

Phylogenetic Trees Pogil Answers

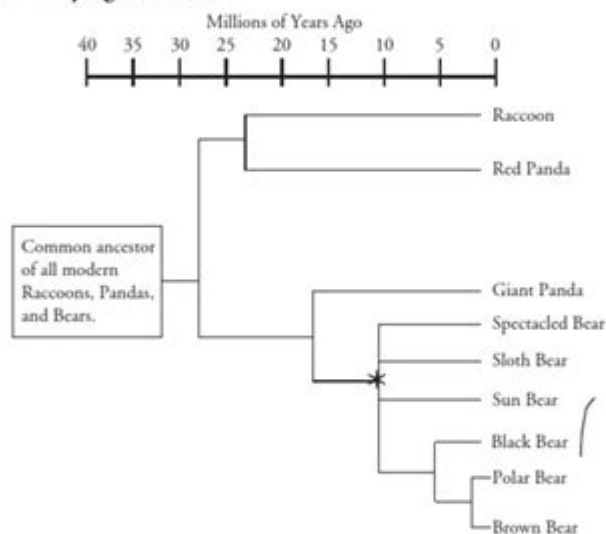
Phylogenetic Trees

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 mi.

- 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.

every thing except
brown and polar

Phylogenetic Trees

Phylogenetic Trees POGIL Answers: A Comprehensive Guide to Understanding Evolutionary Relationships

Are you struggling to decipher the complexities of phylogenetic trees? Finding accurate answers to your POGIL (Process Oriented Guided Inquiry Learning) activities on this topic can be frustrating. This comprehensive guide provides not just the answers to your phylogenetic trees POGIL questions, but a deeper understanding of how to interpret and utilize these powerful tools for visualizing evolutionary history. We'll break down the key concepts, offer solutions to common problem areas, and equip you with the knowledge to confidently tackle any phylogenetic tree challenge.

This post is designed to help you fully grasp the concepts behind phylogenetic trees, providing detailed explanations and insightful answers to your POGIL exercises. We'll go beyond simply providing the answers; we'll teach you how to arrive at those answers, strengthening your understanding of evolutionary relationships and phylogenetic analysis.

What are Phylogenetic Trees?

Phylogenetic trees, also known as evolutionary trees, are branching diagrams that visually represent the evolutionary relationships among various biological species or other entities. They depict the hypothesized evolutionary history, showing how different groups are related through common ancestors. Each branch point (node) represents a common ancestor, while the tips of the branches represent the extant (currently living) or extinct species. The length of branches can sometimes represent evolutionary time or the amount of genetic change.

Understanding the Key Concepts in Phylogenetic Tree Analysis

Before diving into POGIL answers, it's crucial to understand the fundamental concepts:

1. Rooted vs. Unrooted Trees:

Rooted trees: Show the direction of evolutionary time, indicating a single common ancestor for all organisms on the tree.

Unrooted trees: Don't show the direction of time; they only show the relationships between the organisms, not necessarily their ancestral relationships.

2. Clades:

A clade is a group of organisms that includes a common ancestor and all of its descendants. Understanding clades is essential for correctly interpreting phylogenetic trees.

3. Monophyletic, Paraphyletic, and Polyphyletic Groups:

Monophyletic: A clade - a group containing a common ancestor and all of its descendants.

Paraphyletic: A group containing a common ancestor but not all of its descendants.

Polyphyletic: A group containing organisms that do not share a recent common ancestor. These are generally considered incorrect groupings in phylogenetic analyses.

4. Interpreting Branch Lengths:

The length of branches can have different meanings depending on the specific tree. Sometimes, branch length represents evolutionary time (longer branch = longer evolutionary time), while in other cases, it represents the amount of genetic change (longer branch = more genetic difference). It's crucial to understand the scale used in the tree.

