AP BIOLOGY · UNIT 7 · TOPIC 7.9

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. The tool shows the matrix on Build it from the matrix. Copy it, writing 1 where a taxon has the character and 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. (a) Describe what an outgroup is.

(b) Explain how an outgroup is used to determine which character states are derived.

2. (a) Describe what a shared derived character is.

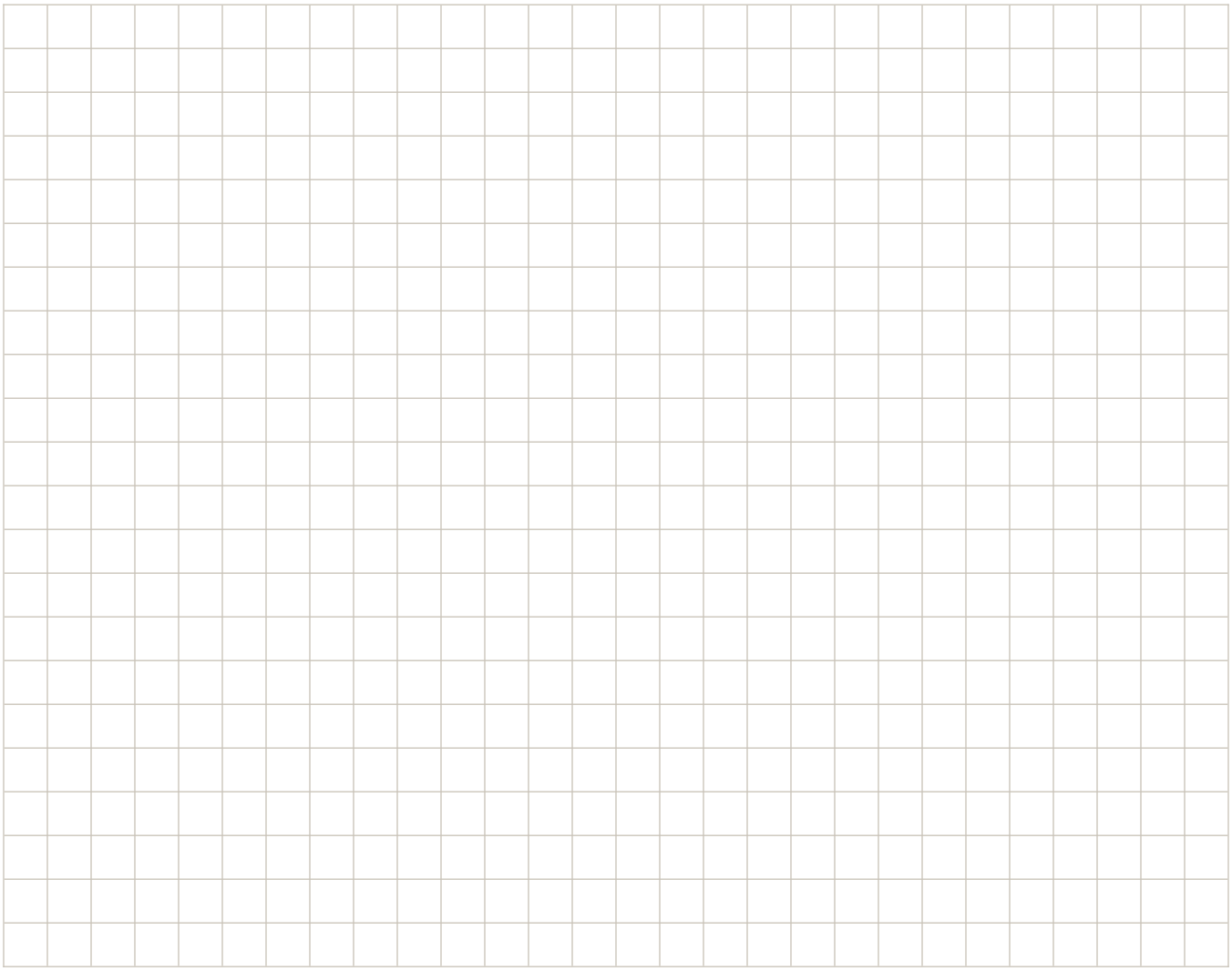
(b) Explain why shared derived characters, and not shared ancestral characters, are used to group taxa.

Part 2 · Building the tree

On Build it from the matrix, click each character. Record how many taxa share it, which taxa they are, and whether it marks one branch of the tree. Six of the characters nest: each group of taxa sits entirely inside the next. One character does not.

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. Construct a cladogram of the eight taxa based on the six nesting characters. On each branch, mark the character that arose there.



4. The fusiform body and fins for swimming are shared by the shark, the salmon and the dolphin.
(a) Explain why this character does not show that these three taxa form a group.

(b) Identify two characters in the matrix that group the dolphin with the land vertebrates rather than with the fish.

Part 3 · Choosing between two trees

Go to **Which tree is better**. Click The tree the characters give to see the tree that the six nesting characters produced, then click Group the dolphin with the fish to see the rival tree. From the table in the panel headed “Every character, on both trees,” copy the minimum number of changes each character needs on each tree. Add each column for the Total row, then click each tree to check your total against its Total changes needed.

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		
Total		

5. (a) Describe the principle of parsimony.

(b) Explain why parsimony is used to choose between phylogenetic trees.

6. The rival tree needs fewer changes for the swimming body than the inferred tree does (1 instead of 3). Using the Part 3 table, explain why the rival tree is still less parsimonious than the inferred tree.

Part 4 · Reading relatedness off a tree

Go to **Reading it**. Click each pair and record its three readouts: how many taxa share the pair's most recent common ancestor, how many tips apart the two names are printed, and how many derived characters the pair shares. Only one of the first two 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. Describe what the nodes on a phylogenetic tree represent.

8. On the tree in the tool, the lamprey and the shark are printed next to each other, and the shark and the dolphin are printed 5 tips apart.
(a) Identify the pair that is more closely related.

(b) Using the Part 4 table, provide reasoning to justify your identification.

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** on Reading it. Then go back to Which tree is better and open Why molecular data usually wins.

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. Describe the difference between a cladogram and a phylogenetic tree.

10. (a) Explain why molecular data usually produce more reliable trees than morphological data.

(b) Identify one situation in which morphological data are the only option.

11. Explain why a phylogenetic tree is considered a hypothesis rather than a record of evolutionary history.

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, and it is the one that morphological analysis most often gets wrong.

Parsimony is used as the criterion for choosing between trees and counted with Fitch's algorithm. Modern analyses 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 tool draws only a cladogram, with no time scale. The Part 5 table describes what a time-scaled phylogenetic tree adds.