Assessing Tree Thinking And Its Role in Understanding Evolution

School of Education

LRDC

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Introduction

Understanding evolution involves knowing something about both the mechanisms involved in evolutionary change and the history of life on Earth. Most introductory biology curricula emphasize models of evolutionary change but do little to explicitly address historical reconstruction. What phylogenetics instruction there is generally emphasizes tree building techniques or learning the evolutionary histories of particular groups. There is very little instruction currently available that addresses basic tree interpretation skills. Interpreting evolutionary trees and relating phylogenies to the broad consequences of descent with modification can provide an important framework for organizing and accessing biological knowledge.

Biologists rely on evolutionary trees as representational tools for organizing and communicating their understanding of life's unity and diversity. In order for students to understand and work with evolutionary trees they need to become familiar with the conventions biologists use when representing evolutionary relationships diagrammatically. This poster presents a collection of questions designed to assess four different aspects of tree interpretation including:

- Understanding how to interpret the topological structure of a tree;
- Understanding the evolutionary relationships among taxa in a tree;
- Understanding how to trace character changes within a tree; and,
- Understanding features of clades and their uses in trees.

The skills addressed in these assessments are important for students to master if we expect them to develop a more sophisticated "tree-thinking" perspective as they learn biology. Understanding the consequences of descent with modification can play a central role in helping students reasoning about patterns in biological phenomena, relate evolutionary concepts to tree diagrams, and organize their biological knowledge.

In developing these categories of tree reading skills my goal was to explore the types of technical knowledge required to interpret phylogenies. These categories are by no means exhaustive and, more seriously, they ignore how these technical skills interact with students beliefs about the nature of species and the relationships between them. I hope that these assessment ideas can be used to help faculty and students become more aware of their understanding of tree reading conventions, and to guide curriculum development that promotes a more sophisticated and systematic approach to teaching reasoning in evolutionary biology.

Acknowledgements

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References

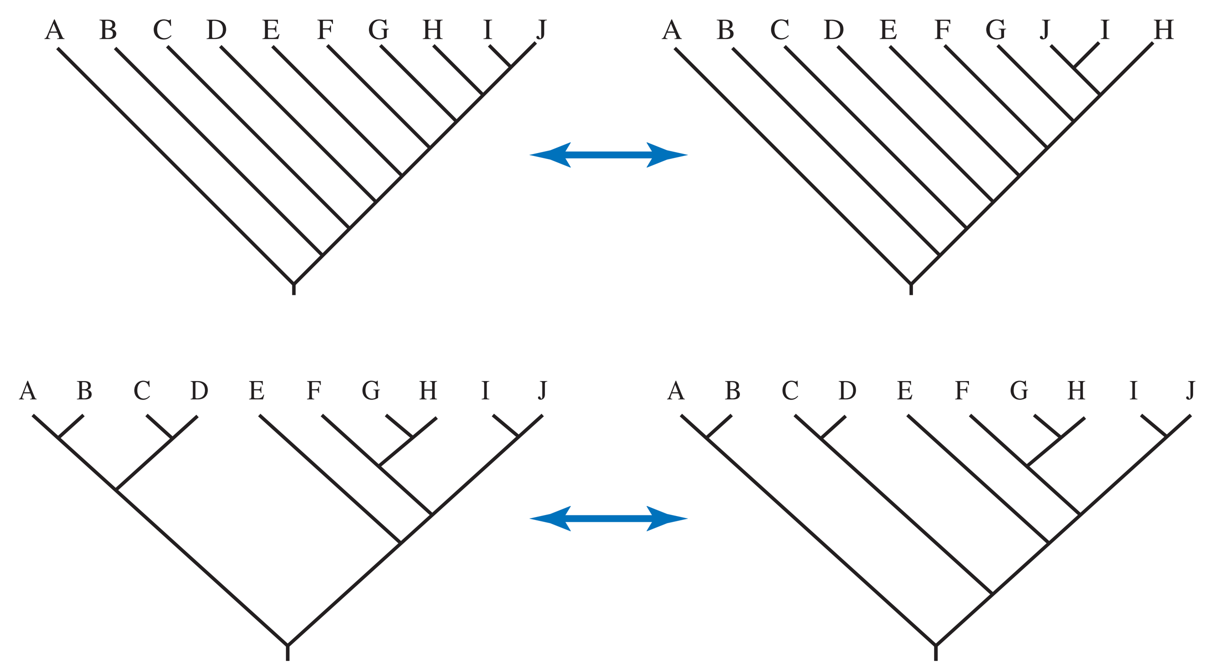
Gatesy, J., C. Hayashi, M. Cronin, & P. Arctander (1996). Evidence from milk casein genes that cetaceans are close relatives of hippopotamid artiodactyls. *Molecular Biology and Evolution* 13:954–963.

