

Phylogeny

Learning objective 7.9.A Describe the types of evidence that can be used to infer an evolutionary relationship, and 7.9.B explain how phylogenetic trees and cladograms can be used to infer evolutionary relatedness.

Name:Date:Period:

Use the tool **What a Tree Claims, and What It Does Not**. Parts 1 and 2 use **Build it from the matrix**, Part 3 uses **Which tree is better**, and Parts 4 and 5 use **Reading it**. A phylogenetic tree is not a picture of the past. It is a **hypothesis** built from evidence, and like any hypothesis it can be tested, compared with a rival and revised. This handout builds one from a character matrix, then measures it against an alternative, then asks what it does and does not claim.

Part 1 • The matrix

Eight taxa and seven characters. **Lancelet** is the outgroup — the lineage known to have branched off before all the others. Fill in a 1 where a taxon has the character and a 0 where it does not.

Character	Lancelet	Lamprey	Shark	Salmon	Frog	Lizard	Mouse	Dolphin
Vertebrae								
Jaws								
Bony skeleton								
Four limbs								
Amniotic egg								
Hair and mammary glands								
Fusiform body and fins for swimming								

1. Explain what an outgroup is and what it is for.

2. Explain what a shared derived character is, and why it is the kind of similarity that groups taxa.

Part 2 · Building the tree

List the characters from the one shared by most taxa to the one shared by fewest. Six of them nest — each group sits entirely inside the next. One does not, and that is the interesting one.

Character	How many taxa share it	Which taxa	Does it mark one branch?
Vertebrae			
Jaws			
Bony skeleton			
Four limbs			
Amniotic egg			
Hair and mammary glands			
Fusiform body and fins for swimming			

3. Draw the cladogram the six nesting characters imply. Label each branch with the character that arose there.

4. The swimming body is shared by the shark, the salmon and the dolphin. Explain why it does not group them, and how you can tell.

Part 3 · Choosing between two trees

Go to **Which tree is better**. One tree puts the dolphin with the fish; the other is the one the six nested characters gave. For each character, record the minimum number of changes it needs on each tree.

Character	Changes on the inferred tree	Changes on the rival tree
Vertebrae		
Jaws		
Bony skeleton		
Four limbs		
Amniotic egg		
Hair and mammary glands		
Fusiform body and fins for swimming		

5. Explain what parsimony means and why it is used to choose between trees.

6. The rival tree makes the swimming body cheaper. Explain why it is still the worse tree.

Part 4 · Reading relatedness off a tree

Go to **Reading it**. For each pair, record how many taxa share their most recent common ancestor, and how many tips apart the two names are printed. Only one of those columns measures relatedness.

Pair	Common ancestor shared with	Tips apart on the page	Derived characters shared
Lamprey and Shark			
Shark and Dolphin			
Salmon and Dolphin			
Mouse and Dolphin			
Frog and Lizard			
Lancelet and Mouse			

7. Explain what the nodes on a phylogenetic tree represent.

8. The lamprey and the shark are printed next to each other, and the shark and the dolphin are 5 tips apart. Explain which pair is more closely related and how you can tell.

Part 5 · What a tree claims, and what it does not

Read the table headed **A cladogram and a phylogenetic tree are not the same claim**, then the panel on molecular against morphological data.

Does it show...	Cladogram	Phylogenetic tree
Shows which lineages are more closely related		
Shows the order in which lineages branched		
Shows how long ago each split happened		
Shows how much change has occurred along a branch		
Can be tested and revised as new evidence arrives		

9. Distinguish between a cladogram and a phylogenetic tree.

10. Explain why molecular data usually produces more reliable trees than morphological data, and name one situation where morphology is the only option.

11. Explain why a phylogenetic tree is described as a hypothesis rather than a record.

What the model simplifies

Seven characters and eight taxa make a clean example precisely because they were chosen to. A real analysis uses hundreds or millions of characters, most of which are uninformative, and reports statistical support values on each branch rather than a single answer.

Characters are scored as simply present or absent. Real characters have multiple states, and deciding that two structures in different organisms are “the same character” at all is itself an inference — the one morphological analysis most often gets wrong.

Parsimony is used as the criterion for choosing between trees and counted with Fitch's algorithm.

Modern analyzes more often use maximum likelihood or Bayesian methods, which weigh how probable each kind of change is rather than treating all changes as equally costly. Parsimony is what the exam asks about and it is the right first idea; it is not the last word.

The rival tree is one specific alternative, chosen because it is the one the convergent character alone would suggest. A real search compares an enormous number of possibilities — for eight taxa there are already 135,135 rooted trees.

The divergence dates on the phylogenetic tree are approximate figures from the fossil record, rounded, and used to show what a scaled tree adds rather than as precise values.