation the author provides key analytical techniques to prove theoretical properties about methods as well as addressing performance in practice for methods for estimating trees research problems requiring novel computational methods are also presented so that graduate students and researchers from varying disciplines will be able to enter the broad and exciting field of computational phylogenetics

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