

Cultural Phylogenetics Concepts And Applications In Archaeology Interdisciplinary Evolution Research

Phylonoms is an implementation of PhyloCode, which is a set of principles, rules, and recommendations governing phylogenetic nomenclature. Nearly 300 clades - lineages of organisms - are defined by reference to hypotheses of phylogenetic history rather than by taxonomic ranks and types. This volume will document the Real World uses of PhyloCode and will govern and apply to the names of clades, while species names will still be governed by traditional codes. Key Features Provides clear regulations for implementing new guidelines for naming lineages of organisms incorporates expressly evolutionary and phylogenetic principles Works with existing codes of nomenclature Eliminates the reliance on rank-based classification in favor of phylogenetic relationships Related Titles: Rieppel, O. Phylogenetic Systematics: Haeckel to Hennig (ISBN 978-1-4987-5488-0) Cantino, P. D. and de Queiroz, K. International Code of Phylogenetic Nomenclature (PhyloCode) (ISBN 978-1-138-33282-9).

Cultural Phylogenetics Concepts and Applications in Archaeology

Phylogenomics: A Primer, Second Edition is for advanced undergraduate and graduate biology students studying molecular biology, comparative biology, evolution, genomics, and biodiversity. This book explains the essential concepts underlying the storage and manipulation of genomics level data, construction of phylogenetic trees, population genetics, natural selection, the tree of life, DNA barcoding, and metagenomics. The inclusion of problem-solving exercises in each chapter provides students with a solid grasp of the important molecular and evolutionary questions facing modern biologists as well as the tools needed to answer them.

Travellers in Time re-evaluates the extent to which the earliest Mediterranean civilizations were affected by population movement. It critiques both traditional culture-history-grounded notions of movement in the region as straightforwardly transformative, and the processual, systemic models that have more recently replaced this view, arguing that newer scholarship too often pays limited attention to the specific encounters, experiences and agents involved in travel. By assessing a broad range of recent archaeological and ancient textual data from the Aegean and central and east Mediterranean via five comprehensive studies, this book makes a compelling case for rethinking issues such as identity, agency, materiality and experience through an understanding of movement as transformative. This innovative and timely study will be of interest to advanced undergraduates, postgraduate students and scholars in the fields of Aegean/Mediterranean prehistory and Classical archaeology, as well as anyone interested in ancient Aegean and Mediterranean culture.

Phylogenetic combinatorics is a branch of discrete applied mathematics concerned with the combinatorial description and analysis of phylogenetic trees and related mathematical structures such as phylogenetic networks and tight spans. Based on a natural conceptual framework, the book focuses on the interrelationship between the principal options for encoding phylogenetic trees: split systems, quartet systems and metrics. Such encodings provide useful options for analyzing and manipulating phylogenetic trees and networks, and are at the basis of much of phylogenetic data processing. This book highlights how each one provides a unique perspective for viewing and perceiving the combinatorial structure of a phylogenetic tree and is, simultaneously, a rich source for combinatorial analysis and theory building.

Graduate students and researchers in mathematics and computer science will enjoy exploring this fascinating new area and learn how mathematics may be used to help solve topical problems arising in evolutionary biology.

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Virtually all aspects of human behavior show enormous variation both within and between cultural groups, including material culture, social organization and language. Thousands of distinct cultural groups exist: about 6,000 languages are spoken today, and it is thought that a far greater number of languages existed in the past but became extinct. Using a Darwinian approach, this book seeks to explain this rich cultural variation. There are a number of theoretical reasons to believe that cultural diversification might be tree-like, that is phylogenetic: material and non-material culture is clearly inherited by descendants, there is descent with modification, and languages appear to be hierarchically related. There are also a number of theoretical reasons to believe that cultural evolution is not tree-like: cultural inheritance is not Mendelian and can indeed be vertical, horizontal or oblique, evidence of borrowing abounds, cultures are not necessarily biological populations and can be transient and complex. Here, for the first time, this title tackles these questions of cultural evolution empirically and quantitatively, using a range of case studies from Africa, the Pacific, Europe, Asia and America. A range of powerful theoretical tools developed in evolutionary biology is used to test detailed hypotheses about historical patterns and adaptive functions in cultural evolution. Evidence is amassed from archaeological, linguist and cultural datasets, from both recent and historical or pre-historical time periods. A unifying theme is that the phylogenetic approach is a useful and powerful framework, both for describing the evolutionary history of these traits, and also for testing adaptive hypotheses about their evolution and co-evolution. Contributors include archaeologists, anthropologists, evolutionary biologists and linguists, and this book will be of great interest to all those involved in these areas.