Approaching Phylogenetic Trees POGIL Activities

POGIL activities encourage active learning and critical thinking. To effectively answer the questions, follow these steps:

1. Carefully read the instructions and background information: Understand the specific concepts being tested in the activity.
2. Analyze the provided phylogenetic tree: Pay close attention to branch points, branch lengths (if applicable), and the labels of the species or groups.
3. Apply the key concepts: Use your understanding of clades, monophyletic groups, and other concepts to answer the questions logically.
4. Check your reasoning: Make sure your answers align with the information presented in the tree and your understanding of evolutionary relationships.

Example POGIL Questions and Answers (Illustrative)

While I can't provide specific answers to your exact POGIL worksheet (as those are unique to your assignment), I can illustrate the type of questions you might encounter and how to approach them:

Example Question 1: Identify the most recent common ancestor of species A and B.

Answer approach: Trace the branches back from species A and B until they converge at a common node. That node represents their most recent common ancestor.

Example Question 2: Is group X a monophyletic group? Justify your answer.

Answer approach: Examine group X on the tree. Determine if it includes a common ancestor and all its descendants. If it does, it's monophyletic; if not, it is paraphyletic or polyphyletic. Clearly explain your reasoning based on the tree structure.

Conclusion

Successfully navigating phylogenetic tree POGIL activities requires a solid understanding of evolutionary relationships and the principles of phylogenetic analysis. By carefully studying the tree, understanding key terms, and applying your knowledge, you can confidently answer any questions presented. Remember to focus on the underlying concepts rather than simply memorizing answers. This approach will strengthen your understanding of evolutionary biology and allow you to confidently tackle more complex analyses in the future.

FAQs

1. What software is commonly used to create phylogenetic trees? Several software packages are used, including MEGA, PhyML, MrBayes, and RAxML. These programs utilize different algorithms to construct trees based on various types of data (e.g., DNA sequences, morphological characteristics).
2. How do scientists determine the evolutionary relationships depicted in phylogenetic trees? They use various data types, including DNA sequences, protein sequences, morphological characteristics, and fossil evidence. Sophisticated computational methods are employed to analyze this data and infer evolutionary relationships.
3. Can phylogenetic trees be incorrect? Yes, phylogenetic trees are hypotheses, not definitive statements of fact. New data or improved analytical methods can lead to revisions of existing trees.
4. What are some common applications of phylogenetic trees? Phylogenetic trees are used in diverse fields, including taxonomy (classifying organisms), epidemiology (tracking disease outbreaks), conservation biology (identifying endangered species), and forensics (analyzing DNA evidence).
5. How can I improve my ability to interpret phylogenetic trees? Practice is key! Work through multiple examples, compare different types of trees, and actively seek feedback on your interpretations. Online resources and educational materials can also be valuable tools.

phylogenetic trees pogil answers: 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.

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Study tips, information organization ideas and misconception warnings are interwoven throughout. New section reviewing the 12 required AP labs. Sample practice exams. The secret to success on the AP Biology exam is to understand what you must know and these experienced AP teachers will guide your students toward top scores!

phylogenetic trees pogil answers: *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.

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PULITZER PRIZE WINNER • A dramatic story of groundbreaking scientific research of Darwin's discovery of evolution that spark[s] not just the intellect, but the imagination (Washington Post Book World). "Admirable and much-needed.... Weiner's triumph is to reveal how evolution and science work, and to let them speak clearly for themselves."—The New York Times Book Review On a desert island in the heart of the Galapagos archipelago, where Darwin received his first inklings of the theory of evolution, two scientists, Peter and Rosemary Grant, have spent twenty years proving that Darwin did not know the strength of his own theory. For among the finches of Daphne Major, natural selection is neither rare nor slow: it is taking place by the hour, and we can watch. In this remarkable story, Jonathan Weiner follows these scientists as they watch Darwin's finches and come up with a new understanding of life itself. *The Beak of the Finch* is an elegantly written and compelling masterpiece of theory and explication in the tradition of Stephen Jay Gould.

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phylogenetic trees pogil answers: 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 Wägele was until recently head of the Department for Animal Systematics (Lehrstuhl für 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 für Biologische Systematik, a Central European society of systematists, and he is actively promoting biodiversity research.

