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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. Reconstructing phylogenetic trees from DNA sequences has become a popular exercise in many branches of biology, and here the well-known geneticist John Avise explains why. Molecular phylogenies provide a genealogical backdrop for interpreting the evolutionary histories of many other types of biological traits (anatomical, behavioral, ecological, physiological, biochemical and even geographical). Guiding readers on a natural history tour along dozens of evolutionary pathways, the author describes how creatures ranging from microbes to elephants came to possess their current phenotypes. Essential reading for college students, professional biologists and anyone interested in natural history and biodiversity, this book is packed with fascinating examples of evolutionary puzzles from across the animal kingdom; how the toucan got its enormous bill, how reptiles grow back lost limbs and why Arctic fish don't freeze. 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. Fossil eggs provide a unique source of information about the reproductive biology of extinct vertebrates. Dinosaur eggshell, eggs, and clutches are of particular interest because of their great diversity in size, shape, microstructure, and clutch configurations relative to extant egg-laying taxa. In order to provide an explicity phylogenetic framework within which to investigate this diversity and to form more rigorous hypotheses about the identities of egg types that lack associations with adult or embryonic remains, cladistic analyses of 36 oological characters were peformed for 48 egg types. This study aimed to achieve a broader ootaxonomic coverage than previous studies, including pterosaur eggs for the first time in an outgroup with crocodilians and turtles in order to better polarize character states. The first set of analyses did not restrict the positions of ingroup eggs; however, the second utilized a backbone constraint to restrict the positions of taxonomically identified eggs on the tree, allowing unidentified ootaxa to fall out freely relative to a stable framework of relationships based on consensus osteological phylogenies. The results of all analyses reveal Chinese spheroolithids and Mongolian dendroolithids grouping together to the exclusion of other members of those oofamilies (and alongside therizinosauroid eggs) suggesting that Spheroolithidae and Dendroolithidae are polyphyletic. The constrained analysis additionally reveals Ovaloolithus and Cairanoolithus as the only egg types unresolved at the base of Dinosauria on an Adams consensus tree, suggesting that they could belong to either saurischians or ornithischians. All other taxonomically unidentified ootaxa fall out as saurischians, suggesting that the lack of ornithischian eggs in the fossil record is the result of real biases acting against their preservation, and is not simply an artifact of a lack of preserved embryos whereby they might be identified. Major transitions in dinosaur eggshell evolution include the evolution of a second structural layer of calcite

within Avetheropoda, and a reversal to a single-layered condition within Therizinosauroidea. As in previous studies, a stepwise accumulation of avian-like character states within theropods precedes the appearance of extant avian clades. This study highlights the need for ongoing application of cladistic and related principles to the study of fossil eggs. " ... the results presented here can be used as a "backbone" for testing hypotheses about the evolution of social organization, religious systems, and material culture in the Pacific" -- Conclusion. The increasing availability of molecular and genetic databases coupled with the growing power of computers gives biologists opportunities to address new issues, such as the patterns of molecular evolution, and re-assess old ones, such as the role of adaptation in species diversification. In the second edition, the book continues to integrate a wide variety of data analysis methods into a single and flexible interface: the R language. This open source language is available for a wide range of computer systems and has been adopted as a computational environment by many authors of statistical software. Adopting R as a main tool for phylogenetic analyses will ease the workflow in biologists' data analyses, ensure greater scientific repeatability, and enhance the exchange of ideas and methodological developments. The second edition is completed updated, covering the full gamut of R packages for this area that have been introduced to the market since its previous publication five years ago. There is also a new chapter on the simulation of evolutionary data. Graduate students and researchers in evolutionary biology can use this book as a reference for data analyses, whereas researchers in bioinformatics interested in evolutionary analyses will learn how to implement these methods in R. The book starts with a presentation of different R packages and gives a short introduction to R for phylogeneticists unfamiliar with this language. The basic phylogenetic topics are covered: manipulation of phylogenetic data, phylogeny estimation, tree drawing, phylogenetic comparative methods, and estimation of ancestral characters. The chapter on tree drawing uses R's powerful graphical environment. A section deals with the analysis of diversification with phylogenies, one of the author's favorite research topics. The last chapter is devoted to the development of phylogenetic methods with R and interfaces with other languages (C and C++). Some exercises conclude these chapters. CD-ROM contains: color photographs -- illustrated glossary -- appendices. A broad, hands on guide with detailed explanations of current methodology, relevant exercises and popular software tools. Never HIGHLIGHT a Book Again! Virtually all of the testable terms, concepts, persons, places, and events from the textbook are included. Cram101 Just the FACTS101 studyguides give all of the outlines, highlights, notes, and quizzes for your textbook with optional online comprehensive practice tests. Only Cram101 is Textbook Specific. Accompanys: 9780878934072 . Incorporating phylogenetic principles and methods throughout, this text moves from the careful explanation of phylogenetic methods and principles to the taxonomic survey of vascular plant families. A much expanded CD-ROM is included, containing over 2,200 colour photos illustrating the diagnostic characters of plant families covered in the text. Appropriate for any course devoted to the systematics of plants, this text assumes no prerequisites other than introductory botany or biology. ABSTRACT: Mitochondrial DNA (mtDNA) has played a major role in human population studies over the past decade due to its maternal inheritance and negligible recombination (Macaulay, 1999). The mtDNA control region has been the focus of these studies due to the highly polymorphic nature of this non-coding region. Forensic scientists also use mtDNA to help determine the identity of missing individuals when nuclear DNA is not present. However, when skeletal remains are unclaimed, identification becomes near impossible. Therefore, mtDNA can play a valuable role in identification in terms of population affiliation, especially in conjunction with morphological analysis. The goals of this research were two-fold: 1) to determine population affiliation of unknown skeletal samples using phylogenetics and 2) to find a method of extraction that leaves a majority of the remains intact. The costs and prevalence of religion present an explanatory challenge for evolutionary theorists. Costs include the opportunity costs of time spent praying, the reproductive costs of abstinent clergy, and the resource costs of sacrificial offerings. The question this raises is how natural selection could have allowed the majority of the global population today to become religious adherents. The emerging field of evolutionary religious studies seeks to explain the prevalence of religion by