Invertebrate Zoology: A Tree of Life Approach is a comprehensive and authoritative textbook adopting an explicitly phylogenetic organization. Most of the classical anatomical and morphological work has not been changed – it established the foundation of Invertebrate Zoology. With the explosion of Next-Generation Sequencing approaches, there has been a sea-change in the recognized phylogenetic relationships among and between invertebrate lineages. In addition, the merger of evolutionary and developmental biology (evo-devo) has dramatically contributed to changes in the understanding of invertebrate biology. Synthesizing these three approaches (classical morphology, sequencing data, and evo-devo studies) offers students an entirely unique perspective of invertebrate diversity. Key Features One of the first textbooks to combine classical morphological approaches and newer evo-devo and Next-Generation Sequencing approaches to address Invertebrate Zoology Organized along taxonomic lines in accord with the latest understanding of invertebrate phylogeny Will provide background in basic systematic analysis useful within any study of biodiversity A wealth of ancillary materials for students and teachers, including downloadable figures, lecture slides, web links, and phylogenetic data matrices

This workshop questioned the reliability of pottery as crisis indicator within the archaeological data set. More particularly, following the perspective of archaeological and anthropological research that assesses pottery technology as a social product, there is an interest in addressing the social and cultural aspects of technological change...

A new system for organizing and classifying living organisms. A phylogenetic code of biological nomenclature.

This volume, A Mathematical Primer of Molecular Phylogenetics, offers a unique perspective on a number of phylogenetic issues that have not been covered in detail in previous publications. The volume provides sufficient mathematical background for young mathematicians and computational scientists, as well as mathematically inclined biology students, to make a smooth entry into the expanding field of molecular phylogenetics. The book will also provide sufficient details for researchers in phylogenetics to understand the workings of existing software packages used. The volume offers comprehensive but detailed numerical illustrations

to render difficult mathematical and computational concepts in molecular phylogenetics accessible to a variety of readers with different academic background. The text includes examples of solved problems after each chapter, which will be particularly helpful for fourth-year undergraduates, postgraduates, and postdoctoral students in biology, mathematics and computer sciences. Researchers in molecular biology and evolution will find it very informative as well.

This volume constitutes a first step towards an ever-deferred interdisciplinary dialogue on cultural traits. It offers a way to enter a representative sample of the intellectual diversity that surrounds this topic, and a means to stimulate innovative avenues of research. It stimulates critical thinking and awareness in the disciplines that need to conceptualize and study culture, cultural traits, and cultural diversity. Culture is often defined and studied with an emphasis on cultural features. For UNESCO, "culture should be regarded as the set of distinctive spiritual, material, intellectual and emotional features of society or a social group". But the very possibility of assuming the existence of cultural traits is not granted, and any serious evaluation of the notion of "cultural trait" requires the interrogation of several disciplines from cultural anthropology to linguistics, from psychology to sociology to musicology, and all areas of knowledge on culture. This book presents a strong multidisciplinary perspective that can help clarify the problems about cultural traits.

Brings together new research demonstrating how evidence based on genetic phenomena should end any lingering controversy over human evolution.

The study of evolution at the molecular level has given the subject of evolutionary biology a new significance. Phylogenetic 'trees' of gene sequences are a powerful tool for recovering evolutionary relationships among species, and can be used to answer a broad range of evolutionary and ecological questions. They are also beginning to permeate the medical sciences. In this book, the authors approach the study of molecular evolution with the phylogenetic tree as a central metaphor. This will equip students and professionals with the ability to see both the evolutionary relevance of molecular data, and the significance evolutionary theory has for molecular studies. The book is accessible yet sufficiently detailed and explicit so that the student can learn the mechanics of the procedures discussed. The book is intended for senior undergraduate and graduate students taking courses in molecular evolution/phylogenetic reconstruction. It will also be a useful supplement for students taking wider courses in evolution, as well as a valuable resource for professionals. First student textbook of phylogenetic reconstruction which uses the tree as a central metaphor of evolution. Chapter summaries and annotated suggestions for further reading. Worked examples facilitate understanding of some of the more complex issues. Emphasis on clarity and accessibility.

