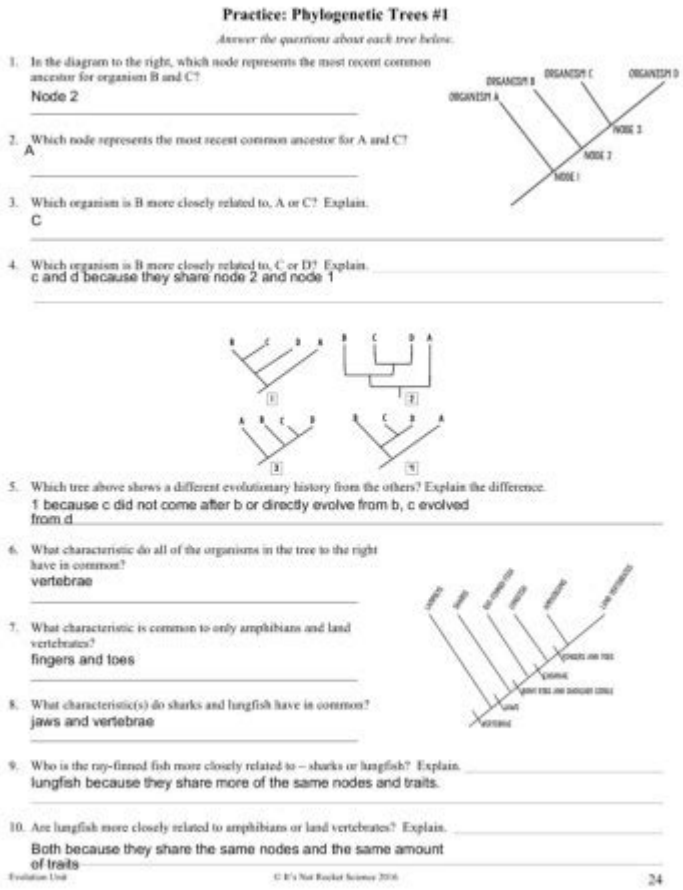
Practice Phylogenetic Trees 1



Practice: Phylogenetic Trees #1

Answer the questions about each tree below.

1. In the diagram to the right, which node represents the most recent common ancestor for organism B and C?
   Node 2
2. Which node represents the most recent common ancestor for A and C?
   A
3. Which organism is B more closely related to, A or C? Explain.
   C
4. Which organism is B more closely related to, C or D? Explain.
   c and d because they share node 2 and node 1
5. Which tree above shows a different evolutionary history from the others? Explain the difference.
   1 because c did not come after b or directly evolve from b, c evolved from d
6. What characteristic do all of the organisms in the tree to the right have in common?
   vertebrae
7. What characteristic is common to only amphibians and land vertebrates?
   fingers and toes
8. What characteristic(s) do sharks and lungfish have in common?
   jaws and vertebrae
9. Who is the ray-finned fish more closely related to – sharks or lungfish? Explain.
   lungfish because they share more of the same nodes and traits.
10. Are lungfish more closely related to amphibians or land vertebrates? Explain.
    Both because they share the same nodes and the same amount of traits

Practice Phylogenetic Trees 1: Mastering the Fundamentals of Evolutionary Relationships

Introduction:

Ever stared at a phylogenetic tree and felt a wave of confusion wash over you? These branching diagrams, representing the evolutionary history of life, can seem intimidating at first. But fear not! This post, "Practice Phylogenetic Trees 1," is your friendly guide to demystifying these powerful tools. We'll move beyond the theory and dive straight into practical exercises, building your confidence in interpreting and even constructing your own phylogenetic trees. Whether you're a student grappling with biology coursework or a curious enthusiast, this beginner-friendly guide will equip you with the fundamental skills to confidently navigate the world of phylogenetic analysis. We will cover key concepts, practice interpreting different tree styles, and offer tips for improving your understanding.

Understanding the Basics: What is a Phylogenetic Tree?

Phylogenetic trees, also known as cladograms or evolutionary trees, are visual representations of the evolutionary relationships among different biological species or groups. Each branch point, or node, signifies a common ancestor, and the branches themselves represent lineages evolving over time. The length of the branches can sometimes (but not always) represent the amount of evolutionary change or time elapsed. Understanding these fundamental elements is crucial before tackling any practice exercises.

