

# MacClade 4

Analysis of Phylogeny and  
Character Evolution



David R. Maddison and Wayne P. Maddison

# Macclade 4 Analysis Of Phylogeny And Character Evolution

**Andy Purvis, John L. Gittleman, Thomas  
M. Brooks**



#### **MacClade 4 Analysis Of Phylogeny And Character Evolution:**

*MacClade* Wayne P. Maddison, David R. Maddison, 1992 *MacClade* is a computer program for graphic and interactive analysis of phylogeny and character evolution for Apple Macintosh computers. It displays a cladogram and paints the branches to indicate reconstructed character evolution. The user can manipulate cladograms on screen as *MacClade* gives diagnostic feedback. Systematics and other evolutionary biologists can use its flexible and analytical tools to examine phylogenies or interpret character evolution in a phylogenetic context; yet its ease of use should allow students to grasp phylogenetic principles in an interactive environment. This is the user's manual. **Plant Systematics** Michael G. Simpson, 2011-08-09 *Plant Systematics* is a comprehensive and beautifully illustrated text covering the most up to date and essential paradigms, concepts, and terms required for a basic understanding of plant systematics. This book contains numerous cladograms that illustrate the evolutionary relationships of major plant groups with an emphasis on the adaptive significance of major evolutionary novelties. It provides descriptions and classifications of major groups of angiosperms including over 90 flowering plant families, a comprehensive glossary of plant morphological terms, as well as appendices on botanical illustration and plant descriptions. Pedagogy includes review questions, exercises, and references that complement each chapter. This text is ideal for graduate and undergraduate students in botany, plant taxonomy, plant systematics, plant pathology, ecology, as well as faculty and researchers in any of the plant sciences. The Henry Allan Gleason Award of The New York Botanical Garden awarded for Outstanding recent publication in the field of plant taxonomy, plant ecology, or plant geography. 2006. Contains numerous cladograms that illustrate the evolutionary relationships of major plant groups with an emphasis on the adaptive significance of major evolutionary novelties. Provides descriptions and classifications of major groups of angiosperms including over 90 flowering plant families. Includes a comprehensive glossary of plant morphological terms, as well as appendices on botanical illustration and plant description. *Excerpts from MacClade* Sinauer Associates, Incorporated, Wayne P. Maddison, David R. Maddison, 1999. Parsimony, Phylogeny, and Genomics Victor A. Albert, 2005-03-24 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. **Phylogenetic treatment and taxonomic revision of the trapdoor spider genus *Aptostichus* Simon (Araneae, Mygalomorphae, Euctenizidae)** Jason E. Bond, 2012-12-19 The Californian Floristic Province, located on the Pacific Coast of North America, is a region recognized as a biodiversity hotspot. The area's rich floristic diversity is also reflected in its remarkable diversity of mygalomorph spiders, the group that includes trapdoor spiders, tarantulas, funnel spiders, and their other close relatives. This monograph documents the species diversity currently attributed to the euctenizid genus *Aptostichus* Simon distributed

primarily throughout California but also found in the habitats of Arizona and Nevada Based on the examination of approximately 2000 specimens from museum and field collections 40 species are assessed 33 of which are new to science A dantrippi A cabrillo A pennjillettei A asmodaeus A nateevansi A chiricahua A icenoglei A isabella A muiri A barackobamai A sinnombre A hedinorum A aguacaliente A chemehuevi A sarlacc A derhamgiulianii A anzaborrego A serrano A mikeradtkei A edwardabbeyi A killerdana A cahuilla A satleri A elisabethae A fornax A lucerne A fisheri A bonoi A cajalco A sierra A huntington A dorothealangeae and A chavezi

**Molecular Evolution** Ziheng Yang, 2014-05-16 Studies of evolution at the molecular level have experienced phenomenal growth in the last few decades due to rapid accumulation of genetic sequence data improved computer hardware and software and the development of sophisticated analytical methods The flood of genomic data has generated an acute need for powerful statistical methods and efficient computational algorithms to enable their effective analysis and interpretation Molecular Evolution a statistical approach presents and explains modern statistical methods and computational algorithms for the comparative analysis of genetic sequence data in the fields of molecular evolution molecular phylogenetics statistical phylogeography and comparative genomics Written by an expert in the field the book emphasizes conceptual understanding rather than mathematical proofs The text is enlivened with numerous examples of real data analysis and numerical calculations to illustrate the theory in addition to the working problems at the end of each chapter The coverage of maximum likelihood and Bayesian methods are in particular up to date comprehensive and authoritative This advanced textbook is aimed at graduate level students and professional researchers both empiricists and theoreticians in the fields of bioinformatics and computational biology statistical genomics evolutionary biology molecular systematics and population genetics It will also be of relevance and use to a wider audience of applied statisticians mathematicians and computer scientists working in computational biology

