PHYLO CLASSROOM GUIDE

Find the common ancestor

Grades 9–12 · one 45-minute period
NGSS HS-LS4-1 · LS4.A Evidence of common ancestry and diversity

Overview

Students use Phylo, a free interactive map of the tree of life, to compare pairs of organisms and find the **most recent group the two share**: the branch that holds their last common ancestor. Some pairs are much closer than they look; others that look alike are not close at all. Along the way students see the tree is built from several lines of evidence (anatomy, fossils, DNA) and that the rank-based classification and the evolutionary tree don't always agree.

Learning goals

- Read a nested classification and identify the most recent group two organisms share.
- Explain that relatedness means sharing a more recent common ancestor, not looking more alike.
- Use DNA similarity and fossil-calibrated divergence estimates as evidence for common ancestry.

You need

Phylo on iPhone or iPad (free, no account): apps.apple.com/us/app/id6827091868, or the web version at phylo-q6r0.onrender.com on any laptop. One device per pair of students works well.

How to compare two organisms in Phylo

1. **Search** for the first organism by common or scientific name (e.g. "humpback whale") and choose it. Its lineage lights up in the tree and the **Info** panel opens.
2. In the Info panel, find **How related?**, type the second organism in *Compare with…* and pick it.
3. Read the result: the **last group they share**, a ladder of the ranks they share and where their lineages part, **when their lineages split** (an estimate, with a range), and for two animals or two plants **their DNA side by side** with the percentage that matches.
4. Switch trees with **Ranks** / **Clades** (in the toolbar; on a phone, under **More**) and read the result again. *Ranks* is the classic kingdom–phylum–class classification; *Clades* is the evolutionary tree, where every group is one whole branch.

Worked example: lion and house cat

Search *lion*, then compare with *house cat*. In both trees Phylo says they last share the family **Felidae**. Their lineages split about **14 million years ago** (likely 12 to 16 million, combined from 19 published studies), and most of their barcode gene (COX1) matches letter for letter. So a lion and a house cat share a recent common ancestor: both descend from one early cat.

Your turn: five pairs

Before you look, predict which two pairs are the closest. Then, for each pair, record the last group they share in each tree, Phylo's estimate of when they split (write *none* if it has no published estimate), and whether they are closer than you expected. Pairs 1, 2, 4 and 5 are all animals, so Phylo can also line up their DNA: note the percentage that matches, and which pair matches most.

Pair (search these names)	Last shared group, **Ranks**	Last shared group, **Clades**	Split (years ago)	Closer than expected?
1. **Humpback whale** and **hippopotamus**				
2. **Chicken** and **American crocodile**				
3. **Human** and **button mushroom**, then **human** and **English oak**				
4. **Little brown bat** and **chicken**				
5. **Great white shark** and **bottlenose dolphin**				

Answer key and discussion

Answer key

Group names come from the GBIF Backbone Taxonomy (Ranks) and the Open Tree of Life (Clades), split estimates from TimeTree. Wording and numbers in the app can change as these sources are updated, so accept answers that name the same group.

Pair	Ranks	Clades	What it means
1. Whale and hippo	Class **Mammalia** (GBIF files whales under order Cetacea, hippos under Artiodactyla)	**Whippomorpha**, the branch of whales and hippos, inside the even-toed hoofed mammals	Whales and hippos share a more recent common ancestor with each other than either does with pigs, cows or deer: the hippo is the whale's closest living relative. Whales got their own order long before DNA evidence.
2. Chicken and crocodile	Phylum **Chordata** (GBIF: class Aves vs class Crocodylia)	**Archosauria**, crocodilians and birds	Birds and crocodilians share a more recent common ancestor than crocodilians do with lizards and snakes. Birds are a branch inside the reptiles, so “Reptilia” without birds is not a natural group.
3. Human and mushroom; human and oak	Different kingdoms for both: “related only through the deepest branches of life”	Human + mushroom: **Opisthokonta**. Human + oak: **Eukaryota**	Animals and fungi share a more recent common ancestor than animals and plants do: in this sense we are closer to a mushroom than to a tree. Separate kingdoms cannot show this.
4. Bat and chicken	Phylum **Chordata**	**Amniota**: mammals, reptiles and birds	Both fly, but their last common ancestor did not: wings evolved separately in bats and birds (convergent evolution). A bat is far closer to a whale than to a bird.
5. Shark and dolphin	Phylum **Chordata**	**Gnathostomata**, the jawed vertebrates	Same streamlined shape, but the dolphin is a mammal: it shares a more recent common ancestor with the hippo, and with us, than with any shark. Shape reflects the job (fast swimming), not ancestry.

Expected DNA results: the whale–hippo pair, the most recent split, matches most; the three deeper splits match less, and at that depth the differences flatten out, because a short gene can only change so much. Pair 3 cannot be lined up: animals, fungi and plants are barcoded with different genes.

Discussion prompts

1. Pair 5 looks alike and pair 1 does not. What does that say about judging relatedness by appearance? What evidence does Phylo use?
2. For which pairs did Ranks and Clades disagree? Why might a classification made before DNA sequencing differ from one built from it?
3. Is “reptiles” (without birds) a natural group? Use pair 2 to explain what makes a group natural: one ancestor and all of its descendants.
4. Phylo shows each split time with a range and the number of studies behind it. Why is a range more honest than one number? What would narrow it?
5. Pick two more organisms you are curious about, predict their last shared group, then check.

Teacher notes

- **“Last shared group”** is the smallest branch holding both organisms; their last common ancestor sits at its base. Closer relatives share a smaller group.
- **Ranks vs Clades.** Ranks is the GBIF classification, which keeps some traditional groups that are not whole branches (dashed ring). Clades is the Open Tree of Life, built from thousands of published phylogenies; where they disagree, it reflects the current evidence.
- **Split times** are TimeTree estimates combining published molecular-clock studies calibrated with fossils. Treat them as “about”; some pairs have none.
- **DNA side by side** compares one barcode gene (COX1 for animals), not whole genomes: a rough guide to relatedness, not a measure of it.
- **Extension (10 min).** With the whale selected, open **Globe** and slide the timeline back to about 50 million years ago, when the earliest whales appear in the fossil record; tap **Now** to see where they are dug up today.

Phylo – Tree of Life Explorer is free, with no account, no ads and no tracking. Data: GBIF, Open Tree of Life, Wikipedia, NCBI, TimeTree (none endorses Phylo). Web version: phylo-q6r0.onrender.com/classroom · patrick@stratosdigitalllc.com · Free to copy for classroom use.

Stratos Digital LLC · 2026