Reconstructing the Evolutionary History of Biological Diversity (Phylogeny) Through the Use of Phylogenetic Trees 1

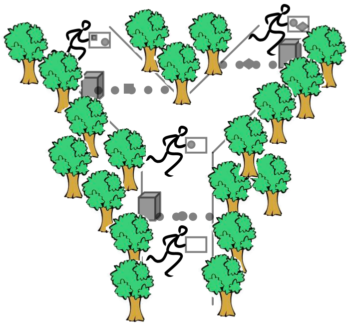
All species on Earth are related by common ancestry. This means that we can learn a lot about one species by knowing which other species are closely related. For example, we know that ungulates – animals who walk on their toes (usually on hooves such as cows) are always herbivores. However, we know that all species in the cat family are carnivores as well. Why is this? Because of the evolutionary history of these species.

Scientists study the evolutionary history of species in many different ways. One way to determine relationships is to study the traits or characteristics of different species. Informative traits can be physical appearance, such as the skeletal five-fingered hand of mammals, molecular comparisons (e.g., DNA sequences), behavioral patterns, geographic distribution, and fossil comparisons. Scientists use these traits to group species together and infer historical relationships. These relationships are represented in phyologenetic trees, which map the evolution of different species. It is important to remember that phylogenies show our best understanding of species relationships today. In the future, new information may lead us to redraw parts of a phylogeny, but many basic phylogenies are well understood and unlikely to change much.

This activity is designed to give you a feel for how scientists construct phylogenetic trees that allow us to understand evolutionary relationships and the world around us.

Part 1: Race in the woods

Imagine a race through the woods with 7 runners (A to G). Although all the runners started at a single starting point, the finish line is anywhere along the far side of the woods. After leaving the starting point, the path branched repeatedly and each runner chose a different course through the woods. Although all the runners crossed the finish line, they did so at different places depending on the route they followed through the woods. Check-in stations were located throughout the race and as each runner passed a station, they received a stamp. We can recreate the route each runner took by referring to the cards each runner had stamped at check in stations.



The following rules apply:

- Runners begin with a blank card
- Runners must collect a stamp from each check-in station they pass
- Each check-in station uses only one stamp and no two check-in stations use the same stamp
- The path always forks into two, and paths never cross or rejoin.

The aim of this activity is to use the information in the cards collected from the 7 runners to reconstruct the course and the placement of check-in stations. Using the stamped runners' cards check-in station symbols (see Runners Cards on page 5), draw a map of the course, labeling the starting point, each check-in station (with the ***symbol*** of the stamp it uses), and each finishing line (with the ***letter*** of the runner who emerged there). Remember that all the runners finished in a unique location, so on your final map you should see one start and 7 finish lines. Work collaboratively and use the Smart Board or white board to draw you final map.

Once your map is completed, answer the following questions.
1) Can you tell if you got the map right? How?

2) Compare your map to those generated by other groups. How are they similar? How do they differ?

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[1] Adapted from an activity developed by David Baum (University of Wisconsin) and Kristin Jenkins (National Evolutionary Synthesis Center). Baum and Jenkins' activity is based on Goldsmith's "The Great Clade Race" and K. Halverson's "Using Pipe Cleaners to Bring the Tree of Life to Life" (Goldsmith, DW, 2003. American Biology Teacher 9: 679-682).

3) Can you tell which should come first: the triangle or the star? Why or why not? No, since we don't have information on where their corresponding check-in stations are located on the path.

