Computational Methods In Phylogenetic Analysis

The Phylogenetic HandbookPhylogenetic Analysis of DNA SequencesComputational Methods in Phylogenetic AnalysisMolecular Evolution and PhylogeneticsSequencing and phylogenetic analysis as a tool in molecular epidemiology of veterinary infectious diseasesRefining Phylogenetic AnalysesParsimony, Phylogeny, and GenomicsConfounding Factors in Phylogenetic AnalysisComparing and Combining Trees and Data in Phylogenetic AnalysisAnalysis of Phylogenetics and Evolution with RFrom Observations to Optimal Phylogenetic TreesPrimates and Their Relatives in Phylogenetic PerspectivePhylogeneticsPhylogenetics and EcologyStudies of Confounding Factors in Phylogenetic AnalysisThe Phylogenetic HandbookPHYLOGENETIC ANALYSIS MORPHOLOBayesian Evolutionary Analysis with BEASTStatistical Methods in Molecular EvolutionFoundations of Phylogenetic Systematics Philippe Lemey Michael M. Miyamoto Arun K. Jagota Masatoshi Nei Iryna Goraichuk Pablo A. Goloboff Victor A. Albert Simon Ho Davide Pisani Emmanuel Paradis Pablo A. Goloboff Ross D.E. MacPhee E. O. Wiley Paul Eggleton Simon Y. W. Ho Marco Salemi WIENS JOHN J Alexei J. Drummond Rasmus Nielsen Johann Wolfgang Wägele

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the phylogenetic handbook is a broad hands on guide to theory and practice of nucleotide and protein phylogenetic analysis this second edition includes six new chapters covering topics such as bayesian inference tree topology testing and the impact of recombination on phylogenies as well as a detailed section on molecular adaptation the book has a stronger focus on hypothesis testing than the previous edition with more extensive discussions on recombination analysis detecting molecular adaptation and genealogy based population genetics many chapters include elaborate practical sections which have been updated to introduce the reader to the most recent versions of sequence analysis and phylogeny software including blast fasta clustal t coffee muscle dambe tree puzzle phylip mega paup iqpnni consel modeltest prottest paml hyphy mrbayes beast lamarc splitstree and rdp many analysis tools are described by their original authors resulting in clear explanations that constitute an ideal teaching guide for advanced level undergraduate and graduate students

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

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

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

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

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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 phylogenetics 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

taxonomists specializing in different groups once based phylogenetic analysis only on morphological data molecular data was used more rarely although molecular systematics is routine today the use of morphological data continues to be important especially for phylogenetic placement of many taxa known only from fossils and rare or difficult to collect species in addition morphological analyses help identify potential biases in molecular analyses and finally scenarios with respect to morphology continue to motivate biologists the beauty of a cheetah or a baobab does not lie in their dna sequence but instead on what they are and do this book is an up to date revision of methods and principles of phylogenetic analysis of morphological data it is also a general guide for using the computer program tnt in the analysis of such data the book covers the main aspects of phylogenetic analysis and general methods to compare classifications derived from molecules and morphology the basic aspects of molecular analysis are covered only as needed to highlight the differences with methods and assumptions for analysis of morphological datasets

this unique volume investigates the relationships of primates at the ordinal and higher classificatory levels from a variety of interdisciplinary viewpoints individual chapters examine the origin and evolution of gliding in early cenozoic dermoptera the ontogeny of the tympanic floor in archontans the role of the neurosciences in primate evolutionary biology and many other subjects the work will be of particular interest to primatologists zoologists and systematists

the long awaited revision of the industry standard on phylogenetics since the publication of the first edition of this landmark volume more than twenty five years ago phylogenetic systematics has taken its place as the dominant paradigm of systematic biology it has profoundly influenced the way scientists study evolution and has seen many theoretical and technical advances as the field has continued to grow it goes almost without saying that the next twenty five years of phylogenetic research will prove as fascinating as the first with many exciting developments yet to come this new edition of phylogenetics captures the very essence of this rapidly evolving discipline written for the practicing systematist and phylogeneticist it addresses both the philosophical and technical issues of the field as well as surveys general practices in taxonomy major sections of the book deal with the nature of species and higher taxa homology and characters trees and tree graphs and biogeography the purpose being to develop biologically relevant species character tree and biogeographic concepts that can be applied fruitfully to phylogenetics the book then turns its focus to phylogenetic trees including an in depth guide to tree building algorithms additional coverage includes parsimony and parsimony analysis parametric phylogenetics including maximum likelihood and bayesian approaches phylogenetic classification critiques of evolutionary taxonomy phenetics and transformed cladistics specimen selection field collecting and curating systematic publication and the rules of nomenclature providing a thorough synthesis of the field this important update to phylogenetics is essential for students and researchers in the areas of evolutionary biology molecular evolution genetics and evolutionary genetics paleontology physical anthropology and zoology