Interpreting Phylogenetic Trees: A Step-by-Step Approach

Let's start with some simple practice. Imagine a tree showing the relationship between four species: A, B, C, and D.

Example Tree 1:

```
/----A
|
|----B
|
|----C
|
|----D
```

In this tree, species A and B are more closely related to each other than they are to C or D. They share a more recent common ancestor. Similarly, C and D are more closely related to each other. This demonstrates the hierarchical nature of evolutionary relationships depicted in a phylogenetic tree.

Identifying Monophyletic Groups (Clades)

A critical skill is identifying monophyletic groups, or clades. A clade includes a common ancestor and all of its descendants. In our example, A and B together form a clade. C and D also form a clade. However, A, B, and C do not form a clade because they don't include all descendants of their common ancestor.

Root vs. Unrooted Trees:

Phylogenetic trees can be rooted (showing the common ancestor of all species) or unrooted (showing only the relationships between species, without explicitly showing the root). Understanding the difference is essential for correct interpretation. Rooted trees provide more information about the evolutionary direction.

Practice Exercise: Analyzing Different Tree Styles

Now, let's analyze some more complex trees:

Example Tree 2 (Rooted):

```
|
|----(Common Ancestor)
| / \
| / \
| / \
| / \
/ / \
/ / \
/ / \
/ / \
A B C D E
```

Example Tree 3 (Unrooted):

```
A---B
| |
| |
C---D
```

Questions for Practice:

1. In Example Tree 2, which species are most closely related? Which species share the most recent common ancestor? Identify a clade.

2. In Example Tree 3, can you definitively say which species are most closely related? Why or why not? What additional information would you need?

3. Try sketching your own simple tree showing the relationships between three hypothetical species: X, Y, and Z, where X and Y are more closely related.

Constructing Phylogenetic Trees: A Glimpse into the Process

While the focus of this "Practice Phylogenetic Trees 1" post is interpretation, it's important to briefly

mention that constructing trees involves analyzing shared characteristics (morphological, genetic, or behavioral). Methods like parsimony (choosing the tree that requires the fewest evolutionary changes) and maximum likelihood (choosing the tree with the highest probability given a model of evolution) are commonly used. More advanced techniques will be explored in subsequent "Practice Phylogenetic Trees" posts.

Conclusion:

Mastering phylogenetic trees requires practice. By working through these examples and practicing with various tree styles, you'll build a solid foundation for understanding evolutionary relationships. This introductory post focused on interpretation, setting the stage for more advanced techniques in future installments. Keep practicing, and you'll soon be confidently navigating the intricacies of phylogenetic analysis.

FAQs:

1. What software can I use to create phylogenetic trees? Several software packages are available, including MEGA X, PhyML, and MrBayes. Many are freely accessible online.

2. What is the difference between a cladogram and a phylogram? Both represent evolutionary relationships. A cladogram focuses on branching patterns, while a phylogram incorporates branch lengths to represent evolutionary change or time.

3. How can I tell if a phylogenetic tree is reliable? Reliability depends on the data used and the methods employed. Bootstrap values (a measure of confidence in the tree's branches) often accompany phylogenetic trees. Higher bootstrap values indicate greater confidence.

4. Are phylogenetic trees always accurate? No, phylogenetic trees are hypotheses based on available data. New data or different analytical methods can lead to revisions in the tree.

5. Where can I find more resources to practice? Online resources, textbooks, and even interactive exercises are readily available. Search for "phylogenetic tree exercises" or "cladogram practice" online to find suitable materials.

practice phylogenetic trees 1: Phylogenetics E. O. Wiley, Bruce S. Lieberman, 2011-10-11 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.

practice phylogenetic trees 1: 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.

