

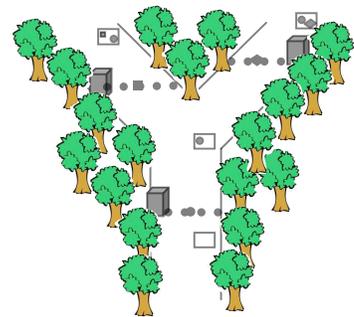
Reconstructing the Evolutionary History of Biological Diversity

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. But we know that all species in the cat family are carnivores. Why is this? Because of the evolutionary history of these species.

Scientists study the evolutionary history of species 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, behavioral patterns, geographic distribution, and fossil comparisons. Scientists use these traits to group species together and infer historical relationships. These relationships are represented in phylogenetic 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. These activities are designed to give you a feel for how scientists make a phylogeny.

Step 1: Race in the woods

Imagine a race through the woods. 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.

Using the stamped runners' cards, 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 seven finish lines.

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?
- 3) Can you tell which should come first: the triangle or the star? Why or why not?

Step 2: A simple study of animal evolution

The problem of determining the evolution of species is very similar to the race map. As species evolve over time they acquire new traits – like the stamps that the runners pick up. Also, sometimes an ancestral species splits into two evolutionary lineages – like the branching of the racecourse.

Your teacher will give you a new set of cards in which the “runners” are living animals and the “stamps” are traits that arose during the animals’ evolution. Use the new cards and the race stamp cards to fill in the following chart of characteristics for each organism.

	Cow	Crocodile	Gecko	Human	Pigeon	Salamander	Trout
Vertebral column							
Four limbs							
Lungs							
Amniotic egg							
Hair							
Rumen							
Antorbital fenestra							
Diapsid skull							
Wishbone							
Feathers							
Pedicellate teeth							
Swim bladder							
Ray fins							

Step 3: Making it 3D

Using colored pipe cleaners, reconstruct the map you drew to make a tree that shows how these animals evolved [Tip: Start by twisting all the pipe cleaners together at the root of the tree about five times]. At each branch point, separate any species that are branching off and twist together the pipecleaners of the species following the same path.

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).

Questions

1. Is a gecko more closely related to a salamander or a cow? Why?
2. Is a crocodile more closely related to a human or a cow? Why?
3. 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?

Teacher Notes

Reading phylogenies is a cognitively challenging task. This activity helps students overcome common misconceptions, allowing them to use phylogenies to understand evolutionary relationships as scientists do. This is a two part activity in which students map a basic phylogeny on paper, and then build a three dimensional representation.

Source: This activity was developed by David Baum, University of Wisconsin, and Kristin Jenkins, National Evolutionary Synthesis Center, and is based on D. Goldsmith's "The Great Clade Race" and K. Halverson's "Using Pipe Cleaners to Bring the Tree of Life to Life."

Level:

This activity is appropriate for students from sixth grade through college. The follow up discussion will vary based on the level.

Time:

This lesson can usually be completed in class periods that are approximately 50 minutes in length.

- **Step 1** takes approximately 30-40 minutes for student map out the race course. An additional 15-20 minutes of discussion time based on their maps. (Typically one class period)
- **Step 2** takes about 15-10 minutes to use their vertebrate cards to complete the chart. Students then use about 10-15 minutes to apply this information to their race maps, they determine which shape represents which shape and which runner represents which animal.
- **Step 3:** The pipecleaner activity should take about 10 minutes, with an additional 10-15 minutes of discussion. Let students discover that their trees may at first appear different, but if you rotate the branches around the nodes they can all be made to look the same.

Materials:

One large sheet of paper and a marker per team. Large post it pads work particularly well, but taping large sheets up works well, too. An alternative is to have each team draw their map on a white board or chalk board.

Two color coded card sets per team. Each team will need one set with symbols and one set with animals and characters. The symbol card template is posted here:

The following color coding system helps with continuity:

Orange – Cow/Runner A

Purple – Crocodile/Runner B

Red – Gecko/Runner C

Yellow – Human/Runner D

Blue – Pigeon/Runner E

Green – Salamander/Runner F

White – Trout/Runner G

Sets of pipecleaners in colors that match the card sets.

Procedure:

Race in the Woods

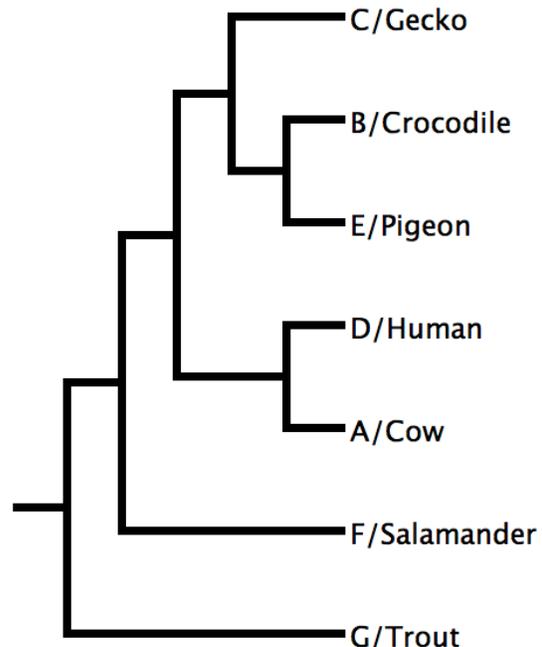
1) Distribute the sheet “Reconstructing Evolutionary History” and give each team of students one set of color coded symbol cards. You may wish to guide students through the introduction to the mapping activity, or have students read the directions to one another. Write the rules for the race on the board to remind students. Do not provide any guidance regarding shape of the paths, location of the check in stations or runner exit sites except to remind students of the rules. Make sure that they understand that each runner finishes the race at a unique finishing line, and that all runners complete the race.

