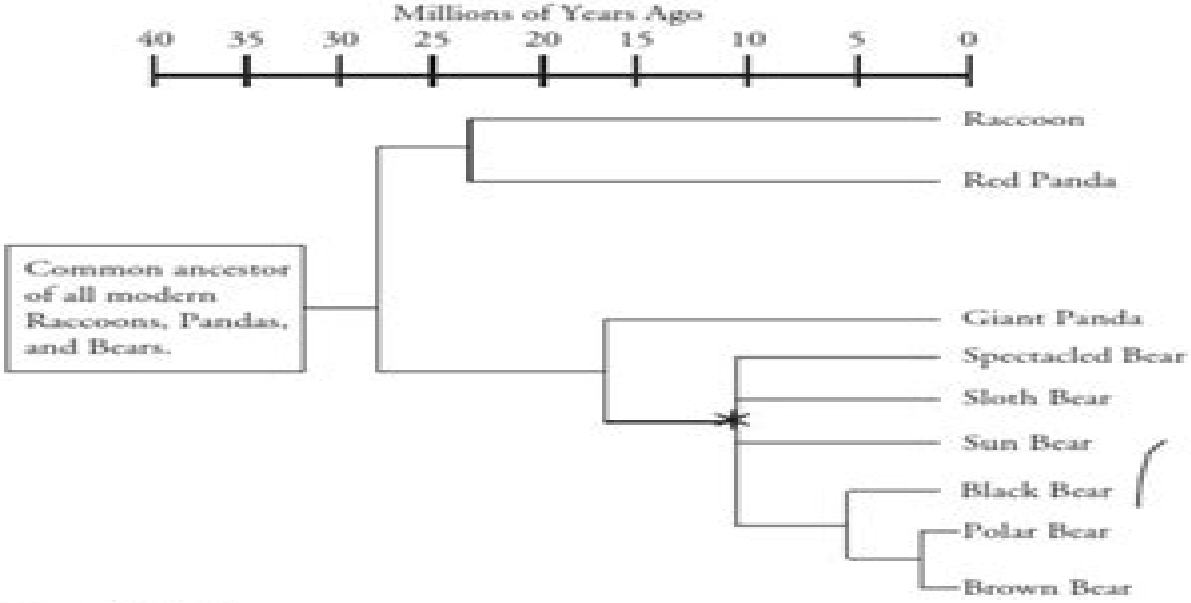
Phylogenetic Trees

How do the changes in gene sequences allow us to reconstruct the evolutionary relationships between related species?

Why?

The saying "Don't judge a book by its cover," could be applied to the topic of evolution. For example, humans share 75% of their DNA with chickens. Biologists point to this as evidence that humans and chickens once shared a common ancestor. The advent of DNA technology has given scientists the tools with which to examine how closely related certain species are. DNA analysis allows scientists to construct phylogenetic trees whose branches link together the relatedness of different organisms.

Model 1 – Phylogenetic Trees



1. Refer to Model 1.
   a. How long ago did the common ancestor of all ~~the~~ organisms on this phylogenetic tree exist?

      35 mil

   b. Which two lines diverged 30 million years ago?

      bear and panda

   c. List all modern descendants of the organism that was alive at the point indicated by the asterisk.

      Everything except brown and polar

Pogil Phylogenic Tree Activity

Albert A Gayle

Pogil Phylogenic Tree Activity:

Automobile Phylogenetic Tree , Al Vogel presents An Automobile Phylogenetic Tree an activity for high school biology or life science classes requiring the construction of a phylogenetic tree for various cars and trucks Access Excellence a service of the nonprofit National Museum of Health provides the activity online The activity was created as part of the National Leadership Program for Teachers of the Woodrow Wilson National Fellowship Foundation **Innovative Teaching Module for Promoting Phylogenetic Tree Understanding for High School Students** Teamjun Sarasan,Mahāwitthayālai Mahidon,Mahāwitthayālai Mahidon. Institute for Innovative Learning,2010 Phylogenetic Trees Made Easy Barry G. Hall,2008 Barry G Hall helps beginners get started in creating phylogenetic trees from protein or nucleic acid sequence data