practice phylogenetic trees 1: Numerical Taxonomy Joseph Felsenstein, 2013-06-29 The NATO Advanced Study Institute on Numerical Taxonomy took place on the 4th - 16th of July, 1982, at the Kur- und Kongresshotel Residenz in Bad Windsheim, Federal Republic of Germany. This volume is the proceedings of that meeting, and contains papers by over two-thirds of the participants in the Institute. Numerical taxonomy has been attracting increased attention from systematists and evolutionary biologists. It is an area which has been marked by debate and conflict, sometimes bitter. Happily, this meeting took place in an atmosphere of GemUtlichkeit, though scarcely of unanimity. I believe that these papers will show that there is an increased understanding by each taxonomic school of each others' positions. This augurs a period in which the debates become more concrete and specific. Let us hope that they take place in a scientific atmosphere which has occasionally been lacking in the past. Since the order of presentation of papers in the meeting was affected by time constraints, I have taken the liberty of rearranging them into a more coherent subject ordering. The first group of papers, taken from the opening and closing days of the meeting, debate philosophies of classification. The next two sections have papers on congruence, clustering and ordination. A notable concern of these participants is the comparison and testing of classifications. This has been missing from many previous discussions of numerical classification.

practice phylogenetic trees 1: *Modern Phylogenetic Comparative Methods and Their Application in Evolutionary Biology* László Zsolt Garamszegi, 2014-07-29 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.

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practice phylogenetic trees 1: *Aristotle's Ladder, Darwin's Tree* J. David Archibald, 2014-08-19 Leading paleontologist J. David Archibald explores the rich history of visual metaphors for biological order from ancient times to the present and their influence on humans' perception of their place in nature, offering uncommon insight into how we went from standing on the top rung of the biological ladder to embodying just one tiny twig on the tree of life. He begins with the ancient but still misguided use of ladders to show biological order, moving then to the use of trees to represent seasonal life cycles and genealogies by the Romans. The early Christian Church then appropriated trees to represent biblical genealogies. The late eighteenth century saw the tree reclaimed to visualize relationships in the natural world, sometimes with a creationist view, but in other instances suggesting evolution. Charles Darwin's On the Origin of Species (1859) exorcised the exclusively creationist view of the tree of life, and his ideas sparked an explosion of trees, mostly by younger acolytes in Europe. Although Darwin's influence waned in the early twentieth century, by midcentury his ideas held sway once again in time for another and even greater explosion of tree building, generated by the development of new theories on how to assemble trees, the birth of powerful computing, and the emergence of molecular technology. Throughout Archibald's far-reaching study, and with the use of many figures, the evolution of tree of life iconography becomes entwined with our changing perception of the world and ourselves.

practice phylogenetic trees 1: Inferring Phylogenies Joseph Felsenstein, 2004-01 Phylogenies, or evolutionary trees, are the basic structures necessary to think about and analyze differences between species. Statistical, computational, and algorithmic work in this field has been ongoing for four decades now, and there have been great advances in understanding. Yet no book has summarized this work. Inferring Phylogenies does just that in a single, compact volume. Phylogenies are inferred with various kinds of data. This book concentrates on some of the central ones: discretely coded characters, molecular sequences, gene frequencies, and quantitative traits. Also covered are restriction sites, RAPDs, and microsatellites.

practice phylogenetic trees 1: Principles of Biology Lisa Bartee, Walter Shiner, Catherine Creech, 2017 The Principles of Biology sequence (BI 211, 212 and 213) introduces biology as a scientific discipline for students planning to major in biology and other science disciplines. Laboratories and classroom activities introduce techniques used to study biological processes and provide opportunities for students to develop their ability to conduct research.

practice phylogenetic trees 1: 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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practice phylogenetic trees 1: International Code of Phylogenetic Nomenclature (PhyloCode) Kevin de Queiroz, Philip Cantino, 2020-04-29 The PhyloCode is a set of principles, rules, and recommendations governing phylogenetic nomenclature, a system for naming taxa by explicit reference to phylogeny. In contrast, the current botanical, zoological, and bacteriological codes define taxa by reference to taxonomic ranks (e.g., family, genus) and types. This code will govern the names of clades; species names will still be governed by traditional codes. The PhyloCode is designed so that it can be used concurrently with the rank-based codes. It is not meant to replace existing names but to provide an alternative system for governing the application of both existing and newly proposed names. Key Features Provides clear regulations for naming clades Based on expressly phylogenetic principles Complements existing codes of nomenclature Eliminates the reliance on taxonomic ranks in favor of phylogenetic relationships Related Titles: Rieppel, O. Phylogenetic Systematics: Haeckel to Hennig (ISBN 978-1-4987-5488-0) de Queiroz, K., Cantino, P. D. and Gauthier, J. A. Phylonyms: A Companion to the PhyloCode (ISBN 978-1-138-33293-5).