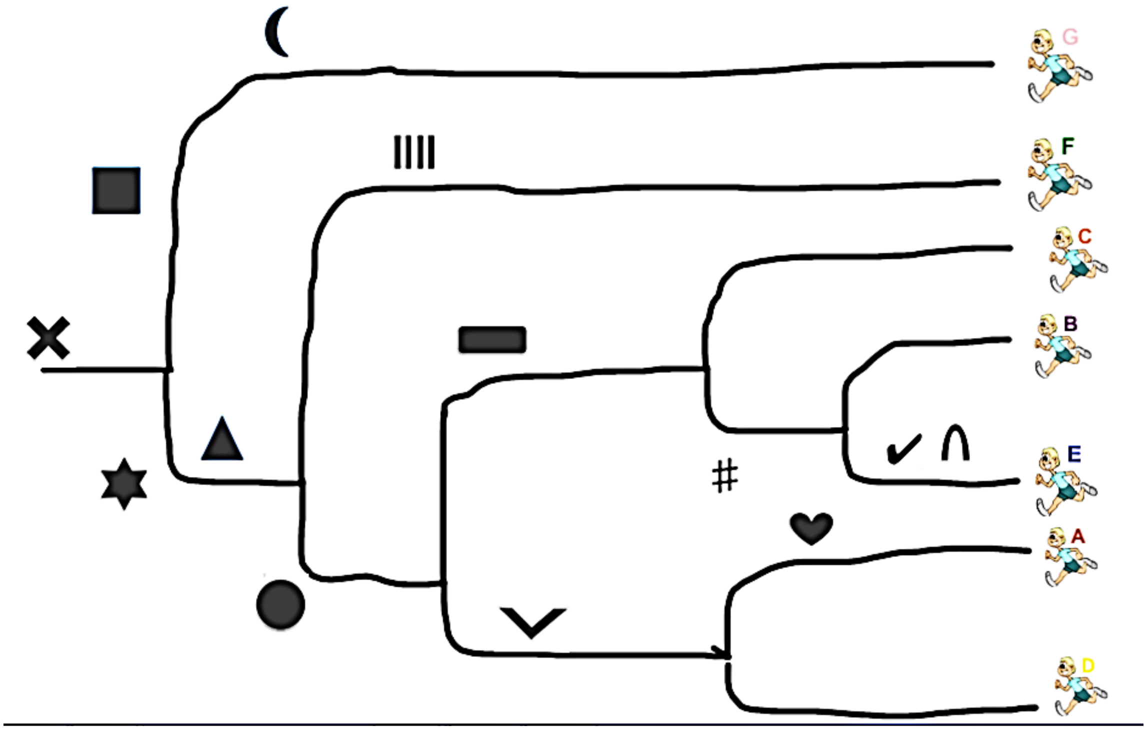
4) In thinking about the analogy to evolution, what would the following represent?

- a. The runners (species)
- b. The check-in stations (evolutionary characteristics or traits)
- c. The race course (lineage)

5) What can you infer about the shape of the tree? Did a particular path go right or left? Are paths straight or not? Are some segments of the course longer or shorter than others? There is no way to know from the stamps information.

6) When there were 2 check-in stations on a segment, can you figure out which came first? No, see question 3.

7) In the biological case, is it valid to assume that the "runners" receive a blank card at the start and that they always gain, but never lose, stamps? No, since species evolve all the time. Along the course of their evolution, they may gain or lose traits.



Part 2: A study of animal evolution

As species evolve over time, they acquire new traits. In addition, sometimes an ancestral species splits into 2 evolutionary lineages. Use the set of "Animals Cards" on page 6 to fill in the following chart of characteristics for each organism. Place a check mark in the appropriate place whenever an animal possesses a particular characteristic.

	Cow	**Crocodile**	**Gecko**	**Human**	**Pigeon**	**Salamander**	**Trout**
Vertebral column	X	X	X	X	X	X	X
Four limbs	X	X	X	X	X	X	
Lungs	X	X	X	X	X	X	
Amniotic egg	X	X	X	X	X		
Hair	X	X					
Rumen	X						
Antorbital fenestra		X			X		
Diapsid skull		X	X		X		

Wishbone					X		
Feathers					X		
Pedicellate teeth						X	
Swim bladder							X
Ray fins							X

Use the characteristics of the animals in the table above to construct a phylogenetic tree (cladogram) that depicts the evolutionary relationships between these animals.

You will see that all living species are all the same distance from the “root” – this shows us that all living species have been evolving for the same amount of time. No species is more or less “advanced” than any other. Even species such as sharks or ceolocanths that have not changed physically for a long time are evolving. Because their physical form is well suited to their environment, selection maintains their appearance. However, if you look at their DNA, you will see that changes have accumulated over time. Another thing to notice is that although living species share traits with their ancestors, no living species is ancestral to another living species. Similarly, although you and your cousins may share some of your grandparents’ physical traits, such as curly hair or eye color, you and your cousins are not ancestral to one another.

We can also use a tree to determine how closely related two species are. Identify the most recent common ancestor of two species by starting at the tips for the two species of interest and tracing the branches back through the tree until you reach a shared node. This is the most recent common ancestor for those two species. Two species that share a more recent common ancestor (one closer to the tips) are more closely related than are two species that share a more distant common ancestor (one that is located deeper in the tree).