The Phylogenetic Handbook Marco Salemi,Anne-Mieke Vandamme,2003-08-27 Sample Text Phylogenetic Supertrees Olaf R.P. Bininda-Emonds,2004-05-31 This is the first book on phylogenetic supertrees a recent but controversial development for inferring evolutionary trees Rather than analyze the combined primary character data directly supertree construction proceeds by combining the tree topologies derived from those data This difference in strategy has allowed for the exciting possibility of larger more complete phylogenies than are otherwise currently possible with the potential to revolutionize evolutionarily based research This book provides a comprehensive look at supertrees ranging from the methods used to build supertrees to the significance of supertrees to bioinformatic and biological research Reviews of many the major supertree methods are provided and four new techniques including a Bayesian implementation of supertrees are described for the first time The far reaching impact of supertrees on biological research is highlighted both in general terms and through specific examples from diverse clades such as flowering plants even toed ungulates and primates The book also critically examines the many outstanding challenges and problem areas for this relatively new field showing the way for supertree construction in the age of genomics Interdisciplinary contributions from the majority of the leading authorities on supertree construction in all areas of the bioinformatic community biology computer sciences and mathematics will ensure that this book is a valuable reference with wide appeal to anyone interested in phylogenetic inference **Data Integration, Manipulation and Visualization of Phylogenetic Trees** Guangchuang Yu,2022-08-26 Data Integration Manipulation and Visualization of Phylogenetic Trees introduces and demonstrates data integration manipulation and visualization of phylogenetic trees using a suite of R packages tidytree treeio ggtree and ggtreeExtra Using the most comprehensive packages for phylogenetic data integration and visualization contains numerous examples that can be used for teaching and learning Ideal for undergraduate readers and researchers with a working knowledge of R and ggplot2 Key Features Manipulating phylogenetic tree with associated data using tidy verbs Integrating phylogenetic data from diverse sources Visualizing phylogenetic data using grammar of graphics **Phylogeny** Mike Steel,2016-09-29 Phylogenetics is a topical and growing area of research Phylogenies phylogenetic trees and networks allow biologists to study and graph evolutionary

relationships between different species These are also used to investigate other evolutionary processes for example how languages developed or how different strains of a virus such as HIV or influenza are related to each other This self contained book addresses the underlying mathematical theory behind the reconstruction and analysis of phylogenies The theory is grounded in classical concepts from discrete mathematics and probability theory as well as techniques from other branches of mathematics algebra topology differential equations The biological relevance of the results is highlighted throughout The author supplies proofs of key classical theorems and includes results not covered in existing books emphasizes relevant mathematical results derived over the past 20 years and provides numerous exercises examples and figures

Phylogenetics E. O. Wiley,Bruce S. Lieberman,2011-06-07 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 Tree Thinking: An Introduction to Phylogenetic Biology David A. Baum,Stacey D. Smith,2012-08-10 Baum and Smith both professors evolutionary biology and researchers in the field of systematics present this highly accessible introduction to phylogenetics and its importance in modern biology Ever since Darwin the evolutionary histories of organisms have been portrayed in the form of branching trees or phylogenies However the broad significance of the phylogenetic trees has come to be appreciated only quite recently Phylogenetics has myriad applications in biology from discovering the features present in ancestral organisms to finding the sources of invasive species and infectious diseases to identifying our closest living and extinct hominid relatives Taking a conceptual approach Tree Thinking introduces readers to the interpretation of phylogenetic trees