For additional information see the Tree Thinking Group Website
http://www.lrdc.pitt.edu/Donovan

Reading Topologies

For many trees, particularly cladograms, the axes of the graph are not scaled. In these situations the information about the relationships between taxa is based exclusively on the branching pattern of the tree and the nested hierarchy of groups of taxa (clades). Another way to think about this is that the tree can be rotated around any node with out affecting the information contained in the graph. The questions below are designed to assess students' facility thinking about topological relationships in a tree.

For the following pairs of trees indicate if the 2 cladograms are equivalent or not. If they are different, mark the diagrams to indicate where they differ.

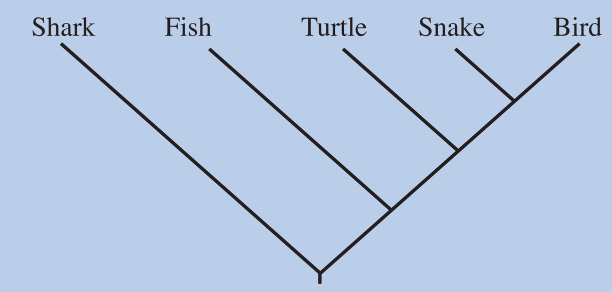


Relationships In Trees

There are a variety of ways that students might make sense of the relationships between taxa represented in trees. Student may rely on the:

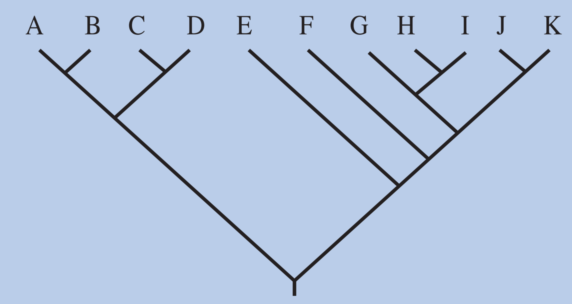
- morphological similarities and differences among taxa;
- spatial arrangement of the taxa in the diagram; or,
- topological relationships (branching structure) between taxa in the tree.

The questions below are designed to assess how students think about the relationships between taxa displayed in a phylogeny.



Which of the following statements is correct given this tree?

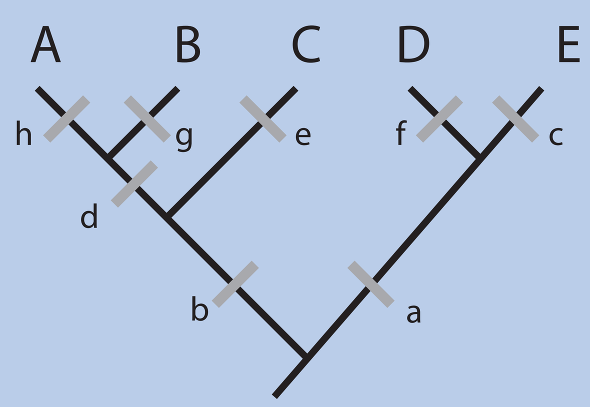
A. The Fish is more closely related to the Bird than it is to the Shark.
B. The Fish is more closely related to the Shark than it is to the Bird.
C. The Fish is about equally related to the Shark and the Bird.
D. The Fish is more closely related to the Turtle than it is to the Bird.
E. The Fish is more closely related to the Bird than it is to the Turtle.



1. Based on this tree, E is most closely related to:
   a) A b) D c) K d) not sure e) cannot be determined
2. Based on this tree, E is most closely related to:
   a) A b) D c) F d) not sure e) cannot be determined
3. Based on this tree, E is most closely related to:
   a) D b) F c) K d) not sure e) cannot be determined

Tracing Character Change

Discussing evolutionary patterns such as homology and analogy in the context of a phylogeny involves tracing character changes within a tree. The questions below are designed to assess students understanding of parsimony, homology, analogy and other evolutionary concepts as they address character change in the context of a tree.



Suppose that only taxa A and B have simple leaves and that all the other taxa have compound leaves. Which of the following statements represents the most parsimonious explanation of the evolutionary history of the character?