In interviews with today's major figures in evolutionary biology--including Stephen Jay Gould, E. O. Wilson, Ernst Mayr, and John Maynard Smith--Ruse offers an unparalleled account of evolutionary theory, from popular books to museums to the most complex theorizing, at a time when its status as science is under greater scrutiny than ever before.

Much of what we are comes from our ancestors. Through cultural and biological inheritance mechanisms, our genetic composition, instructions for constructing artifacts, the structure and content of languages, and rules for behavior are passed from parents to

children and from individual to individual. Mapping Our Ancestors demonstrates how various genealogical or "phylogenetic" methods can be used both to answer questions about human history and to build evolutionary explanations for the shape of history. Anthropologists are increasingly turning to quantitative phylogenetic methods. These methods depend on the transmission of information regardless of mode and as such are applicable to many anthropological questions. In this way, phylogenetic approaches have the potential for building bridges among the various subdisciplines of anthropology; an exciting prospect indeed. The structure of Mapping Our Ancestors reflects the editors' goal of developing a common understanding of the methods and conditions under which ancestral relations can be derived in a range of data classes of interest to anthropologists. Specifically, this volume explores the degree to which patterns of ancestry can be determined from artifactual, genetic, linguistic, and behavioral data and how processes such as selection, transmission, and geography impact the results of phylogenetic analyses. Mapping Our Ancestors provides a solid demonstration of the potential of phylogenetic methods for studying the evolutionary history of human populations using a variety of data sources and thus helps explain how cultural material, language, and biology came to be as they are.

This book explores the potential and challenges of implementing evolutionary phylogenetic methods in archaeological research, by discussing key concepts and presenting concrete applications of these approaches. The volume is divided into two parts: The first covers the theoretical and conceptual implications of using evolution-based models in the sociocultural domain, illustrates the sorts of questions that these methods can help answer, and invites the reader to reflect on the opportunities and limitations of these perspectives. The second part comprises case studies that address relevant empirical issues, such as inferring patterns and rates of cultural transmission, detecting selective pressures in cultural evolution, and explaining the nature of cultural variation. This book will appeal to archaeologists interested in applying evolutionary thinking and inferential methods to their field, and to anyone interested in cultural evolution studies.

Widens traditional concepts of forensic science to include humanitarian, social, and cultural aspects Using the preservation of the dignity of the deceased as its foundation, Forensic Science and Humanitarian Action: Interacting with the Dead and the Living is a unique examination of the applications of humanitarian forensic science. Spanning two comprehensive volumes, the text is sufficiently detailed for forensic practitioners, yet accessible enough for non-specialists, and discusses both the latest technologies and real-world interactions. Arranged into five sections, this book addresses the 'management of the dead' across five major areas in humanitarian forensic science. Volume One presents the first three of these areas: History, Theory, Practice, and Legal Foundation; Basic Forensic Information to Trace Missing Persons; and Stable Isotopes Forensics. Topics covered include: Protection of The Missing and the Dead Under International Law Social, Cultural and Religious Factors in Humanitarian Forensic Science Posthumous Dignity and the Importance in Returning Remains of the Deceased The New Disappeared – Migration and Forensic Science Stable Isotope Analysis in Forensic Anthropology Volume Two covers two further areas of interest: DNA Analysis and the Forensic Identification Process. It concludes with a comprehensive set of case studies focused on identifying the

deceased, and finding missing persons from around the globe, including: Forensic Human Identification from an Australian Perspective Skeletal Remains and Identification Processing at the FBI Migrant Deaths along the Texas/Mexico Border Humanitarian Work in Cyprus by The Committee on Missing Persons (CMP) Volcán De Fuego Eruption – Natural Disaster Response from Guatemala Drawing upon a wide range of contributions from respected academics working in the field, Forensic Science and Humanitarian Action is a unique reference for forensic practitioners, communities of humanitarian workers, human rights defenders, and government and non-governmental officials.

