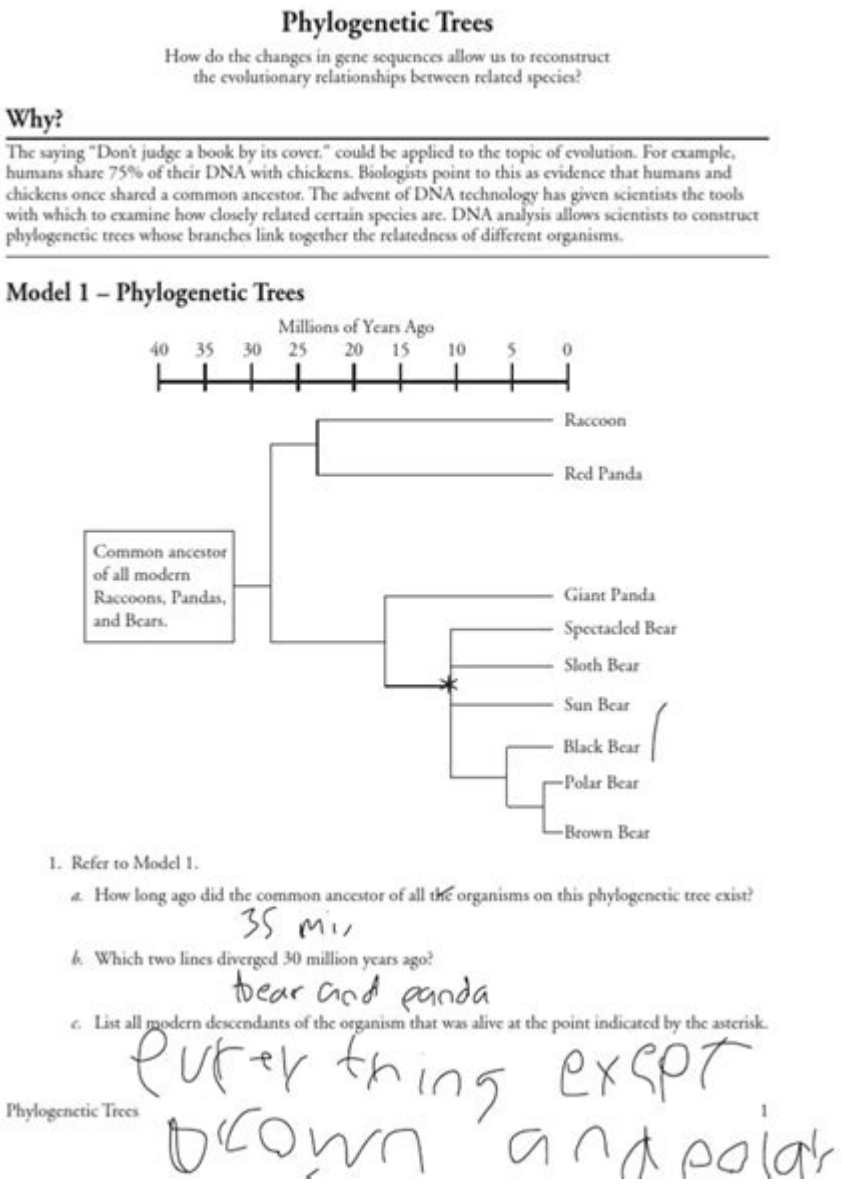
Pogil Phylogenetic Trees Answer Key



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

Millions of Years Ago
40 35 30 25 20 15 10 5 0

Raccoon
Red Panda
Common ancestor of all modern Raccoons, Pandas, and Bears.
Giant Panda
Spectacled Bear
Sloth Bear
Sun Bear
Black Bear
Polar Bear
Brown Bear

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.
   every thing except brown and polar

