# The Vertebrate Clade Race: Reconstructing Evolutionary History

## Step 1: Race in the woods

Last year, race organizers held a very successful race in a local park and they want to run the race again this year. Unfortunately, they lost the course map. In this race, runners all started at one point on the west 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 tokens. In this race, runners could finish anywhere on the east side of the park, rather than at a single finish point. Although all the runners crossed the finish line (the far side of the park), they did so at different places depending on the route they followed through the woods.



Your task is to help the race organizers reconstruct the route each runner took by referring to the tokens each runner collected at check-in stations.

The following rules apply:

* Runners begin with no tokens.
* Runners must collect a token from each check-in station they pass.
* Each check-in station hands out only one token and no two check-in stations use the same token.
* The path always forks in two, and paths never cross or rejoin.
* Runners cannot backtrack.

### Reconstructing the race route

The yarn represents the runners’ pathways. Clip the yarn to a single starting point on the felt board, twisting all the yarn together to reflect a single starting path. Show the location of check-in stations by clipping the appropriate token where the station was. Clip the runners’ rings on the far side of the felt board to represent where they emerged on the far side of the park. Remember that all the runners finished in a unique location, so on your final map you should see one start and six finishes.

### 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 wing nut or the wooden bead? 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 populations evolve over time they acquire new traits – like the stamps that the runners pick up - leading to speciation. As populations evolve, they split into different evolutionary lineages – like the branching of the racecourse. Scientists use these traits to infer organisms’ evolutionary pathways. The map of ancestral relationships is called a phylogenetic tree.

In this activity the “runners” represent modern animals and the “tokens” are traits that arose during the animals’ evolution. Can you use the clothespins to label each trait and animal? Use the information to fill in the following chart of characteristics for each organism. This kind of chart, called a matrix, can be used to organize data for a phylogenetic tree.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Cow** | **Crocodile** | **Trout** | **Human** | **Pigeon** | **Iguana** |
| **Four limbs (bead)** |  |  |  |  |  |  |
| **Lungs (wing nut)** |  |  |  |  |  |  |
| **Swim Bladder (rubber gasket)** |  |  |  |  |  |  |
| **Hair (button)** |  |  |  |  |  |  |
| **Rumen (sponge)** |  |  |  |  |  |  |
| **Non-overlapping scales (hose clamp)** |  |  |  |  |  |  |
| **Diapsid skull (pipe)** |  |  |  |  |  |  |
| **Feathers (die)** |  |  |  |  |  |  |

### Reading the Tree

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 and 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 anatomical, genetic 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 phylogenies are well understood and unlikely to change much. These activities are designed to give you a feel for how scientists make a phylogeny.

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 physical form. 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). Note however, that you cannot determine relationships by looking which tips sit next to one another. Branches on the tree rotate around nodes, where branches split, similar to the way sections of a hanging art mobile rotate freely. For this reason, it is important to read down the branches to reach a common ancestor before drawing conclusions about evolutionary relationships.

### Questions

1. Is an iguana more closely related to a trout 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 of salamander that has four limbs, lungs, and four toes on the front feet, where would it be placed on your tree? Would adding this new species change the relationships of the other species?