# Reconstructing the Evolutionary History of Biological Diversity

**Teacher Notes**

Reading phylogenies and thinking clearly about evolutionary history is a cognitively challenging task. This activity helps students overcome common misconceptions, allowing them to use phylogenies to understand evolutionary relationships as scientists do. In this activity students solve the logic puzzle of reconstructing the map of a hypothetical race course. The race course is actually the phylogenetic tree for six familiar animals. Students then explore the evolutionary concepts represented by the map. This variation was developed by D.A. Baum and K.P. Jenkins, based on an activity by D. Goldsmith (ABT, 2001).

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

**Time:**

The activity should take about 30-45 minutes for the introduction and time for students to map the race. An additional 15-30 minutes of discussion time around the maps allows students to explore the evolutionary concepts behind the map and practice their tree reading skills.

**Materials:**

One copy of the student directions per student or per team.

One set of cards with stamps and runner letters A-F per team.

One set of cards with characters and organism names per team.

**Procedure**

***Race in the Woods***

1) Distribute the sheet “Reconstructing Evolutionary History” and give each team of students one set of runner cards with stamps. You may wish to guide students through the introduction to the mapping activity, or have students read the directions to one another. 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 all runners started at the same starting line, but that each runner finished the race at a unique finishing line, and that all runners completed the race.

2) Have students share their maps with the class. 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 sites are in different locations on branches, 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 tokens correspond to the check-in stations that they passed on their way from the starting line.

Important ideas to highlight include:

- the check in point can be anywhere along the path between branch points or right at the branch point

- if there are two check in stations on a given branch, the order in which they are drawn is arbitrary

- 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. By analogy, 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. Phylogenies are drawn in many styles which are typically driven by page space constraints or aesthetics.

The check in stations represent traits evolving somewhere along an ancestral branch between forks. Students may place check in stations at the nodes (branching points) or anywhere along a branch. Either option is valid, but given how little of the race course is exactly at the nodes, it is more likely that check in stations are located somewhere along a branch. In evolution, we usually cannot pinpoint the exact time when a trait evolves, and the positioning of check in stations reflects this uncertainty in the timing of trait evolution. For this reason, it is more accurate to represent the stamps being collected sometime along the branches of the course rather than marking where paths split.

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). We do this by understanding how evolution occurs over time, and reconstructing how events (like check-in stations/evolution of traits and path splitting/speciation events) occurred based on the data we have available in extant species’ morphology and DNA, and fossils.

***Converting runners to species***

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

***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 between two organisms (node counting is another common mistake students make). The total number of traits that organisms share is also not the determinant of whether or not organisms are more or less closely related. For example in this tree, a crocodile has one difference from an iguana and one from a pigeon, but is more closely related to a pigeon. This is because it would be impractical to place all of a species’ traits on a tree. Trees are typically drawn using traits that clearly differentiate between species.

The check in stations now represent traits that have evolved over time somewhere along an ancestral branch between branch points (“nodes”). As with stamps on the runner cards, it is more likely that trait evolution happened between nodes. A trait is rarely a marker of a speciation event. A branching event corresponds to an ancestral population splitting into two populations which *then* started accumulating differences. Students often assume that major trait changes occur at the node, where population splits are represented.

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. You might ask whether the human “runner” covered more distance than a shark “runner.” The answer is that a living human and living shark are exactly equally distant in years from their last common ancestor.

In this guide, teacher notes are provided in color throughout the student handout. Problem spots are highlighted, and answers to the questions are provided.

**The Great Clade Race (Teacher Guide)**

Based on: D. W. Goldsmith (2003) American Biology Teacher 9: 679-682

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? It is 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, 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 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. These activities are designed to give you a feel for how scientists make a phylogeny.

**Step 1: Race in the woods**

Last year, race organizers held a very successful race in a local park and they want to use the same course again. Unfortunately, they lost the course map. In this race, runners all started at one point on one side of the park. As they ran through the park, the paths branched repeatedly and each runner took different routes. Throughout the course there were check-in stations where the runners collected stamps. In this race, runners could finish anywhere on the far side of the park, rather than at a single finish point. Although all the runners crossed the finish line, they did so at different places depending on the route they followed through the woods. The race organizers believe that they can recreate the route each runner took by referring to the stamps each runner collected at check in stations.



Can you use the runners’ stamps to reconstruct their pathways? The following rules apply:

* Runners began with a blank card.
* Runners collected a stamp from each check-in station they passed.
* Each check-in station used only one stamp and no two check-in stations used the same stamp.
* The path always forked into two, and paths never crossed or rejoined.
* Runners could not backtrack.
* All runners reached the far side of the park and finished the race

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 where each runner finished (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 six finish points. (Teacher note: emphasize that all runners must reach the far side of the park.)

Questions

1) Can you tell if you got the map right? How?

Yes. Trace each runner’s path and check it against the race card. The stamps on the card and path should match up.