how these trees can be reconstructed and how they can be used to answer biological questions Examples and vivid metaphors are incorporated throughout and each chapter concludes with a set of problems valuable for both students and teachers Tree Thinking is must have textbook for any student seeking a solid foundation in this fundamental area of evolutionary biology **Reconstructing the Tree of Life** Trevor R. Hodkinson,John A.N. Parnell,2006-12-26 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 b Mathematics of Evolution and Phylogeny Olivier Gascuel,2005-02-24 Table of contents **Shortest Connectivity** Dietmar Cieslik,2006-06-02 The aim in this graduate level text is to outline the key mathematical concepts that underpin these important questions in applied mathematics These concepts involve discrete mathematics particularly graph theory optimization computer science and several ideas in biology **Analysis of Phylogenetics and Evolution with R** Emmanuel Paradis,2011-11-06 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 **The Phylogenetic Handbook** Marco Salemi,Anne-Mieke Vandamme,Philippe Lemey,2009-03-26 A broad hands on guide with detailed explanations of current methodology relevant exercises and popular software tools **A Phylogenetic Tree of the Animal Kingdom** Jarmila Kukalova-Peck,1990-07 **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 **The Compleat Cladist** E. O. Wiley,1991 **Foundations of Phylogenetic Systematics** Johann Wolfgang Wägele,2005 Phylogeny inference and the classification of organisms are indispensable for all fields of biology On the basis of a well corroborated tree of life it is possible to understand the evolution of structure and function of genomes of gene families of cascades of developmental genes and the origin of genes of medical importance Ecologists need a stable classification of organisms to identify organisms to find their correct names and thus further information on relevant species This book offers an introduction to the theory of Phylogenetic Systematics and is a companion for all biologists who want to analyze morphological or molecular data with classical methods or with modern computer programs The first part of the book explains the epistemological basis that is independent of the type of method used to construct phylogenetic trees Unlike other empirical sciences the estimation of data quality in phylogenetics is still little developed and very often neglected Here a theoretical basis is presented that enables the systematist to assess critically and objectively the quality of different data sets and to make statements on the plausibility of results This requires a conception of the notions of information content probability of homology probability of cognition probability of events the principle of parsimony the differentiation of phenomenological and modelling methods Willi Hennig s original method is compared with modern numerical systematics and an updated Hennigian procedure of data analysis is discussed The difference between phenetic and phylogenetic cladistics is explained Popular tools for data evaluation implemented in computer programs are explained including their axiomatic assumptions sources of error and possible applications For the more common tools the mathematical background is explained in a simple easy to understand way Johann Wolfgang Wagele was until recently head of the Department for Animal Systematics Lehrstuhl fur Spezielle Zoologie at the University of Bochum and is now director of the Museum Alexander Koenig in Bonn Germany His main research interests are the taxonomy phylogeny and biodiversity of Isopoda which implies observations of life history biogeography and ecology in combination with phylogeny inference Further subjects include arthropod phylogeny and tools for explorative data analyses The author is president of the Gesellschaft fur Biologische Systematik a Central European society of systematists and he is actively promoting biodiversity research

Phylogenetic Comparative Methods Luke J. Harmon,2018-05-23 An introduction to statistical analyses of phylogenetic trees using comparative methods **Phylogenetics** Charles Semple,Mike Steel,Both in the Department of Mathematics and Statistics Mike Steel,2003 Phylogenetics is the reconstruction and analysis of phylogenetic evolutionary trees and networks

based on inherited characteristics It is a flourishing area of intereaction between mathematics statistics computer science and biology The main role of phylogenetic techniques lies in evolutionary biology where it is used to infer historical relationships between species However the methods are also relevant to a diverse range of fields including epidemiology ecology medicine as well as linguistics and cognitive psychologyThis graduate level book based on the authors lectures at The University of Canterbury New Zealand focuses on the mathematical aspects of phylogenetics It brings together the central results of the field providing proofs of the main theorem outlines their biological significance and indicateshow algorithms may be derived The presentation is self contained and relies on discrete mathematics with some probability theory A set of exercises and at least one specialist topic ends each chapter This book is intended for biologists interested in the mathematical theory behind phylogenetic methods and for mathematicians statisticians and computer scientists eager to learn about this emerging area of discrete mathematics Phylogenetics in the 24th volume in the Oxford Lecture Series in Mathematics and its Applications This series contains short books suitable for graduate students and researchers who want a well written account of mathematics that is fundamental to current to research The series emphasises futuredirections of research and focuses on genuine applications of mathematics to finance engineering and the physical and biological sciences

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