Paleobiology struggled for decades to influence our understanding of evolution and the history of life because it was stymied by a focus on microevolution and an incredibly patchy fossil record. But in the 1970s, the field took a radical turn, as paleobiologists began to investigate processes that could only be recognized in the fossil record across larger scales of time and space. That turn led to a new wave of macroevolutionary investigations, novel insights into the evolution of species, and a growing prominence for the field among the biological sciences. In *The Quality of the Archaeological Record*, Charles Perreault shows that archaeology not only faces a parallel problem, but may also find a model in the rise of paleobiology for a shift in the science and theory of the field. To get there, he proposes a more macroscale approach to making sense of the archaeological record, an approach that reveals patterns and processes not visible within the span of a human lifetime, but rather across an observation window thousands of years long and thousands of kilometers wide. Just as with the fossil record, the archaeological record has the scope necessary to detect macroscale cultural phenomena because it can provide samples that are large enough to cancel out the noise generated by micro-scale events. By recalibrating their research to the quality of the archaeological record and developing a true macroarchaeology program, Perreault argues, archaeologists can finally unleash the full contributive value of their discipline. Comparison is fundamental to evolutionary anthropology. When scientists study chimpanzee cognition, for example, they compare chimp performance on cognitive tasks to the performance of human children on the same tasks. And when new fossils are found, such as those of the tiny humans of Flores, scientists compare these remains to other fossils and contemporary humans. Comparison provides a way to draw general inferences about the evolution of traits and therefore has long been the cornerstone of efforts to understand biological and cultural diversity. Individual studies of fossilized remains, living species, or human populations are the essential units of analysis in a comparative study; bringing these elements into a broader comparative framework allows the puzzle pieces to fall into place, creating a means of testing adaptive hypotheses and generating new ones. With this book, Charles L. Nunn intends to ensure that evolutionary anthropologists and organismal biologists have the tools to realize the potential of comparative research. Nunn provides a wide-ranging investigation of the comparative foundations of evolutionary anthropology in past and present research, including studies of animal behavior, biodiversity, linguistic evolution, allometry, and cross-cultural variation. He also points the way to the future, exploring the new phylogeny-based comparative approaches and offering a how-to manual for scientists who wish to incorporate these new methods into their research. *Evolutionary Research in Archaeology* seeks to provide a comprehensive overview of contemporary evolutionary research in

archaeology. The book will provide a single source for introduction and overview of basic and advanced evolutionary concepts and research programs in archaeology. Content will be organized around four areas of critical research including microevolutionary and macroevolutionary process, human ecology studies (evolutionary ecology, demography, and niche construction), and evolutionary cognitive archaeology. Authors of individual chapters will address theoretical foundations, history of research, contemporary contributions and debates, and implications for the future for their respective topics. As appropriate, authors present or discuss short empirical case studies to illustrate key arguments. ?

This book will appeal to archaeologists interested in applying evolutionary thinking and inferential methods to their field, and to anyone interested in cultural evolution studies. This book explores the potential and challenges of implementing evolutionary phylogenetic methods in archaeological research, by discussing key concepts and presenting concrete applications of these approaches. Cultural Phylogenetics, assembles seven articles dealing both theoretically and practically with the prospects and challenges of phylogenetic methods in archaeology. I consider the book to be an interesting contribution, worth being read by everyone who is interested in quantitative methods applied to historical sciences.

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: <http://www.mpcm-evolution.com>), where the authors post and permanently update practical materials to help embed methods into practice.

No question in theoretical biology has been more perennially controversial or perplexing than "What is a species?" Recent advances in phylogenetic theory have called into question traditional views of species and spawned many concepts that are currently competing for general acceptance. Once the subject of esoteric intellectual exercises, the "species problem" has emerged as a critically important aspect of global environmental concerns. Completion of an inventory of biodiversity, success in conservation, predictive knowledge about life on earth, management of material resources, formulation of scientifically credible public policy and law, and more depend upon our adoption of the "right" species concept. Quentin D. Wheeler and Rudolf Meier present a debate among top systematic biology theorists to consider the strengths and weaknesses of five competing concepts.

Debaters include (1) Ernst Mayr (Biological Species Concept), (2) Rudolf Meier and Rainer Willmann (Hennigian species concept), (3) Brent Mishler and Edward Theriot (one version of the Phylogenetic Species Concept), (4) Quentin Wheeler and Norman Platnick (a competing version of the Phylogenetic Species Concept), and (5) E. O. Wiley and Richard Mayden (the Evolutionary Species Concept). Each author or pair of authors contributes three essays to the debate: first, a position paper with an opening argument for their respective concept of species; second, a counterpoint view of the weakness of competing concepts; and, finally, a rebuttal of the attacks made by other authors. This unique and lively debate format makes the comparative advantages and disadvantages of competing species concepts clear and accessible in a single book for the first time, bringing to light numerous controversies in phylogenetic theory, taxonomy, and philosophy of science that are important to a wide audience. *Species Concepts and Phylogenetic Theory* will meet a need among scientists, conservationists, policy-makers, and students of biology for an explicit, critical evaluation of a large and complex literature on species. An important reference for professionals, the book will prove especially useful in classrooms and discussion groups where students may find a concise, lucid entrée to one of the most complex questions facing science and society.

