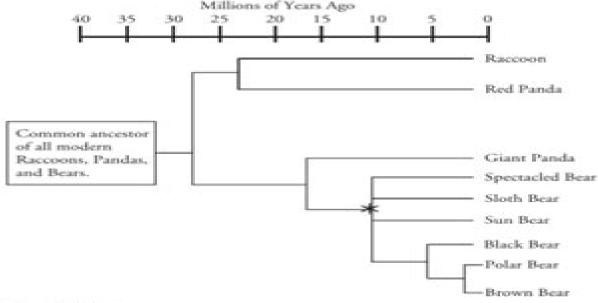
# Phylogenetic Trees

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?
  - b. Which two lines diverged 30 million years ago?
  - c. List all modern descendants of the organism that was alive at the point indicated by the asterisk.

# **Model Phylogenetic Trees Answer Key**

**Ramit Mehr, Miles Davenport** 

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College Biology Learning Exercises & Answers Textbook Equity,2014-08-22 This textbook is designed as a quick reference for College Biology volumes one through three It contains each Chapter Summary Art Connection Review and Critical Thinking Exercises found in each of the three volumes It also contains the COMPLETE alphabetical listing of the key terms black white version College Biology intended for capable college students is adapted from OpenStax College s open CC BY textbook Biology It is Textbook Equity s derivative to ensure continued free and open access and to provide low cost print formats For manageability and economy Textbook Equity created three volumes from the original that closely match typical semester or quarter biology curriculum No academic content was changed from the original See textbookequity org tbq\_biology This supplement covers all 47 chapters ReCombinatorics Dan Gusfield,2014-07-11 Combinatorial structure and algorithms for deducing genetic recombination history represented by ancestral recombination graphs and other networks and their role in the emerging field of phylogenetic networks In this book Dan Gusfield examines combinatorial algorithms to construct genealogical and exact phylogenetic networks particularly ancestral recombination graphs ARGs The

algorithms produce networks or information about networks that serve as hypotheses about the true genealogical history of observed biological sequences and can be applied to practical biological problems Phylogenetic trees have been the traditional means to represent evolutionary history but there is a growing realization that networks rather than trees are often needed most notably for recent human history. This has led to the development of ARGs in population genetics and more broadly to phylogenetic networks ReCombinatorics offers an in depth rigorous examination of current research on the combinatorial graph theoretic structure of ARGs and explicit phylogenetic networks and algorithms to reconstruct or deduce information about those networks ReCombinatorics a groundbreaking contribution to the emerging field of phylogenetic networks connects and unifies topics in population genetics and phylogenetics that have traditionally been discussed separately and considered to be unrelated It covers the necessary combinatorial and algorithmic background material the various biological phenomena the mathematical population genetic and phylogenetic models that capture the essential elements of these phenomena the combinatorial and algorithmic problems that derive from these models the theoretical results that have been obtained related software that has been developed and some empirical testing of the software on simulated and real biological data Identification and functional analysis of differentially expressed genes in plant response to abiotic stresses Xuke Lu, Wagar Afzal Malik, Ting Zhao, Yupeng Cui, Libei Li, 2023-08-24 Models in Biology Elizabeth Spencer Allman, John A. Rhodes, 2004 This introductory textbook on mathematical biology focuses on discrete models across a variety of biological subdisciplines Biological topics treated include linear and non linear models of populations Markov models of molecular evolution phylogenetic tree construction genetics and infectious disease models The coverage of models of molecular evolution and phylogenetic tree construction from DNA sequence data is unique among books at this level Computer investigations with MATLAB are incorporated throughout in both exercises and more extensive projects to give readers hands on experience with the mathematical models developed MATLAB programs accompany the text Mathematical tools such as matrix algebra eigenvector analysis and basic probability are motivated by biological models and given self contained developments so that mathematical prerequisites are minimal **Emerging Applications of Algebraic Geometry** Mihai Putinar, Seth Sullivant, 2008-12-10 Recent advances in both the theory and implementation of computational algebraic geometry have led to new striking applications to a variety of fields of research The articles in this volume highlight a range of these applications and provide introductory material for topics covered in the IMA workshops on Optimization and Control and Applications in Biology Dynamics and Statistics held during the IMA year on Applications of Algebraic Geometry The articles related to optimization and control focus on burgeoning use of semidefinite programming and moment matrix techniques in computational real algebraic geometry. The new direction towards a systematic study of non commutative real algebraic geometry is well represented in the volume Other articles provide an overview of the way computational algebra is useful for analysis of contingency tables reconstruction of phylogenetic trees

and in systems biology The contributions collected in this volume are accessible to non experts self contained and informative they quickly move towards cutting edge research in these areas and provide a wealth of open problems for future research

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