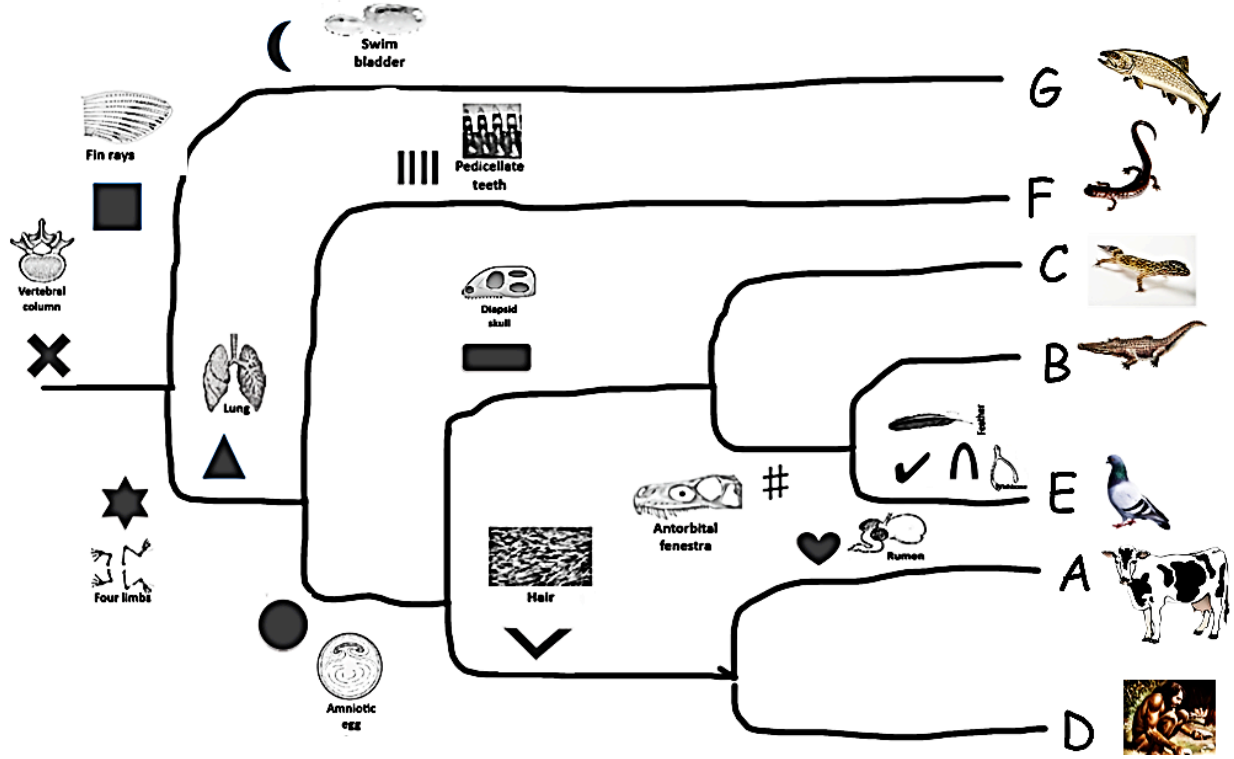
Once your cladogram is completed, answer the following questions.
1) Compare your tree to those generated by other groups. How are they similar? How do they differ?

2) Which species is the outgroup? Trout

3) Is a gecko more closely related to a salamander or a cow? Why? Equally related, since it shares a distant common ancestry with both.

4) Is a crocodile more closely related to a human or a cow? Why? Equally related, since it shares a distant common ancestry with both.

6) If scientists discovered a new species that has a vertebral column, four limbs, lungs and an amniote egg, where would it be placed on your tree? Would adding this new species change the relationships of the other species? As a branch of the amniotes in common with the crocodile, gecko, pigeon, cow, and human. Adding the new species should not the relationships of the other amniotic species on the tree.



Part 3: Use of a simple DNA sequence similarity to construct cladograms

The following are 5 different sequences of DNA (written 5' to 3') from 4 different organisms.
Organism A Sequence: ---ATGATCCAGT---
Organism B Sequence: ------AGGACTCAGT-----
Organism C Sequence: ----TTGATCCAGT----
Organism D Sequence: ---CGGACGCAGT---
Organism E Sequence: ---GCGAGAGT--

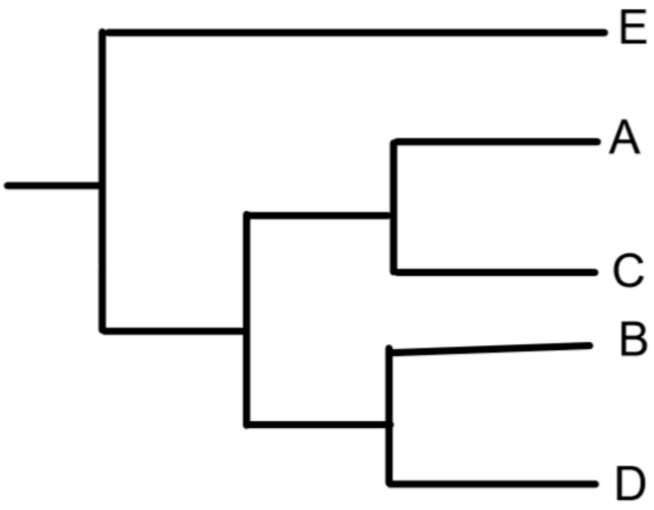
Dashes represent bases unimportant to the comparison. Match-aligning the sequences with each other could result in the following alignment pattern:
Organism A Sequence: ---ATGATCCAGT---
Organism B Sequence: ------AGGACTCAGT-----
Organism C Sequence: ----TTGATCCAGT----
Organism D Sequence: ---CGGACGCAGT---
Organism E Sequence: ---GCGAGAGTGT--

This alignment pattern could be used to compare the level of sequence similarity between the organisms as illustrated in Part A.