This book is intended to help transform epistemology - the traditional study of knowledge - into a rigorous discipline by removing conceptual roadblocks and developing formal tools required for a fully naturalized epistemology. The evolutionary approach which Harms favours begins with the common observation that if our senses and reasoning were not reliable, then natural selection would have eliminated them long ago. The challenge for some time has been how to transform these informal musings about evolutionary epistemology into a rigorous theoretical discipline capable of complementing current scientific studies of the evolution of cognition with a philosophically defensible account of meaning and justification.

To document the world's diversity of species and reconstruct the tree of life we need to undertake some simple but mountainous tasks. Most importantly, we need to tackle species rich groups. We need to collect, name, and classify them, and then position them on the tree of life. We need to do this systematically across all groups of organisms and because of the biodiversity crisis we need to do it quickly. With contributions from key systematic and taxonomic researchers, *Reconstructing the Tree of Life: Taxonomy and Systematics of Species Rich Taxa* outlines the core of the problem and explores strategies that bring us closer to its solution. The editors split the book into three parts: introduction and general concepts, reconstructing and using the tree of life, and taxonomy and systematics of species rich groups (case studies). They introduce, with examples, the concept of species rich groups and discuss their importance in reconstructing the tree of life as well as their conservation and sustainable utilization in general. The book highlights how phylogenetic trees are becoming "supersized" to handle species rich groups and the methods that are being developed to deal with the computational complexity of such trees. It discusses factors that have lead some groups to speciate to a staggering degree and also provides case studies that highlight the problems and prospects of dealing with species rich groups in taxonomy. To understand species rich taxa, evolution has set scientists a difficult, but not unattainable, challenge that requires the meshing together of phylogenetics and taxonomy, considerable advances in informatics, improved and increased collecting, training of taxonomists, and significant financial support. This book provides the tools and methods needed to meet that challenge.

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"This book impressively chronicles the burgeoning field of experimental evolutionary biology. Controlled field and lab experiments are among the newest pillars of evolution. Assembled by two of the most articulate and effective practitioners, this volume provides a stimulating and often inspiring introduction to experimental evolution; it is ideal for a graduate seminar and is certain to fuel rewarding discussion and innovative research."--Rick Grosberg, University of California, Davis "Although experimental evolution has been a major element in the biological toolkit for decades, many still think of evolutionary biology as a descriptive science. This timely, authoritative review of the broad sweep and deep insights of experimental evolution should permanently change that impression by firmly establishing an approach that has now grounded many evolutionary hypotheses in sound experimental logic. The authors, who include many who built the field, have written eloquently; the editors, themselves major practitioners of the method, have chosen wisely; this book, their product, now defines the field."--Steve Stearns, Yale University "Experiments provide a powerful complement to observational and comparative studies. For this reason, evolutionary biology is increasingly an experimental science, not only in the laboratory, but also in the field. This textbook provides an excellent introduction to the manner in which evolutionary experiments are conducted and the types of questions and organisms to which they are applied."--Jonathan B. Losos, Museum of Comparative Zoology and Department of Organismic and Evolutionary Biology, Harvard University

Much of what we are comes from our ancestors. Through cultural and biological inheritance mechanisms, our genetic composition, instructions for constructing artifacts, the structure and content of languages, and rules for behavior are passed from parents to children and from individual to individual. Mapping Our Ancestors demonstrates how various genealogical or "phylogenetic" methods can be used both to answer questions about human history and to build evolutionary explanations for the shape of history. Anthropologists are increasingly turning to quantitative phylogenetic methods. These methods depend on the transmission of information regardless of mode and as such are applicable to many anthropological questions. In this way, phylogenetic approaches have the potential for building bridges among the various subdisciplines of anthropology; an exciting prospect indeed. The structure of Mapping Our Ancestors reflects the editors' goal of developing a common understanding of the methods and conditions under which ancestral relations can be derived in a range of data classes of interest to anthropologists. Specifically, this volume explores the degree to which patterns of ancestry can be determined from artifactual, genetic, linguistic, and behavioral data and how processes such as selection, transmission, and geography impact the results of phylogenetic analyses. Mapping Our Ancestors provides a solid demonstration of the potential of phylogenetic methods for studying the evolutionary history of human populations using a variety of data sources and thus helps explain how cultural material, language, and biology came to be as they are. Carl P. Lipo is assistant professor of anthropology at California State University in Long Beach. Michael O'Brien is professor of anthropology and director of the Museum of Anthropology at the University of Missouri. Mark Collard is assistant professor of anthropology at the University of British Columbia, Stephen J. Shennan is a professor and director of the Institute of Archaeology at the University College London. Niles Eldredge is a curator in the department of invertebrates at the American Museum of Natural History, and adjunct professor at the City University of New York.