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

Students may use different styles of lines for their maps, but the most important difference is that the order of the runners from one side of the finish line to the other may not match between races. This is because phylogenies can rotate at the nodes. For example: F,D,A,C,E,B could be the equivalent of F, A, D, B, E, C. Have students check the pathways to confirm that the order at the end of the race can be different and still correct (assuming that the pathways have been marked correctly).

3) Can you tell which should come first: the X or the pentagon? Explain your reasoning.

We cannot distinguish which stamp/trait came first in this map/phylogeny because we do not have any information about *when* these stamps were collected/traits evolved. Because we do not know the placement of the check in stations, tamps may be placed anywhere along the branch or right at the node. Similarly, if we do not know when a trait evolved, it may be placed anywhere along the branch or at the node. Scientists use a variety of evidence to determine when traits arose, including molecular clocks and fossils.

In this case, lungs arose first. See this article for an interesting explanation of how lungs evolved: https://evolution.berkeley.edu/evolibrary/article/fishtree\_09

**Teacher Guide Step 2: Converting “runners” to species**

The problem of determining the evolutionary pathway 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.

The racecourse the students built reflects extant animals and their traits. Have the students convert the stamps and runners in their phylogenies to traits and organism using the second set of cards. You may want to provide students with the chart that explains each trait.

(See the phylogenetic tree below for the key)



(Teacher note: In general, it is easier for students to read this “bracket” style phylogenetic tree, rather than a “V” shaped tree. Trees with the root and tips horizontal, instead of vertical, also avoid confusion about the direction of time. With more advanced students, it can be useful to ask them to convert their race course between the “bracket” style and the diagonal, “V” shaped style.)

|  |  |  |
| --- | --- | --- |
| **Trait** | **Stamp** | **Description** |
| Vertebral column | Arch | A picture containing text, map  Description automatically generated  The vertebral column runs along the dorsal side of vertebrates and supports the spinal cord, part of the nervous system.  By Ruth Lawson. Otago Polytechnic |
| Lungs | Pentagon | A picture containing drawing  Description automatically generatedLungs are used for respiration by vertebrates to bring in oxygen and remove CO2 from the blood to support energy production through cellular respiration and maintain homeostasis. Birds have a unique respiratory system that is more efficient than the mammalian system.  Image: Dorothy Sigler Norton |
| Tetrapod | X | A picture comparing skeletons of lobe finned f ish and amphibians.  Description automatically generatedTetrapods have four limbs and evolved from the lobe finned fishes. Tetrapods may be aquatic, semi-aquatic, or land based. Some members of the superclass Tetrapoda have lost their limbs, for example snakes and whales, but we know they are tetrapods because their skeletons have vestigial limbs.  Image: Conty: Crossopterygii tetrapod hips |
| Hair | Circle | Hair is an identifying characteristic of mammals. Even aquatic mammals, such as whales, retain hair follicles and some hair.  A close up of a map  Description automatically generated |
| Diapsid Skull | Rectangle | Screen shot 2015-03-01 at 9A distinguishing characteristic of Sauria (the taxonomic group for reptiles, including lizards, crocodiles, turtles, and birds!). Diapsid skulls have two holes behind the eye socket that may have evolved to increase jaw movement and/or decrease weight of the skull.  Image Gagae |
| Rumen | Square | Ruminants (grazers like cows and sheep) have a unique section of the digestive system, the rumen, that houses bacteria. These symbiotic bacteria digest cellulose from grasses to a form that the ruminant can absorb and metabolize. In exchange, the ruminant provides a safe living space and lots of food to the bacteria.    ACARA: <https://www.learnaboutwool.com/lesson-plans/ruminant-digestion/> |
| Non-overlapping scales | Hourglass | Archosauria (birds and crocodiles) have non-overlapping scales. Lepidosauria (lizards and snakes) have overlapping scales.  Overlapping scales of a snake    **By AshLin Keeled scales**    Non-overlapping scales of a crocodile  **Hans Hillewaert** |
| Feathers | Star | A picture containing pen, implement, stationary, bird  Description automatically generatedA close up of a bird  Description automatically generatedOnly aves (birds) have feathers. Feathers evolved in the dinosaur ancestors of birds.  Image: K.Jenkins  Emily Willoughby |

**Reading the Tree**

Looking at the map, note that all living species are all the same distance from the “root” or base of the tree – 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 coelacanths that have not changed physically for a long time are evolving. Because their physical form is well suited to their environment, selection maintains their physical form but changes have accumulated over time in their DNA. 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 (endpoints) for the two species of interest and tracing the branches back through the tree until you reach a shared node, or point where two branches meet. 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, closer to the root).

Questions

1) Is an iguana more closely related to a shark or a cow? Why?

An iguana is more closely related to a cow than a shark, because the cow and iguana share a more recent common ancestor than either shares with the shark.

The most recent common ancestor of the iguana and cow is represented at the node splitting above the branch with lungs and tetrapod traits (pentagon and X). The most recent common ancestor for the iguana and the shark is represented at the first branch of the tree, immediately above the root.

2) Is a crocodile more closely related to a human or a cow? Why?