A. Simple leaves evolved from compound leaves on branch b.
B. Compound leaves evolved from simple leaves on branches e and a.
C. Simple leaves evolved from compound leaves on branch d.
D. Simple leaves evolved from compound leaves on branches h and g.
E. Compound leaves evolved from simple leaves on branch e.

Suppose that only taxa D and E have spines and that all the other taxa do not have spines. Which of the following statements represents the most parsimonious explanation of the evolutionary history of the character?

A. Spines evolved on branch a.
B. Spines evolved on branches f and c.
C. Either spines evolved on branch a or they evolved on branches f and c.
D. Spines were lost on branch b.
E. Either spines evolved on branch a or they were lost on branch b.

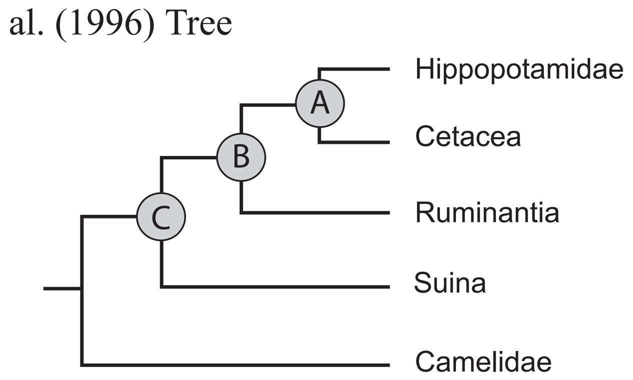
Modified from an assessment by David Baum.

Understanding Clades

Tree diagrams are made up of nested groups or clades. Clades can be collapsed, expanded, and repositioned (as long as the topology is not changed) without changing their status in a tree. Understanding a tree as a collection of clades makes it possible to consider trees as collections of hypothetical relationships and compare trees even when they don't initially appear to be similar. The questions below are designed to require students to think about trees as collections of clades.

An early molecular analysis done by Gatesy, et al. (1996) produced the following tree. The nodes labeled A, B and C can be thought of as 3 hypotheses about the evolutionary relationships among these groups. For the two trees built from new molecular data determine if they support or refute the hypotheses identified in the original tree.

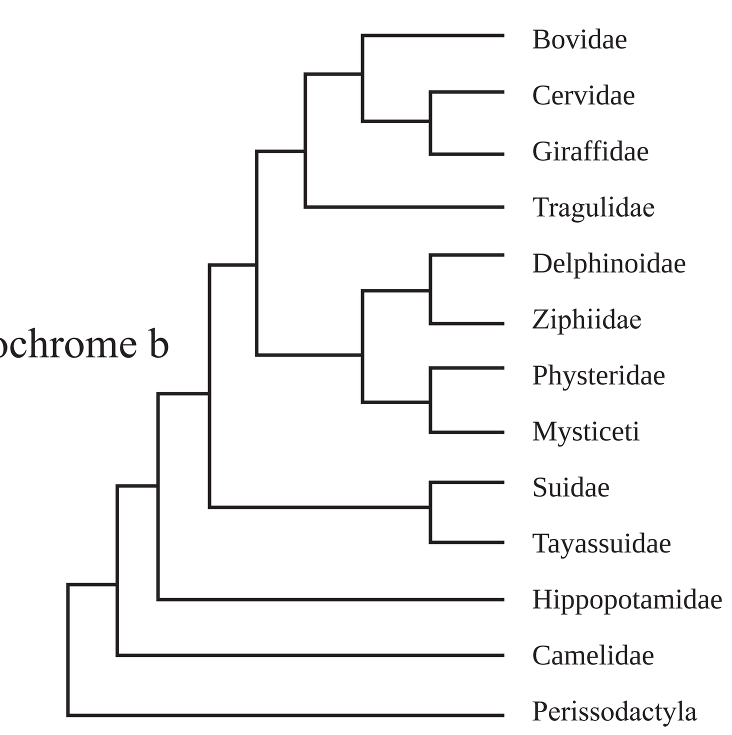
Gatesy et al. (1996) Tree



Key to taxonomic groups

- **Ruminantia** include: antelopes, deer (Cervidae), giraffe, and chevrotains (Tragulidae)
- **Cetacea** include: dolphins (Delphinoidae), porpoises, and whales (Ziphiidae, Physteridae, Mysticeti)
- **Hippopotamidae** includ:e hippos
- **Suina** include: pigs and peccaries (Tayassuidea)
- **Camelidae** include: camels and llamas
- **Perissodactyla** are the odd-toed ungulates

cytochrome b



γ-fibrinogen