A map/phylogeny key is provided below. Remember that branches can rotate around nodes, so the order of the tips can change. Check in stations may be represented at branch points or anywhere along a branch.

2) Have students post their maps around the room. Ask a volunteer group to guide the class through their map. Ask the class if the map is correct, and if not, correct any errors. Select a second map that looks different (check in site are in a different location, the paths are drawn in a different style, the runners do not emerge in the same order reading left to right across the finish line, etc). Point out the differences and ask the class if this map is also correct. Allow some class discussion and repeat with another map if desired. Students can often see that the solutions are “correct” and “equivalent” even when they are drawn quite differently. This is worth complimenting them on, as it is a major stumbling block in reading phylogenies. If students are unsure if a map is correct, ask them to consider each runner in turn and confirm that the stamps on the card correspond to the check-in stations that they passed on their way from the starting line.

The key points here are:

- the check in point can be anywhere along the path between branch points or right at the branch point
- the order of runners (reading left to right) across the finish line can vary
- the map does not have to be in a particular orientation (bottom to top is most common, probably because of the introductory prompts)
- the shape of the paths does not change the overall map pattern (curvy lines vs. straight lines, short vs. long, etc)
- all the runners completed the race. All extant organisms (all living organisms) are at the same point in the evolutionary race. No species is more or less evolved than any other.



These points are important because students often read phylogenies “across the tips.” This is incorrect because branches can rotate around nodes (think of a mobile). Students are often confused if the shape of the phylogeny changes. There are many styles of drawing phylogenies which are typically driven by space constraints or aesthetics. The check in stations represent traits that have evolved over time somewhere along an ancestral branch between forks. You can say that either is valid, but given how little of the race course is exactly at the branching points (nodes), it is probably more likely that check in stations are between nodes. We usually cannot pinpoint the exact time of trait evolution, so students will need to see that trait (or traits) as appearing sometime during the evolution of that group rather than the marker of a speciation event. It is a very common misconception that “simpler” organisms are less evolved than others. This is an example of thinking of evolution as a progressive process, leading to a more desirable endpoint (like humans!). Evolution is not progressive, and it is not directional.

Another important point is that we could reconstruct the race course even though none of us were there to see the race. This is an illustration of the nature of science. Scientists are often able to study things or events that we cannot directly see, whether because they are too small, too big, or too far away (in space or time).

A simple study of animal evolution

1) Give each team the second set of cards with animals and traits listed. Give them a few minutes to match the runners and the animals on the worksheet. You may want to have them relabel their maps with the animals and traits replacing the runners and stamps.

Taking it 3D

1) Give each student a set of pipecleaners. Have the students build a three dimensional representation of the race map with the pipecleaners. You may want to demonstrate twisting all the pipecleaners together 3-5 turns, then twisting all the pipecleaners except the trout to make the first branch point. When the students have formed all the branches, they can stick the animal cards on the tips. You may also want to print up labels for the traits and have students place the labels along the pipecleaner branches.

2) Discuss with students how the shape of the phylogeny does not alter the relationships of the organisms, and demonstrate how branches rotate around nodes. Another interesting demonstration is to add or remove an organism from the phylogeny, again without altering any of the other relationships.

Reading the tree

1) Relationships between organisms on a tree are determined by the most recent common ancestor. To identify the most recent common ancestor between any two organisms, start at the tip and trace back through the phylogeny until you reach a shared node. That node represents the most recent common ancestor. Note that the ancestor did not necessarily look like either of the extant organisms, or a blend of them. It simply represents an (often unknown) organism that had all the traits shared by the two species of interest.

Have students trace the evolutionary pathway of humans back through the tree. They should notice that we share traits with many other organisms, we are related more or less closely to various organisms based on the number of shared traits (not the number of nodes – node counting is another common mistake students make).

Variation:

Withhold Runner B/crocodile (purple) from the entire exercise. After students have drawn the map and built their pipecleaner phylogenies, take them through the following extension:

When West Nile virus first arrived in the USA, it was observed in birds, horses and occasionally people. The normal host for West Nile virus is birds, and it is easily transmitted between birds. It is much rarer and less deadly in horses and humans. However West Nile virus had a big impact on crocodile farms. Why do you think that might be?

Have students discuss why. The key point is that crocodiles are more closely related to birds, the natural host of West Nile, than mammals are. Give students the crocodile card and a purple pipecleaner. Ask the students to add crocodiles to the phylogeny.

The key points here are:

- understanding evolutionary relationships can help us understand the world around us
- species may be added or removed from a phylogeny without altering the relationships of the remaining species

References and additional resources:

Goldsmith, D. 2003. The Great Clade Race. American Biology Teacher, Vol 65(9) pp679-682

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Tree Thinking Assessment from Baum, etal. 2005 Science Vol 310 p979
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Gregory, T.R. 2008. Understanding Evolutionary Trees. Evo Edu Outreach (2008) 1:121–137 DOI 10.1007/s12052-008-0035-x (Free download: <http://www.springer.com/life+sciences/evolutionary+%26+developmental+biology/journal/12052?hideChart=1#realtime>)

Tree of Life Video

From the Peabody Museum

<http://archive.peabody.yale.edu/exhibits/treeoflife/films.html>

Understanding Evolution (<http://evolution.berkeley.edu/evolibrary/home.php>)