1. Calculate the percentage of similarity between the organisms and complete the following table.

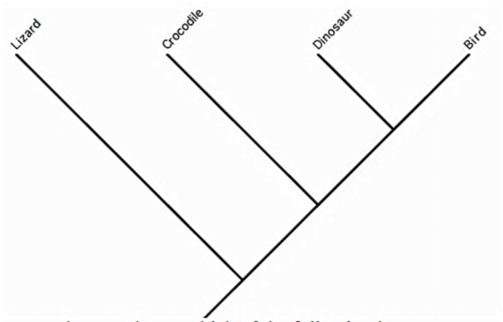
Organisms and Percentage Similarity					
	A	**B**	**C**	**D**	**E**
A	100	70	90	60	40
B		100	60	80	40
C			100	60	40
D				100	40
E					100

2. Use your answers in the table to construct a cladogram.



Clicker Questions

1. By reference to the tree below, which of the following is an accurate statement of relationships?



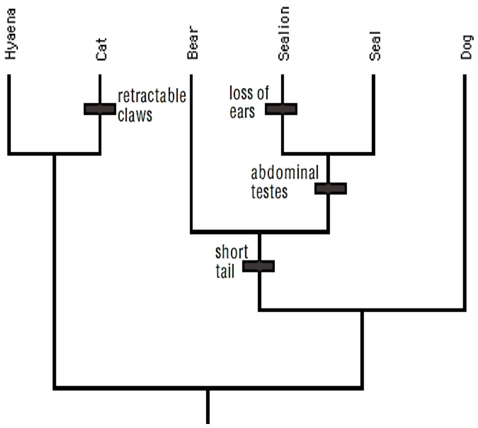
  - A. A crocodile is more closely related to a lizard than to a bird
  - B. A crocodile is more closely related to a bird than to a lizard
  - C. A crocodile is equally related to a lizard and a bird
  - D. A crocodile is related to a lizard, but is not related to a bird

2. A molecular biologist studying fungi discovers a gene family that is similar to a fruit-fly gene family. If she wants to determine whether the fungi and fruit-fly gene families are homoplastic or homologous, she should:

  - A. Determine whether the functions of the gene families are similar in fungi and insects.
  - B. Sequence some other fungi and fruit-fly gene families.
  - C. See if organisms in lines that branched off between fungi and insects have similar gene families.
  - D. Determine whether any bacteria have similar gene families.

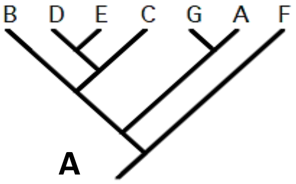
3. In the tree below, assume that the ancestor had a long tail, ears, external testes, and fixed claws. Based on the tree and assuming that all evolutionary changes in these traits are shown, what traits does a seal have?

  - A. long tail, ears, external testes, and fixed claws
  - B. short tail, no ears, external testes, and fixed claws
  - C. short tail, no ears, abdominal testes, and fixed claws
  - D. short tail, ears, abdominal testes, and fixed claws
  - E. long tail, ears, abdominal testes, and retractable claws

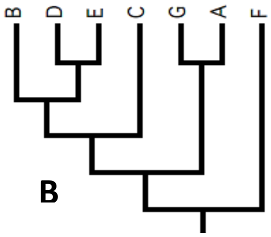


4. Which of the 4 trees below depicts a different pattern of relationship than the others?

A. Tree A
B. Tree B
C. Tree C
D. Tree D

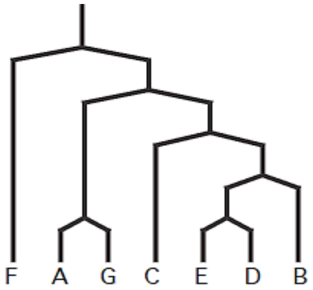


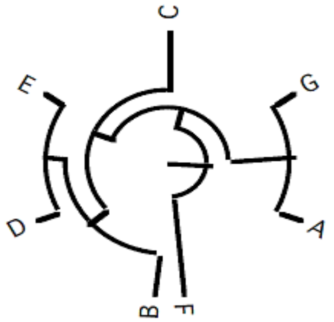
A



B

C





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