Phylogenetic Trees 1

POGIL Phylogenetic Trees Answer Key: Mastering Evolutionary Relationships

Are you grappling with the complexities of phylogenetic trees and struggling to understand the relationships between different organisms? Have you been assigned a POGIL (Process Oriented Guided Inquiry Learning) activity on phylogenetic trees and feel lost in the branching pathways? You're not alone! Many students find constructing and interpreting phylogenetic trees challenging. This comprehensive guide provides a detailed look at common POGIL phylogenetic tree activities, offers insights into understanding the answers, and helps you master this crucial concept in

evolutionary biology. We'll equip you with the knowledge to confidently navigate your POGIL assignment and achieve a deeper understanding of phylogenetic analysis. This isn't just about finding the "answer key"; it's about mastering the underlying principles.

Understanding Phylogenetic Trees: A Foundation

Before diving into specific POGIL activities, let's establish a solid understanding of phylogenetic trees. These diagrams visually represent the evolutionary relationships among various species or groups of organisms. They are built using various data points, including morphological characteristics, genetic sequences, and fossil evidence. Each branch point, or node, represents a common ancestor, while the tips of the branches represent the extant (currently living) or extinct organisms.

The length of the branches can sometimes represent evolutionary time or the amount of genetic change, depending on the specific tree construction method used. Understanding these fundamental elements is crucial for interpreting any POGIL activity focused on phylogenetic trees.

Deciphering POGIL Phylogenetic Trees Activities: Common Challenges

POGIL activities on phylogenetic trees often present scenarios requiring you to:

Construct a phylogenetic tree: This involves analyzing provided data (e.g., character matrices) and arranging the organisms based on shared derived characteristics. This requires careful consideration of homologous and analogous traits.
Interpret an existing phylogenetic tree: This involves understanding the relationships represented in a given tree, identifying common ancestors, and inferring evolutionary history.
Analyze different tree construction methods: POGIL activities might compare and contrast different methods, such as parsimony analysis or maximum likelihood, highlighting their strengths and weaknesses.
Evaluate the limitations of phylogenetic trees: Understanding that phylogenetic trees are hypotheses, subject to revision based on new data and methodologies, is essential. POGIL activities often explore the uncertainties inherent in reconstructing evolutionary history.

Approaching POGIL Phylogenetic Trees Activities Strategically

To successfully complete a POGIL activity on phylogenetic trees, follow these steps:

1. Thoroughly read the instructions: Understand the specific goals and objectives of the activity.

2. Define key terms: Ensure you have a clear understanding of terms such as "clade," "monophyletic," "paraphyletic," and "polyphyletic."
3. Analyze the data carefully: If constructing a tree, systematically compare the characteristics of different organisms. Pay close attention to shared derived characters, which are traits that evolved in a common ancestor and are unique to its descendants.
4. Use the provided resources: POGIL activities often include hints, diagrams, or background information that can guide your analysis.
5. Collaborate with your peers: Discussing your interpretations and approaches with classmates can help clarify any misconceptions.
6. Review your work: After completing the activity, check your answers against the provided solutions (if available) and reflect on any mistakes made. Focus on understanding why your initial answer was incorrect, rather than just memorizing the correct answer.

Why a "POGIL Phylogenetic Trees Answer Key" Isn't Always Enough

While a simple answer key might seem attractive, it often hinders true learning. Understanding the underlying processes of phylogenetic analysis is far more valuable than simply matching answers. The POGIL method is designed to promote critical thinking and problem-solving, and relying solely on an answer key defeats this purpose. Use the answer key (if available) as a tool for checking your understanding, not as a shortcut to bypass the learning process.

Beyond the Answer Key: Mastering Phylogenetic Analysis

Ultimately, mastering phylogenetic trees involves understanding the principles of evolution, recognizing patterns in data, and applying logical reasoning. Focus on building a strong foundation in these areas, and you'll find that tackling POGIL activities, and indeed, any challenge related to phylogenetic analysis, becomes significantly easier. The "answer key" is just a stepping stone; the true reward lies in developing a deep conceptual understanding.