**Phylogeny and Conservation** Andy Purvis, John L. Gittleman, Thomas M. Brooks, 2005-09-22 Phylogeny is a potentially powerful tool for conserving biodiversity This book explores how it can be used to tackle questions of great practical importance and urgency for conservation Using case studies from many different taxa and regions of the world the volume evaluates how useful phylogeny is in understanding the processes that have generated today's diversity and the processes that now threaten it The urgency with which conservation decisions have to be made as well as the need for the best possible decisions make this volume of great value to researchers practitioners and policy makers

**Computational Molecular Evolution** Ziheng Yang, 2006-10-05 The field of molecular evolution has experienced explosive growth in recent years due to the rapid accumulation of genetic sequence data continuous improvements to computer hardware and software and the development of sophisticated analytical methods The increasing availability of large genomic data sets requires powerful statistical methods to analyse and interpret them generating both computational and conceptual challenges for the field Computational Molecular Evolution provides an up to date and comprehensive coverage of modern statistical and computational methods used in molecular evolutionary

analysis such as maximum likelihood and Bayesian statistics Yang describes the models methods and algorithms that are most useful for analysing the ever increasing supply of molecular sequence data with a view to furthering our understanding of the evolution of genes and genomes The book emphasizes essential concepts rather than mathematical proofs It includes detailed derivations and implementation details as well as numerous illustrations worked examples and exercises It will be of relevance and use to students and professional researchers both empiricists and theoreticians in the fields of molecular phylogenetics evolutionary biology population genetics mathematics statistics and computer science Biologists who have used phylogenetic software programs to analyze their own data will find the book particularly rewarding although it should appeal to anyone seeking an authoritative overview of this exciting area of computational biology **The Hawaiian**

**Honeycreepers** H. Douglas Pratt, 2005-05-12 Publisher Description Endogenous ADP-Ribosylation Friedrich

Koch-Nolte, 2014-10-24 This volume gathers the latest exciting findings on ADP ribosylation from renowned experts in the field It includes ten chapters organized into the following three thematic sections Evolution and detection of endogenous ADP ribosylation ADP ribosylation by the ARTC family of ADP ribosyltransferases R S E ARTs ADP ribosylation by the ARTD family of ADP ribosyltransferases H Y E ARTs The book will provide readers a better understanding of ADP ribosylating toxins and their endogenous relatives This provides a basis for developing novel toxin neutralizing drugs and drugs targeting endogenous ADP ribosyltransferase relatives *Practical Aspects of Declarative Languages* Matthew Flatt, Hai-Feng

Guo, 2013-12-09 This book constitutes the refereed proceedings of the 16th International Symposium on Practical Aspects of Declarative Languages PADL 2014 held in San Diego CA USA in January 2014 co located with POPL 2014 the 41st Symposium on Principles of Programming Languages The 15 revised papers presented were carefully reviewed and selected from 27 submissions They cover a wide range of topics related to logic and functional programming including language support for parallelism and GPUs constructs and techniques for modularity and extensibility and applications of declarative programming to document processing and DNA simulation *The Science of Forensic Entomology* David B. Rivers, Gregory

A. Dahlem, 2022-09-27 A thoroughly updated introduction to forensic entomology In the newly revised second edition of *The Science of Forensic Entomology* two distinguished entomologists deliver a foundational and practical resource that equips students and professionals to be able to understand and resolve questions concerning the presence of specific insects at crime scenes Each chapter in the book addresses a topic that delves into the underlying biological principles and concepts relevant to the insect biology that grounds the use of insects in legal and investigational contexts In addition to non traditional topics including the biology of maggot masses temperature tolerances of necrophagous insects chemical attraction and communication reproductive strategies of necrophagous flies and archaeoentomology the book also offers readers A thorough introduction to the role of forensic science in criminal investigations and the history of forensic entomology Comprehensive discussions of the biology taxonomy and natural history of forensically important insects Fulsome