understanding its evolutionary origins and potential functions. In support of functional explanations, previous cross-cultural research has found that features of religion, such as belief in big gods, are associated with larger and more complex societies. However, this research is subject to Galton's Problem and is based on the effects of modern world religions under conditions very different to most of our evolutionary history. Rigorous cross-cultural research is needed to test functions of religion in traditional cultures. In Chapter 1 I provide an overview of evolutionary religious studies and explain how phylogenetic comparative methods have the power to identify the co-evolution of religion and society in traditional Austronesian cultures. Phylogenetic methods can be used to reconstruct cultural history, address Galton's Problem, and infer the direction of causality based on the order that traits tend to arise. Traditional Austronesian cultures had a diverse range of supernatural beliefs, practices and social structures, and can be linked to a language based genealogy. In Chapter 2 I present the Pulotu database which provides quantitative variables on the traditional religious and social systems of Austronesian cultures. I then use phylogenetic methods and the Pulotu database to test three prominent evolutionary theories of religion. In Chapter 3 I find evidence that belief in punishment by a broad range of supernatural agents helped build political complexity, but that big gods arose after political complexity in Austronesia. In Chapter 4 I find that human sacrifice functioned to help build and maintain social inequality in early human societies. In Chapter 5 I show that political systems facilitated the recent spread of Christianity. I finish in Chapter 6 by suggesting five directions for the future development of evolutionary religious studies. A comprehensive introduction to vascular plant phylogeny, the third edition of "Plant Systematics" reflects changes in the circumscription of many orders and families to represent monophyletic groups, following the most recent classification of the Angiosperm Phylogeny Group. Molecular taxonomic methods are fully presented, as are the results of many recent studies, both molecular and morphological. 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. The long-awaited revision of the industry standard on phylogenetics Since the publication of the first edition of this landmark volume more than twenty-five years ago, phylogenetic systematics has taken its place as the dominant paradigm of systematic biology. It has profoundly influenced the way scientists study evolution, and has seen many theoretical and technical advances as the field has continued to grow. It goes almost without saying that the next twenty-five years of phylogenetic research will prove as fascinating as the first, with many exciting developments yet to come. This new edition of Phylogenetics captures the very essence of this rapidly evolving discipline. Written for the practicing systematist and phylogeneticist, it addresses both the philosophical and technical issues of the field, as well as surveys general practices in taxonomy. Major sections of the book deal with the nature of species and higher taxa, homology and characters, trees and tree graphs, and biogeography—the purpose being to develop biologically relevant species, character, tree, and biogeographic concepts that can be applied fruitfully to phylogenetics. The book then turns its focus to phylogenetic trees, including an in-depth

guide to tree-building algorithms. Additional coverage includes: Parsimony and parsimony analysis Parametric phylogenetics including maximum likelihood and Bayesian approaches Phylogenetic classification Critiques of evolutionary taxonomy, phenetics, and transformed cladistics Specimen selection, field collecting, and curating Systematic publication and the rules of nomenclature Providing a thorough synthesis of the field, this important update to Phylogenetics is essential for students and researchers in the areas of evolutionary biology, molecular evolution, genetics and evolutionary genetics, paleontology, physical anthropology, and zoology. A cladistic analysis based on parsimony is undertaken to test hypotheses concerning the monophyly of the family and examine the relationships among their various clades. The data matrix comprised a total of 98 species representing 16 families scored for 146 characters, all but six taken from various morphological systems; the remaining are behavioral attributes.

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