Computational Methods In Phylogenetic Analysis

Phylogenetic Analysis of DNA SequencesSequencing and phylogenetic analysis as a tool in molecular epidemiology of veterinary infectious diseasesThe Phylogenetic HandbookComputational Methods in Phylogenetic AnalysisA Descriptive and Phylogenetic Analysis of Plumulaceous Feather Characters in CharadriiformesMorphology, Shape and PhylogenyRefining Phylogenetic AnalysesMolecular Evolution and PhylogeneticsBioinformatics for BeginnersPhylogenetic Analysis of the Rhabdomesine BryozoansAnalysis of Phylogenetics and Evolution with RA Phylogenetic Analysis of the Major Lineages of the Crambinae and of the Genera of Crambini of North America (Lepidoptera: Pyralidae)Parsimony, Phylogeny, and GenomicsPhylogenetic Analysis of DNA SequencesFrom Observations to Optimal Phylogenetic TreesPhylogenetic Studies in Vespoidea (Hymenoptera)Bayesian Evolutionary Analysis with BEASTThe Nature and Evidential Interpretation of Phylogenetic Character DataPhylogenetic Systematics of Dart-poison Frogs and Their Relatives (Amphibia:Athesphatanura:Dendrobatidae)The Hierarchy of Life Michael M. Miyamoto Iryna Goraichuk Philippe Lemey Arun K. Jagota Carla J. Dove Norman MacLeod Pablo A. Goloboff Masatoshi Nei Supratim Choudhuri Kurt D. Spearing Emmanuel Paradis Bernard Landry Victor A. Albert Michael M. Miyamoto Pablo A. Goloboff James Michael Carpenter Alexei J. Drummond Benjamin Adam Salisbury Taran Grant Bo Fernholm

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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 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

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

generally biologists and mathematicians who study the shape and form of organisms have largely been working in isolation from those who work on evolutionary relationships through the analysis of common characteristics increasingly however dialogue between the two communities is beginning to develop but other than a handful of journal papers there has been no formal published discussion on this subject this timely book summarises the interdisciplinary work that has taken place and will stimulate additional research into these topics any scientist working on evolutionary relationships will find this volume invaluable

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

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

bioinformatics for beginners genes genomes molecular evolution databases and analytical tools provides a coherent and friendly treatment of bioinformatics for any student or scientist within biology who has not routinely performed bioinformatic analysis the book discusses the relevant principles needed to understand the theoretical underpinnings of bioinformatic analysis and demonstrates with examples targeted analysis using freely available web based software and publicly available databases eschewing non essential information the work focuses on principles and hands on analysis also pointing to further study options avoids non essential coverage yet fully describes the field for beginners explains the molecular basis of evolution to place bioinformatic analysis in biological context provides useful links to the vast resource of publicly available bioinformatic databases and analysis tools contains over 100 figures that aid in concept discovery and illustration

as a result the inference of phylogenies often seems divorced from any connection to other methods of analysis of scienti c 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 elds in science it involves observations from very di erent 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 eld 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 eld studies of small mammals and es mation of demographic parameters things changed in 1996 when my interest was attracted by the question of the e ect of demographic parameters on bird diversi cation this was a new issue for me so i searched for relevant data analysis methods but i failed to nd 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 o ered to phylogeneticists at this time was inappropriate

parsimony analysis cladistics has long been one of the most widely used methods of phylogenetic inference in the fields of systematic and evolutionary biology moreover it has mathematical attributes that lend itself for use with complex genomic scale data sets this book demonstrates the potential that this powerful hierarchical data summarization method also has for both structural and functional comparative genomic research

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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

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

the known diversity of dart poison frog species has grown from 70 in the 1960s to 247 at present with no sign that the discovery of new species will wane in the foreseeable future although this growth in knowledge of the diversity of this group has been accompanied by detailed investigations of many aspects of the biology of dendrobatids their phylogenetic relationships remain poorly understood this study was designed to test hypotheses of dendrobatid diversification by combining new and prior genotypic and phenotypic evidence in a total evidence analysis dna sequences were sampled for five mitochondrial and six nuclear loci approximately 6 100 base pairs bp x arithmetic mean 53 740 bp per terminal total dataset composed of approximately 1 55 million bp and 174 phenotypic characters were scored from adult and larval morphology alkaloid profiles and behavior these data were combined with relevant published dna sequences ingroup sampling targeted several previously unsampled species including aromobates nocturnus which was hypothesized previously to be the sister of all other dendrobatids undescribed and problematic species were sampled from multiple localities when possible the final dataset consisted of 414 terminals 367 ingroup terminals of 156 species and 47 outgroup terminals of 46 species direct optimization parsimony analysis of the equally weighted evidence resulted in 25 872 optimal trees forty nodes collapse in the strict consensus with all conflict restricted to conspecific terminals dendrobatids were recovered as monophyletic and their sister group consisted of crossodactylus hylodes and megaelosia recognized herein as hylodidae among outgroup taxa centrolenidae was found to be the sister group of all athesphatanurans except hylidae leptodactyidae was polyphyletic thoropa was nested within cycloramphidae and ceratophryinae was paraphyletic with respect to telmatobiinae among dendrobatids the monophyly and content of mannophryne and phyllobates were corroborated aromobates nocturnus and colostethus saltuensis were found to be nested within nephelobates and minyobates was paraphyletic and nested within dendrobates colostethus was shown to be rampantly nonmonophyletic with most species falling into two unrelated cis and trans andean clades a morphologically and behaviorally diverse clade of median lingual process possessing species was discovered in light of these findings and the growth in knowledge of the diversity of this large clade over the past 40 years we propose a new monophyletic taxonomy for dendrobatids recognizing the inclusive clade as a superfamily dendrobatoidea composed of two families one of which is new six subfamilies three new and 16 genera four new although poisonous frogs did not form a monophyletic group the three poisonous lineages are all confined to the revised family dendrobatidae in keeping with the traditional application of this name we also propose changes to achieve a monophyletic higher level taxonomy for the athesphatanuran outgroup taxa analysis of character evolution revealed multiple origins of phytotelm breeding parental provisioning of nutritive oocytes for larval consumption larval oophagy and endotrophy available evidence indicates that transport of tadpoles on the dorsum of parent nurse frogs a dendrobatid synapomorphy is carried out primitively by male nurse frogs with three independent origins of female transport and five independent origins of biparental transport reproductive amplexus is optimally explained as having been lost in the most recent common ancestor of dendrobatoidea with cephalic amplexus arising independently three times

the goal of the symposium on which these proceedings are based was to reach a consensus on the hierarchy of life in some well studied areas there is a good agreement between molecular data and morphology for example among vertebrates and insects in other well studied groups such as birds and bacteria fundamental disagreements reported in these proceedings may result from the use and interpretation of different methods all these points were discussed during the meeting and several problem areas were also indentified resulting in new ideas and plans for future work in this field

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