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Lewis, 2014-05-27 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.

practice phylogenetic trees 1: Brenner's Encyclopedia of Genetics Stanley Maloy, Kelly Hughes, 2013-03-03 The explosion of the field of genetics over the last decade, with the new technologies that have stimulated research, suggests that a new sort of reference work is needed to keep pace with such a fast-moving and interdisciplinary field. Brenner's Encyclopedia of Genetics, Second Edition, Seven Volume Set, builds on the foundation of the first edition by addressing many of the key subfields of genetics that were just in their infancy when the first edition was published. The currency and accessibility of this foundational content will be unrivalled, making this work useful for scientists and non-scientists alike. Featuring relatively short entries on genetics topics written by experts in that topic, Brenner's Encyclopedia of Genetics, Second Edition, Seven Volume Set provides an effective way to quickly learn about any aspect of genetics, from Abortive Transduction to Zygotes. Adding to its utility, the work provides short entries that briefly define key terms, and a guide to additional reading and relevant websites for further study. Many of the entries include figures to explain difficult concepts. Key terms in related areas such as biochemistry, cell, and molecular biology are also included, and there are entries that describe historical figures in genetics, providing insights into their careers and discoveries. This 7-volume set represents a 25% expansion from the first edition, with over 1600 articles encompassing this burgeoning field Thoroughly up-to-date, with many new topics and subfields covered that were in their infancy or not inexistence at the time of the first edition. Timely coverage of emergent areas such as epigenetics, personalized genomic medicine, pharmacogenetics, and genetic enhancement technologies Interdisciplinary and global in its outlook, as befits the field of genetics Brief articles, written by experts in the field, which not only discuss, define, and explain key elements of the field, but also provide definition of key terms, suggestions for further reading, and biographical sketches of the key people in the history of genetics

practice phylogenetic trees 1: The Invertebrate Tree of Life Gonzalo Giribet, Gregory D. Edgecombe, 2020-03-03 The most up-to-date book on invertebrates, providing a new framework for understanding their place in the tree of life In The Invertebrate Tree of Life, Gonzalo Giribet and Gregory Edgecombe, leading authorities on invertebrate biology and paleontology, utilize phylogenetics to trace the evolution of animals from their origins in the Proterozoic to today. Phylogenetic relationships between and within the major animal groups are based on the latest molecular analyses, which are increasingly genomic in scale and draw on the soundest methods of tree reconstruction. Giribet and Edgecombe evaluate the evolution of animal organ systems, exploring how current debates about phylogenetic relationships affect the ways in which aspects of invertebrate nervous systems, reproductive biology, and other key features are inferred to have developed. The authors review the systematics, natural history, anatomy, development, and fossil records of all major animal groups, employing seminal historical works and cutting-edge research in evolutionary developmental biology, genomics, and advanced imaging techniques. Overall, they provide a synthetic treatment of all animal phyla and discuss their relationships via an integrative approach to invertebrate systematics, anatomy, paleontology, and genomics. With numerous detailed illustrations and phylogenetic trees, The Invertebrate Tree of Life is a must-have reference for biologists and anyone interested in invertebrates, and will be an ideal text for courses in

invertebrate biology. A must-have and up-to-date book on invertebrate biology Ideal as both a textbook and reference Suitable for courses in invertebrate biology Richly illustrated with black-and-white and color images and abundant tree diagrams Written by authorities on invertebrate evolution and phylogeny Factors in the latest understanding of animal genomics and original fossil material

practice phylogenetic trees 1: 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.