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anoline lizards epitomize. Readers who are drawn to nature by its beauty or its intellectual challenges—or both—will find his book rewarding.—Douglas J. Futuyma, State University of New York, Stony Brook This book is destined to become a classic. It is scholarly, informative, stimulating, and highly readable, and will inspire a generation of students.—Peter R. Grant, author of *How and Why Species Multiply: The Radiation of Darwin's Finches* Anoline lizards experienced a spectacular adaptive radiation in the dynamic landscape of the Caribbean islands. The radiation has extended over a long period of time and has featured separate radiations on the larger islands. Losos, the leading active student of these lizards, presents an integrated and synthetic overview, summarizing the enormous and multidimensional research literature. This engaging book makes a wonderful example of an adaptive radiation accessible to all, and the lavish illustrations, especially the photographs, make the anoles come alive in one's mind.—David Wake, University of California, Berkeley This magnificent book is a celebration and synthesis of one of the most eventful adaptive radiations known. With disarming prose and personal narrative Jonathan Losos shows how an obsession, beginning at age ten, became a methodology and a research plan that, together with studies by colleagues and predecessors, culminated in many of the principles we now regard as true about the origins and maintenance of biodiversity. This work combines rigorous analysis and glorious natural history in a unique volume that stands with books by the Grants on Darwin's finches among the most informed and engaging accounts ever written on the evolution of a group of organisms in nature.—Dolph Schluter, author of *The Ecology of Adaptive Radiation*

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Gascuel, 2005-02-24 Table of contents

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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.

phylogenetic trees pogil answers: 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.

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and develop the skills they need to interpret patterns in the tree of life. Covers every major method of modern phylogenetic comparative analysis in R Explains the basics of R and discusses topics such as trait evolution, diversification, trait-dependent diversification, biogeography, and visualization Features a wealth of exercises and challenge problems Serves as an invaluable resource for students and researchers, with applications in ecology, evolution, anthropology, disease transmission, conservation biology, and a host of other areas Written by two of today's leading developers of phylogenetic comparative methods

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phylogenetic trees pogil answers: From Observations to Optimal Phylogenetic Trees Pablo A. Goloboff, 2022-07-22 Taxonomists specializing in different groups once based phylogenetic analysis only on morphological data; molecular data was used more rarely. Although molecular systematics is routine today, the use of morphological data continues to be important, especially for phylogenetic placement of many taxa known only from fossils and rare or difficult to collect species. In addition, morphological analyses help identify potential biases in molecular analyses. And finally, scenarios with respect to morphology continue to motivate biologists: the beauty of a cheetah or a baobab does not lie in their DNA sequence, but instead on what they are and do! This book is an up-to-date revision of methods and principles of phylogenetic analysis of morphological data. It is also a general guide for using the computer program TNT in the analysis of such data. The book covers the main aspects of phylogenetic analysis and general methods to compare classifications derived from molecules and morphology. The basic aspects of molecular analysis are covered only as needed to highlight the differences with methods and assumptions for analysis of morphological datasets.

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to analyze them have led to a revolution in the study of cospeciation. *Tangled Trees* provides an up-to-date review and synthesis of current knowledge about phylogeny, cospeciation, and coevolution. The opening chapters present various methodological and theoretical approaches, ranging from the well-known parsimony approach to jungles and Bayesian statistical models. Then a series of empirical chapters discusses detailed studies of cospeciation involving vertebrate hosts and their parasites, including nematodes, viruses, and lice. *Tangled Trees* will be welcomed by researchers in a wide variety of fields, from parasitology and ecology to systematics and evolutionary biology. Contributors: Sarah Al-Tamimi, Michael A. Charleston, Dale H. Clayton, James W. Demastes, Russell D. Gray, Mark S. Hafner, John P. Huelsenbeck, J.-P. Hugot, Kevin P. Johnson, Peter Kabat, Bret Larget, Joanne Martin, Yannis Michalakis, Roderic D. M. Page, Ricardo L. Palma, Adrian M. Paterson, Susan L. Perkins, Andy Purvis, Bruce Rannala, David L. Reed, Fredrik Ronquist, Theresa A. Spradling, Jason Taylor, Michael Tristem

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