treatments of the postmortem decomposition of human remains and vertebrate carrion In depth introduction to the concepts of accumulated degree days and the use of insect development for estimation of the postmortem interval New chapters dedicated to forensic entomotoxicology aquatic insects in forensic investigations microbiomes of forensic insects and carrion professional standards and case studies Perfect for graduate and advanced undergraduate students in forensic entomology forensic biology and general forensic science The Science of Forensic Entomology will also earn a place in the libraries of law enforcement and forensic investigators as well as researchers in forensic entomology *The Quintessential Naturalist* Douglas A. Kelt, 2007-07-31 Oliver P Pearson's studies on mammalian biology remain standard reading for ecologists physiologists taxonomists and biogeographers Reflecting this the papers gathered here continue to expand our understanding of the ecology and evolution of subterranean mammals and of ecology taxonomy and biogeography of Neotropical mammals a group that was central to the latter half of Pearson's career **Functional and Evolutionary Ecology of Bats** Akbar Zubaid, Gary F. McCracken, Thomas Kunz, 2006-01-05 Every three years a major international conference on bats draws the leading workers in the field to a carefully orchestrated presentation of the research and advances and current state of understanding of bat biology Bats are the second most populous group of mammalia species after rodents and they are probably the most intensively studied group of mammals Virtually all mammalogists and a large proportion of organismic biologists are interested in bats The earlier two edited books deriving from previous bat research conferences as well as this one have been rigorously edited by Tom Kunz and others with all chapters subjected to peer review The resulting volumes published first by Academic Press and most recently by Smithsonian have sold widely as the definitive synthetic treatments of current scientific understanding of bats **Systematics, Evolution, and Ecology of Melastomataceae** Renato Goldenberg, Fabián A. Michelangeli, Frank Almeda, 2022-07-20 This book presents a synthesis of critical new information for the Melastomataceae one of the ten richest families among flowering plants with over 5 800 species that has its diversity highly concentrated in tropical or subtropical areas It describes the family's global diversity and distribution and summarizes recent advances in systematics evolution biogeography reproductive biology and ecology *Developmental Genetics and Plant Evolution* Quentin C.B. Cronk, Richard M. Bateman, Julie A. Hawkins, 2004-01-29 A benchmark text Developmental Genetics and Plant Evolution integrates the recent revolution in the molecular developmental genetics of plants with mainstream evolutionary thought It reflects the increasing cooperation between strongly genomics influenced researchers with their strong grasp of technology and evolutionary morphogenetists and sys Encyclopedia of Marine Mammals William F. Perrin, Bernd Würsig, J.G.M. Thewissen, 2009-02-26 This thorough revision of the classic Encyclopedia of Marine Mammals brings this authoritative book right up to date Articles describe every species in detail based on the very latest taxonomy and a host of biological ecological and sociological aspects relating to marine mammals The latest information on the biology ecology anatomy behavior and interactions with man is provided by a cast of expert

authors all presented in such detail and clarity to support both marine mammal specialists and the serious naturalist Fully referenced throughout and with a fresh selection of the best color photographs available the long awaited second edition remains at the forefront as the go to reference on marine mammals More than 20% NEW MATERIAL includes articles on Climate Change Pacific White sided Dolphins Sociobiology Habitat Use Feeding Morphology and more Over 260 articles on the individual species with topics ranging from anatomy and behavior to conservation exploitation and the impact of global climate change on marine mammals New color illustrations show every species and document topical articles FROM THE FIRST EDITION This book is so good a bargain full of riches packed with fascinating up to date information I recommend it unreservedly it to individuals students and researchers as well as libraries Richard M Laws MARINE MAMMALS SCIENCE establishes a solid and satisfying foundation for current study and future exploration Ronald J Shusterman SCIENCE

Molecular Phylogeny, Biogeography and an e-Monograph of the Papaya Family (Caricaceae) as an Example of Taxonomy in the Electronic Age Fernanda Antunes Carvalho, 2015-06-05 Fernanda Antunes Carvalho addresses an issue of key importance to the field of systematics namely how to foster taxonomic work and the dissemination of scientific knowledge about species by taking full advantage of electronic data and bioinformatics tools The first part focuses on the development of an electronic monograph of the papaya family Caricaceae using existing infrastructures of Information Technology IT and bioinformatic tools that together set the stage for a new era of systematics Based on the plastid and nuclear DNA data the author inferred historical processes in the second part that may have shaped the evolution of the Caricaceae and explain their current geographic distribution The last part is dedicated to the evolution of chromosome numbers in the Caricaceae and includes counts for species from three genera Cylicomorpha Horovitzia Jarilla that have never been investigated before