Conclusion:

While searching for a "POGIL Phylogenetic Trees Answer Key" might seem like a shortcut, the real benefit comes from actively engaging with the POGIL activity itself. By understanding the principles of phylogenetic analysis, employing strategic problem-solving, and collaborating with peers, you can confidently tackle these activities and solidify your understanding of evolutionary relationships. Remember, the process of learning is more valuable than the final answer.

FAQs:

1. Where can I find reliable resources to learn more about phylogenetic trees beyond my POGIL activity? Numerous online resources, including educational websites, videos, and interactive simulations, can provide supplementary learning. Textbooks on evolutionary biology are also invaluable.

2. What software is commonly used for constructing phylogenetic trees? Several software packages,

such as MEGA X, PhyML, and MrBayes, are widely used for phylogenetic analysis.

3. How can I tell the difference between homologous and analogous traits? Homologous traits are similar due to shared ancestry, while analogous traits are similar due to convergent evolution (independent evolution of similar features in unrelated organisms).

4. What are some common mistakes students make when constructing phylogenetic trees? Common mistakes include misinterpreting character data, ignoring the principle of parsimony, and failing to consider the possibility of convergent evolution.

5. Is there a single "correct" phylogenetic tree? Phylogenetic trees are hypotheses, and different methods or datasets may result in slightly different trees. The best tree is the one that is best supported by the available evidence.

pogil phylogenetic trees answer key: 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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experienced AP teachers will guide your students toward top scores!

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pogil phylogenetic trees answer key: Discipline-Based Education Research National Research Council, Division of Behavioral and Social Sciences and Education, Board on Science Education, Committee on the Status, Contributions, and Future Directions of Discipline-Based Education Research, 2012-08-27 The National Science Foundation funded a synthesis study on the status, contributions, and future direction of discipline-based education research (DBER) in physics, biological sciences, geosciences, and chemistry. DBER combines knowledge of teaching and learning with deep knowledge of discipline-specific science content. It describes the discipline-specific difficulties learners face and the specialized intellectual and instructional resources that can facilitate student understanding. Discipline-Based Education Research is based on a 30-month study built on two workshops held in 2008 to explore evidence on promising practices in undergraduate science, technology, engineering, and mathematics (STEM) education. This book asks questions that are essential to advancing DBER and broadening its impact on undergraduate science teaching and learning. The book provides empirical research on undergraduate teaching and learning in the sciences, explores the extent to which this research currently influences undergraduate instruction,

and identifies the intellectual and material resources required to further develop DBER. Discipline-Based Education Research provides guidance for future DBER research. In addition, the findings and recommendations of this report may invite, if not assist, post-secondary institutions to increase interest and research activity in DBER and improve its quality and usefulness across all natural science disciples, as well as guide instruction and assessment across natural science courses to improve student learning. The book brings greater focus to issues of student attrition in the natural sciences that are related to the quality of instruction. Discipline-Based Education Research will be of interest to educators, policy makers, researchers, scholars, decision makers in universities, government agencies, curriculum developers, research sponsors, and education advocacy groups.

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pogil phylogenetic trees answer key: *Scientific Teaching* Jo Handelsman, Sarah Miller, Christine Pfund, 2007 Seasoned classroom veterans, pre-tenured faculty, and neophyte teaching assistants alike will find this book invaluable. HHMI Professor Jo Handelsman and her colleagues at the Wisconsin Program for Scientific Teaching (WPST) have distilled key findings from education, learning, and cognitive psychology and translated them into six chapters of digestible research points and practical classroom examples. The recommendations have been tried and tested in the National Academies Summer Institute on Undergraduate Education in Biology and through the WPST. Scientific Teaching is not a prescription for better teaching. Rather, it encourages the reader to approach teaching in a way that captures the spirit and rigor of scientific research and to contribute to transforming how students learn science.

pogil phylogenetic trees answer key: Excerpts from MacClade Wayne P. Maddison, 1992 MacClade is a computer program for graphic and interactive analysis of phylogeny and character evolution for Apple Macintosh computers. It displays a cladogram and paints the branches to indicate reconstructed character evolution. The user can manipulate cladograms on screen as MacClade gives diagnostic feedback. Systematics and other evolutionary biologists can use its flexible and analytical tools to examine phylogenies or interpret character evolution in a phylogenetic context, yet its ease of use should allow students to grasp phylogenetic principles in an interactive environment. This is chapters 3-6 of the user's manual.