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 biology has increasingly relied upon tools developed in molecular biology that allow for the structure and function of macromolecules to be used as data for exploring the patterns and processes of evolutionary change. *Integrated Molecular Evolution, Second Edition* is a textbook intended to expansively and comprehensive review evolutionary studies now routinely using molecular data. This new edition has been thoroughly updated and expanded, and provides a basic summary of evolutionary biology as well as a review of current phylogenetics and phylogenomics. Reflecting a burgeoning pedagogical landscape, this new edition includes nearly double the number of chapters, including a new section on molecular and bioinformatic methods. Dedicated chapters were added on: Evolution of the genetic code Mendelian genetics and population genetics Natural selection Horizontal gene transfers Animal development and plant development Cancer Extraction of biological molecules Analytical methods Sequencing methods and sequencing analyses Omics Phylogenetics and phylogenetic networks Protein trafficking Human genomics More than 400 illustrations appear in this edition, doubling the number included in the first edition, and over 100 of these diagrams are now in color. The second edition combines and integrates extensive summaries of genetics and evolutionary biology in a manner that is accessible for students at either the graduate or undergraduate level. It also provides both the basic foundations of molecular evolution, such as the structure and function of DNA, RNA and proteins, as well as more advanced chapters reviewing analytical techniques for obtaining sequences, and interpreting and archiving molecular and genomic data.

The evolutionary history of species is traditionally represented using a rooted phylogenetic tree. However, when reticulate events such as hybridization, horizontal gene transfer or recombination are believed to be involved, phylogenetic networks that can accommodate non-treelike evolution have an important role to play. This book provides the first interdisciplinary overview of phylogenetic networks. Beginning with a concise introduction to both phylogenetic trees and phylogenetic networks, the fundamental concepts and results are then presented for both rooted and unrooted phylogenetic networks. Current approaches and algorithms available for computing phylogenetic networks from different types of datasets are then discussed, accompanied by examples of their application to real biological datasets. The book also summarises the algorithms used for drawing phylogenetic networks, along with the existing software for their computation and evaluation. All datasets, examples and other additional information and links are available from the book's companion website at www.phylogenetic-networks.org.

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, t

Decapod crustaceans are of tremendous interest and importance evolutionarily, ecologically, and economically. There is no shortage of publications reflecting the wide variety of ideas and hypotheses concerning decapod phylogeny, but until recently, the world's leading decapodologists had never assembled to elucidate and discuss relationships among the major decapod lineages and between decapods and other crustaceans. Based on the findings presented by an international group of scientists at a symposium supported by the Society for Integrative and Comparative Biology, The Crustacean Society, and several other societies, and with major funding from the National Science

Foundation, Decapod Crustacean Phylogenetics provides a comprehensive synopsis of the current knowledge of this vast and important group of animals. This volume contains state-of-the-art reviews of literature and methodologies for elucidating decapod phylogeny. The contributions include studies on the fossil origin of decapods, morphological and molecular phylogenetic analyses, the evolution of mating and its bearing on phylogeny, decapod "evo-devo" studies, decapod spermiocladistics, and phylogenetic inference. The experts also present research on preliminary attempts to construct the first known phylogenetic tree for various groups of decapods. Several contributions offer the most comprehensive analyses to date on major clades of decapods, and others introduce data or approaches that could be used in the future to help resolve the phylogeny of the Decapoda. Currently, the Decapoda contain an estimated 15,000 species, some of which support seafood and marine industries worth billions of dollars each year to the world's economy. This volume is a fascinating overview of where we are currently in our understanding of these important creatures and their phylogeny and also provides a window into the future of decapod research. This work will be of great interest to researchers, instructors, and students in marine biology, evolutionary biology, crustacean biology, resource management, and biodiversity database management.

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 (<http://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.