Evolutionary Ecology of Social and Sexual Systems J. Emmett Duffy, Martin Thiel, 2007-09-06 Understanding of animal social and sexual evolution has seen a renaissance in recent years with discoveries of frequent infidelity in apparently monogamous species the importance of sperm competition active female mate choice and eusocial behavior in animals outside the traditional social insect groups Each of these findings has raised new questions and suggested new answers about the evolution of behavioral interactions among animals This volume synthesizes recent research on the sexual and social biology of the Crustacea one of the dominant invertebrate groups on earth Its staggering diversity includes ecologically important inhabitants of nearly every environment from deep sea trenches through headwater streams to desert soils The wide range of crustacean phenotypes and environments is accompanied by a comparable diversity of behavioral and social systems including the elaborate courtship and wildly exaggerated morphologies of fiddler crabs the mysterious queuing behavior of migrating spiny lobsters and even eusociality in coral reef shrimps This diversity makes crustaceans particularly valuable for exploring the comparative evolution of sexual and social systems Despite exciting recent advances however general recognition of the value of Crustacea as models has lagged behind that of the better studied insects and

vertebrates This book synthesizes the state of the field in crustacean behavior and sociobiology and places it in a conceptually based comparative framework that will be valuable to active researchers and students in animal behavior ecology and evolutionary biology It brings together a group of internationally recognized and rising experts in fields related to crustacean behavioral ecology ranging from physiology and functional morphology through mating and social behavior to ecology and phylogeny Each chapter makes connections to other non crustacean taxa and the volume closes with a summary section that synthesizes the contributions discusses anthropogenic impacts highlights unanswered questions and provides a vision for profitable future research

**Microbial Nitrogen Cycling Dynamics in Coastal Systems** Annika Carlene Mosier, 2011 Human influence on the global nitrogen cycle e g through fertilizer and wastewater runoff has caused a suite of environmental problems including acidification loss of biodiversity increased concentrations of greenhouse gases and eutrophication These environmental risks can be lessened by microbial transformations of nitrogen nitrification converts ammonia to nitrite and nitrate which can then be lost to the atmosphere as  $N_2$  gas via denitrification or anammox Microbial processes thus determine the fate of excess nitrogen and yet recent discoveries suggest that our understanding of these organisms is deficient This dissertation focuses on microbial transformations of nitrogen in marine and estuarine systems through laboratory and field studies using techniques from genomics microbial ecology and microbiology Recent studies revealed that many archaea can oxidize ammonia AOA ammonia oxidizing archaea in addition to the well described ammonia oxidizing bacteria AOB Considering that these archaea are among the most abundant organisms on Earth these findings have necessitated a reevaluation of nitrification to determine the relative contribution of AOA and AOB to overall rates and to determine if previous models of global nitrogen cycling require adjustment to include the AOA I examined the distribution diversity and abundance of AOA and AOB in the San Francisco Bay estuary and found that the region of the estuary with low salinity and high C N ratios contained a group of AOA that were both abundant and phylogenetically distinct In most of the estuary where salinity was high and C N ratios were low AOB were more abundant than AOA despite the fact that AOA outnumber AOB in soils and the ocean the two end members of an estuary This study suggested that a combination of environmental factors including carbon nitrogen and salinity determine the niche distribution of the two groups of ammonia oxidizers In order to gain insight into the genetic basis for ammonia oxidation by estuarine AOA we sequenced the genome of a new genus of AOA from San Francisco Bay using single cell genomics The genome data revealed that the AOA have genes for both autotrophic and heterotrophic carbon metabolism unlike the autotrophic AOB These AOA may be chemotactic and motile based on numerous chemotaxis and motility associated genes in the genome and electron microscopy evidence of flagella Physiological studies showed that the AOA grow aerobically but they also oxidize ammonia at low oxygen concentrations and may produce the potent greenhouse gas  $N_2O$  Continued cultivation and genomic sequencing of AOA will allow for in depth studies on the physiological and metabolic potential of this novel group of organisms that will ultimately



advance our understanding of the global carbon and nitrogen cycles Denitrifying bacteria are widespread in coastal and estuarine environments and account for a significant reduction of external nitrogen inputs thereby diminishing the amount of bioavailable nitrogen and curtailing the harmful effects of nitrogen pollution I determined the abundance community structure biogeochemical activity and ecology of denitrifiers over space and time in the San Francisco Bay estuary Salinity carbon nitrogen and some metals were important factors for denitrification rates abundance and community structure Overall this study provided valuable new insights into the microbial ecology of estuarine denitrifying communities and suggested that denitrifiers likely play an important role in nitrogen removal in San Francisco Bay particularly at high salinity sites

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