A crocodile is equally related to a human and a cow, because the most recent common ancestor for the crocodile and human and the crocodile and cow is the same. The most recent common ancestor for all three animals is represented by the node splitting above the branch with lungs and tetrapod traits (pentagon and X).

Additional questions:

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

* 1. The runners - Species
  2. The check-in stations – evolution of traits
  3. The race course – evolutionary pathways over time

Can you determine relationships between runners by looking at their relative positions on the finish line? In other words, if you go from left to right, do the runners always emerge in the same order? Why or why not?

The order of the runners from one side of the finish line to the other may not match between races. This is because phylogenies can rotate at the nodes. For example: F,D,A,C,E,B is the equivalent of F, A, D, B, E, C. Have students check the pathways to confirm that the order at the end of the race can be different and still correct (assuming that the pathways have been marked correctly).

In the biological case, is it valid to assume that the “runners” receive an empty card at the start and that they always gain, but never lose, stamps?

The stamps/traits used in this tree are a small subset of the traits that these species have. These traits were selected to differentiate between the species. Many other traits could be added to the tree, but it would become cluttered and difficult to read quickly! Additionally, species may gain or lose traits over time.

(Teacher Note: Loss of traits can be a difficult idea for students. As a case in point, archosaurs (represented by crocodiles and pigeons in this activity) are characterized by “socket teeth” (thecodont) teeth, but birds have lost this trait. One more complicating factor is that traits may be gained or lost independently in different lineages. These events are called homoplasies.)

Amniote eggs protect the embryo with membranes, and were a key evolutionary development that allowed organisms to move beyond aquatic environments to terrestrial environments. Amniote eggs were not represented in this tree, however all these organisms except the shark have this trait. If the trait was added to the tree, where would it be added and would it change the structure of the tree?

It would be added anywhere between the first and second branch of the tree, with the stamps for lungs and tetrapods. Adding this trait would not change the relationships represented in this tree.

(For more on amniotes, check this site: <https://ucmp.berkeley.edu/vertebrates/tetrapods/amniota.html>; and for some very interesting information on shark eggs, check this site: https://www.nhm.ac.uk/discover/do-sharks-lay-eggs.html)

Which organism has the most traits in this tree? (Pigeon) By comparison, how many traits do humans have? (3) Does this indicate that “Birds are more evolved” than other organisms on the tree?

No. All organisms are equally distant in time from the “start” of the evolutionary “race” and all are at the same time point in their evolutionary pathways. In this this phylogeny, more traits were required to distinguish birds from other organisms. Only a tiny subset of all traits were included, but we might expect that if we studied enough traits, including both DNA and “physical” traits, each living species would have approximately the same of differences from the root of the tree.

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?

Crocodiles are more closely related to birds, the natural host of West Nile, than mammals are. As such, they are susceptible to the virus.

**Additional Resources**

These are additional resources for understanding building and reading phylogenies. These resources may be more useful after students complete this activity.

Understanding Evolution Evo101 Introduction to Phylogenies: (https://evolution.berkeley.edu/evolibrary/article/0\_0\_0/evo\_04)

Kahn Academy on Building Phylogenetic Trees: <https://www.youtube.com/watch?v=6_XMKmFQ_w8>

The pipecleaner activity described in this article provides another way of visualizing phylogenies and is particularly useful at demonstrating rotation around nodes, and how organisms may be added to or removed from a tree without changing the existing relationships. Halverson, K. 2010. Using Pipe Cleaners to Bring the Tree of Life to Life. American Biology Teacher, Vol 72 (4) pp223-224. DOI: 10.1525/abt.2010.72.4.4

These paired articles provide a deeper dive into phylogenies.

Baum, D. 2008. Reading a Phylogenetic Tree: The Meaning of Monophyletic Groups. Nature Education 1(1) (<http://www.nature.com/scitable/topicpage/reading-a-phylogenetic-tree-the-meaning-of-41956>)

Baum, D. (2008) Trait evolution on a phylogenetic tree: Relatedness, similarity, and the myth of evolutionary advancement. Nature Education 1(1) (<http://www.nature.com/scitable/topicpage/trait-evolution-on-a-phylogenetic-tree-relatedness-41936>)

This article is appropriate for faculty. It provides information about how to read phylogenies, but also explores common student misconceptions about reading phylogenies.

Gregory, T.R. 2008. Understanding Evolutionary Trees. Evo Edu Outreach (2008) 1:121–137 DOI 10.1007/s12052-008-0035-x

**References**

This activity was developed by David Baum, University of Wisconsin, and Kristin Jenkins, National Evolutionary Synthesis Center/BioQUEST, and is based on D. Goldsmith’s “The Great Clade Race”.

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

Baum, D.A., Smith, S. D., Donovan, S.S. 2005. The Tree Thinking Challenge. Science Vol 310(5750):979-980. DOI: 10.1126/science.1117727

Baum, D.A. and Smith, S.D. 2013. Tree Thinking: An introduction to Phylogenetic Biology. Roberts and Co. ISBN: 9781936221165



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