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utilities from the web site. Some conventions used in this book. Tutorial: create a tree. Why create phylogenetic trees. Otaining related sequences by a BLAST search. Creating the multiple alignment. Phylogenetic analysis. Methods for constructing phylogenies. Using PAUP* to create a tree. Additional methods for creating trees. Presenting and printing your trees. Fine-tuning alignments. Using MrBayes to reconstruct ancestral DNA sequences. Dealing with some common problems. File formats and their interconversion using PAUP*. Printing alignments. Index to major program discussed. Subject index.

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pogil phylogenetic trees answer key: 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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pogil phylogenetic trees answer key: *Probability and Stochastic Processes* Roy D. Yates, David J. Goodman, 2014-01-28 This text introduces engineering students to probability theory and stochastic processes. Along with thorough mathematical development of the subject, the book presents intuitive explanations of key points in order to give students the insights they need to apply math to practical engineering problems. The first five chapters contain the core material that is essential to any introductory course. In one-semester undergraduate courses, instructors can select material from the remaining chapters to meet their individual goals. Graduate courses can cover all chapters in one semester.

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education. In each section, experts set out powerful ideas followed by two eminent discussant responses that both respond to and provoke additional ideas from the lead papers. In the associated website highly distinguished, nationally recognized STEM education scholars and policymakers engage in deep conversations and considerations addressing core practices that guide STEM education.

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by algae in a variety of complex freshwater ecosystems. As concern over environmental health escalates, the keystone and pivotal role played by algae is becoming more apparent. This volume in the Aquatic Ecology Series represents an important compilation of the latest research on the crucial niche occupied by algae in aquatic ecosystems. - Presents algae as the important player in relation to environmental health - Prepared by leading authorities in the field - Includes comprehensive treatment of the functions of benthic algae as well as the factors that affect these important aquatic organisms - Acts as an important reference for anyone interested in understanding and managing freshwater ecosystems

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Rosemary Grant, 2011-05-29 Trace the evolutionary history of fourteen different species of finches on the Galapagos Islands that were studied by Charles Darwin.

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pogil phylogenetic trees answer key: Social Computing and Social Media Gabriele H. Meiselwitz, 2019 This two-volume set LNCS 11578 and 11579 constitutes the refereed proceedings of the 11th International Conference on Social Computing and Social Media, SCSM 2019, held in July 2019 as part of HCI International 2019 in Orlando, FL, USA. HCII 2019 received a total of 5029 submissions, of which 1275 papers and 209 posters were accepted for publication after a careful reviewing process. The 81 papers presented in these two volumes are organized in topical sections named: Social Media Design and Development, Human Behaviour in Social Media, Social Network Analysis, Community Engagement and Social Participation, Computer Mediated Communication, Healthcare Communities, Social Media in Education, Digital Marketing and Consumer Experience.

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10 cách dùng ChatGPT - OpenAI Chat miễn phí tại Việt Nam
Apr 22, 2024 · ChatGPT (OpenAI chat gpt) đang trở thành một trào lưu tại Việt Nam. Đây là trí tuệ nhân tạo AI sử dụng trên trình duyệt web và chưa có ứng dụng chính thức. Sau đây là ...

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GitHub - 0xk1h0/ChatGPT_DAN: ChatGPT DAN, Jailbreaks prompt
Mar 21, 2023 · NOTE: As of 20230711, the DAN 12.0 prompt is working properly with Model GPT-3.5 All contributors are constantly investigating clever workarounds that allow us to utilize the …

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