

MacClade 4

Analysis of Phylogeny and
Character Evolution



David R. Maddison and Wayne P. Maddison

Macclade 4 Analysis Of Phylogeny And Character Evolution

Ziheng Yang



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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** Wayne P. 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 chapters 3-6 of the user's manual. **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*.

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.

Anatomy, Phylogeny and Palaeobiology of Early Archosaurs and Their Kin Sterling J. Nesbitt, Julia Brenda Desojo, Randall B. Irmis, 2013 Archosaurs, an important reptile group that includes today's crocodiles and birds, arose during the Triassic in the aftermath of the greatest mass extinction of all time. In the last 20 years, our understanding of the early evolution of the group has improved substantially with the discovery of new fossils and species of early archosaurs and their closest relatives, a better understanding of the relationships of these animals, and new insights into their palaeobiology. In order to synthesize these new data, researchers of early archosaurs from around the world met at the first symposium of early archosaur evolution at the IV Congreso Latinoamericano de Paleontología y de Vertebrados, September 2011, in San Juan, Argentina. This symposium facilitated collaboration and strove to paint a better understanding of these extraordinary animals. The resultant body of work is a state-of-the-art examination of early archosaur groups and their close relatives, including historical anatomical, biogeographical, evolutionary, and palaeobiological data. This contribution furthers our knowledge of the anatomy, relationships, and palaeobiology of species-level taxa, as well as more global patterns of archosaur evolution during the Triassic.

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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

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

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

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