Bees are flying insects of the order Hymenoptera closely related to wasps and ants. The ancestors of bees are assumed to be predatory wasps, which switched to pollen consumption. Further, bees co-evolved with flowering plants and divided into several species according to climatic conditions. Widely known bees are western bees *Apis mellifera*, and eastern bees *Apis cerana*. This book sheds light on features of evolution, phylogenesis, speciation, adaptation to environment, and taxonomy of bees. It will be of particular relevance to evolutionists, geneticists, taxonomists, ecologists, population geneticist, and breeders.

L'Annuario della Scuola Archeologica di Atene e delle Missioni Italiane in Oriente è pubblicato dal 1914. Presenta articoli originali e di sintesi sull'arte, l'archeologia, l'architettura, la topografia, la storia, le religioni, l'antropologia del mondo antico, l'epigrafia e il diritto. L'interesse è rivolto alla Grecia e alle aree della grecità attraverso il tempo, dalla preistoria all'età bizantina e oltre, nonché alle interazioni con l'Oriente, l'Africa e l'Europa continentale. L'Annuario è composto da tre sezioni: Saggi, Scavi e Ricerche e Atti della Scuola 2019, a cura di Emanuele Papi. Gli articoli vengono approvati dal Comitato Editoriale e da due valutatori anonimi. I contributi sono pubblicati in una delle seguenti lingue: italiano, greco, inglese, spagnolo e tedesco, con riassunti in italiano, greco e inglese.

Like previous series entries, this volume covers rock art research and management all over the world over a 5-year period, in this case 2015-19. Contributions once again show the wide variety of approaches that have been taken in different parts of the world and reflect the expansion and diversification of perspectives and research questions.

This book offers a unique balance between a basic introductory knowledge of bioinformatics and a detailed study of algorithmic techniques.

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Bioinformatics and RNA: A Practice-Based Approach is a complete guide on the fundamental concepts, applications, algorithms, protocols, new trends, challenges, and research results in the area of bioinformatics and RNA. The book offers a broad introduction to the explosively growing new discipline of bioinformatics. It covers theoretical topics along with computational algorithms. It explores RNA bioinformatics, which contribute to therapeutics and drug discovery. Implementation of algorithms in a DotNet Framework with code and complete insight on the state-of-the-art and recent advancements are presented in detail. The book targets both novice readers as well as practitioners in the field. FEATURES Offers a broad introduction to the explosively growing new discipline of bioinformatics Covers theoretical topics and computational algorithms Explores RNA bioinformatics to unleash the potential from therapeutics to drug discovery Discusses implementation of algorithms in DotNet Frameworks with code Presents insights into the state of the art and recent advancements in bioinformatics The book is useful to undergraduate students with engineering, science, mathematics, or biology backgrounds. Researchers will be equally interested. Phylogenetic Systematics: Haeckel to Hennig traces the development of phylogenetic systematics against the foil of idealistic morphology through 100 years of German biology. It starts with the iconic Ernst Haeckel-the German Darwin from Jena-and the evolutionary morphology he developed. It ends with Willi Hennig, the founder of modern phylogenetic

Explore the latest research in anthropological genetics and understand the genome's role in cultural and social development A Companion to Anthropological Genetics illustrates the role of genetic analysis in advancing the modern study of human origins, populations, evolution, and diversity. Broad in scope, this essential reference work establishes and explores the relationship between genetic research and the major questions of anthropological study. Through contributions by leading researchers, this collection explores molecular genetics and evolutionary mechanisms in the context of macro- and microevolution, paleontology, phylogeny, diet, and disease, with detailed explanations of quantitative methods, including coalescent and approximate Bayesian computation. With an emphasis on contextualizing new and developing genetic research within anthropological frameworks, this text offers critical perspective on the conditions of molecular evolution that accompany cultural and social transformation, while also addressing critical disciplinary questions, such as the ethical issues surrounding ancestry testing and community-based genetic research. Acts as an essential reference on the contributions of genetic science to the field of anthropology Features new work by leading researchers of the field Explores the evolution of immunity, including the genetics and epigenetics of pathogens, chronic illness, and disease resistance Provides in-depth examination of mutation and dietary adaptation, including AMY1, lactase persistence, and sensory polymorphisms Explains essential quantitative and phylogenetic methods for aligning genomic analysis with evolution and migration time scales Offering thorough coverage on leading questions and developing research, A Companion to Anthropological Genetics is a comprehensive resource for students and scholars.

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