practice phylogenetic trees 1: *Molecular Evolution* Ziheng Yang, 2014 Studies of evolution at the molecular level have experienced phenomenal growth in the last few decades, due to rapid accumulation of genetic sequence data, improved computer hardware and software, and the development of sophisticated analytical methods. The flood of genomic data has generated an acute need for powerful statistical methods and efficient computational algorithms to enable their effective analysis and interpretation. Molecular Evolution: a statistical approach presents and explains modern statistical methods and computational algorithms for the comparative analysis of genetic sequence data in the fields of molecular evolution, molecular phylogenetics, statistical phylogeography, and comparative genomics. Written by an expert in the field, the book emphasizes conceptual understanding rather than mathematical proofs. The text is enlivened with numerous examples of real data analysis and numerical calculations to illustrate the theory, in addition to the working problems at the end of each chapter. The coverage of maximum likelihood and Bayesian methods are in particular up-to-date, comprehensive, and authoritative. This advanced textbook is aimed at graduate level students and professional researchers (both empiricists and theoreticians) in the fields of bioinformatics and computational biology, statistical genomics, evolutionary biology, molecular systematics, and population genetics. It will also be of relevance and use to a wider audience of applied statisticians, mathematicians, and computer scientists working in computational biology.

practice phylogenetic trees 1: Molecular Evolution Roderick D.M. Page, Edward C. Holmes, 2009-07-14 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.

practice phylogenetic trees 1: Handbook of Trait-Based Ecology Francesco de Bello, Carlos P. Carmona, André T. C. Dias, Lars Götzenberger, Marco Moretti, Matty P. Berg, 2021-03-11 Trait-based ecology is rapidly expanding. This comprehensive and accessible guide covers the main concepts and tools in functional ecology.

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practice phylogenetic trees 1: Biology Workbook For Dummies Rene Fester Kratz, 2012-05-08 From genetics to ecology — the easy way to score higher in biology Are you a student baffled by biology? You're not alone. With the help of Biology Workbook For Dummies you'll quickly and painlessly get a grip on complex biology concepts and unlock the mysteries of this fascinating and ever-evolving field of study. Whether used as a complement to Biology For Dummies or on its own, Biology Workbook For Dummies aids you in grasping the fundamental aspects of Biology. In plain English, it helps you understand the concepts you'll come across in your biology class, such as physiology, ecology, evolution, genetics, cell biology, and more. Throughout the book, you get plenty of practice exercises to reinforce learning and help you on your goal of scoring higher in biology. Grasp the fundamental concepts of biology Step-by-step answer sets clearly identify where you went wrong (or right) with a problem Hundreds of study questions and exercises give you the skills and confidence to ace your biology course If you're intimidated by biology, utilize the friendly, hands-on information and activities in Biology Workbook For Dummies to build your skills in and out of the science lab.

practice phylogenetic trees 1: Phylogenetic Trees and Molecular Evolution David R. Bickel, 2022-09-29 This book serves as a brief introduction to phylogenetic trees and molecular evolution for biologists and biology students. It does so by presenting the main concepts in a variety of ways: first visually, then in a history, next in a dice game, and finally in simple equations. The content is primarily designed to introduce upper-level undergraduate and graduate students of biology to phylogenetic tree reconstruction and the underlying models of molecular evolution. A unique feature also of interest to experienced researchers is the emphasis on simple ways to quantify the uncertainty in the results more fully than is possible with standard methods.

practice phylogenetic trees 1: Evolutionary Genetics Glenn-Peter Sætre, Mark Ravinet, 2019 With recent technological advances, vast quantities of genetic and genomic data are being generated at an ever-increasing pace. The explosion in access to data has transformed the field of evolutionary genetics. A thorough understanding of evolutionary principles is essential for making sense of this, but new skill sets are also needed to handle and analyze big data. This contemporary textbook covers all the major components of modern evolutionary genetics, carefully explaining fundamental processes such as mutation, natural selection, genetic drift, and speciation. It also draws on a rich literature of exciting and inspiring examples to demonstrate the diversity of evolutionary research, including an emphasis on how evolution and selection has shaped our own species. Practical experience is essential for developing an understanding of how to use genetic and genomic data to analyze and interpret results in meaningful ways. In addition to the main text, a

series of online tutorials using the R language serves as an introduction to programming, statistics, and analysis. Indeed the R environment stands out as an ideal all-purpose source platform to handle and analyze such data. The book and its online materials take full advantage of the authors' own experience in working in a post-genomic revolution world, and introduces readers to the plethora of molecular and analytical methods that have only recently become available. Evolutionary Genetics is an advanced but accessible textbook aimed principally at students of various levels (from undergraduate to postgraduate) but also for researchers looking for an updated introduction to modern evolutionary biology and genetics.

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