the relationship between systematics and ecology has recently been invigorated and developed a long way from the old field of comparative biology this change has been two fold advances in phylogenetic research have allowed explicit phylogenetic hypotheses to be constructed for a range of different groups of organisms and ecologists are now more aware that organism traits are influenced by the interaction of past and present this volume discusses the impact of these modern phylogenetic methods on ecology especially those using comparative methods although unification of these areas has proved difficult a number of conclusions can be drawn from the text these include the need for a working bridge between evolutionary biologists using logic based cladistic methods and those using probability based statistical methods for care in the selection of tree types for comparative studies and for systematists to attempt to analyse ecologically important groups comparative ecologists and systematists need to come together to develop these ideas further but this volume presents a very useful starting point for all those interested in systematics and ecology

sample text

biologists some with specialties and a paleontologist summarize research on selected topics relating to using a phylogenetic framework to understand how plants and animals their traits and interactions between species evolve the eight studies are from the 1996 symposium morphological data in phylogenetic analysis recent progress and unresolved problems held in st louis missouri annotation copyrighted by book news inc portland or

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 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 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

in the field of molecular evolution inferences about past evolutionary events are made using molecular data from currently living species with the availability of genomic data from multiple related species molecular evolution has become one of the most active and fastest growing fields of study in genomics and bioinformatics most studies in molecular evolution rely heavily on statistical procedures based on stochastic process modelling and advanced computational methods including high dimensional numerical optimization and markov chain monte carlo this book provides an overview of the statistical theory and methods used in studies of molecular evolution it includes an introductory section suitable for readers that are new to the field a section discussing practical methods for data analysis and more specialized sections discussing specific models and addressing statistical issues relating to estimation and model choice the chapters are written by the leaders of field and they will take the reader from basic introductory material to the state of the art statistical methods this book is suitable for statisticians seeking to learn more about applications in molecular evolution and molecular evolutionary biologists with an interest in learning more about the theory behind the statistical methods applied in the field the chapters of the book assume no advanced mathematical skills beyond basic calculus although familiarity with basic probability theory will help the reader most relevant statistical concepts are introduced in the book in the context of their application in molecular evolution and the book should be accessible for most biology graduate students with an interest in quantitative methods and theory rasmus nielsen received his ph d form the university of california at berkeley in 1998 and after a postdoc at harvard university he assumed a faculty position in statistical genomics at cornell university he is currentlyan ole rømer fellow at the university of copenhagen and holds a sloan research fellowship his is an associate editor of the journal of molecular evolution and has published more than fifty original papers in peer reviewed journals on the topic of this book from the reviews overall this is a very useful book in an area of increasing importance journal of the royal statistical society i find statistical methods in molecular evolution very interesting and useful it delves into problems that were considered very difficult just several years ago the book is likely to stimulate the interest of statisticians that are unaware of this exciting field of applications it is my hope that it will also help the wet lab molecular evolutionist to better understand mathematical and statistical methods marek kimmel for the journal of the american statistical association september 2006 who should read this book we suggest that anyone who deals with molecular data who does not and anyone who asks evolutionary questions who should not ought to consult the relevant chapters in this book dan graur and dror berel for biometrics september 2006 coalescence theory facilitates the merger of population genetics theory with phylogenetic approaches but still there are mostly two camps phylogeneticists and population geneticists only a few people are moving freely between them rasmus nielsen is certainly one of these researchers and his work so far has merged many population genetic and phylogenetic aspects of biological research under the umbrella of molecular evolution although nielsen did not contribute a chapter to his book his work permeates all its chapters this book gives an overview of his interests and current achievements in molecular evolution in short this book should be on your bookshelf peter beerli for evolution 60 2 2006

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

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