

Name:

Date:

Student Exploration: Cladograms

Gizmo Warm-up

Cladistics is a method of hypothesizing the **evolutionary** relationships between species. A **cladogram** is a branching diagram that illustrates these relationships.

To begin, make sure **Plants** is selected for the **Organism group** and **Morphological** is selected for the **Data** type. Click on one of the characteristics to the left of the table on the TABLE tab. Information about the characteristic will be shown on the ORGANISMS tab.

Activity A:	Get the Gizmo ready:	
Morphological cladogram	 Check that Plants and Morphological are still selected for the group and data type. 	

Question: How do you build a simple cladogram based on physical characteristics?

- <u>Fill in</u>: Clicking one of the boxes of the table will add a check mark to indicate the presence of a characteristic. Fill in the table, then select **Check table** and adjust any of the boxes you may have filled in incorrectly.
- 2. <u>Organize:</u> Now you are ready to organize the table.
 - A. Drag the arrows () below the table to order the organism columns from fewest characteristics on the left to most on the right.
 - B. Drag the arrows to the right of the table to order the characteristics from fewest organisms on the top to most on the bottom.
- 3. <u>Build</u>: Select the CLADOGRAM tab at the top left. The goal of a cladogram is to show the relationships among a group of organisms. Organisms that are most closely related should share the most recent common ancestor (highest branch on the tree). Organisms that are most distantly related should share the oldest common ancestor (lowest branch on the tree).

Click the segments on the cladogram template to build your own cladogram that shows how you think the different plants are related.

Sketch you cladogram in the space to the right.

Answer the following questions based on your cladogram.

- A. Which two organisms are most closely related?
- B. Which organisms are most distantly related?





- organisms B and C descended from a common ancestor (D)
- common ancestor (D) is more recent than the common ancestor (E) of
- organisms A, B, and C descended from a common ancestor (E).

Describe how the organisms in your cladogram are related through common ancestors. A. Which two organisms share the most recent common ancestor?

- B. How many common ancestors between algae and moss are represented in the cladogram?
- 5. <u>Label</u>: The purple lines represent a characteristic change, or **adaptation**. On the cladogram above, organisms B and C share characteristic 3. Organism B gained characteristic 1 after diverging from organism C. Only organism C possesses characteristic 2.

In the Gizmo, select a purple line to open a text box and fill in the characteristics.

Based on your cladogram, from oldest to newest, in what order did the three characteristics (flowers, multicellularity, and xylem/ phloem) evolve?

Activity B:	Get the Gizmo ready:	0
Cladogram practice	 Select Insects for the organism group and Morphological for the data type. Select the ORGANISMS tab. 	10

Introduction: In this activity, you will practice creating larger, more complex cladograms.

Question: How do you create cladograms with more complex branching?

 <u>Build</u>: As you did in activity A, use the information provided to fill in the table of characteristics for insects. Check that your table is correct. On the CLADOGRAM tab, use your table to create an insect cladogram. Make adjustments until you achieve the lowest possible parsimony score, and then compare your cladogram to the accepted cladogram. When you are done, sketch your cladogram in the space to the right.



Which two insects are most closely related?

Based on your cladogram, from oldest to newest, in what order did the four characteristics (foldable wings, larval stage, stinger, and wings) evolve?



Activity C:	Get the Gizmo ready:	4
Molecular cladograms	 Select the ORGANISMS tab, Primates, and Molecular data. 	1

Introduction: The creation of cladograms has been improved with protein and DNA sequencing. As organisms evolve, some parts of these sequences may change as one amino acid is substituted for another. Scientists can count these changes to try to reconstruct evolutionary relationships. In this activity, you will use protein sequence data to create a cladogram.

Question: How do scientists use molecular data to construct cladograms?

- <u>Collect data</u>: On the ORGANISMS tab, the amino acid sequences for the protein cytochrome c oxidase in six primate species are listed.
 - Select the top organism name on the table.
 - Check "Show differences."
 - Compare the amino acids in that species to the amino acids in the other five species. Use this data to fill in the table on the TABLE tab.

Select the organism in the second row. Compare the amino acids in this organism to the other four below. Fill in the table. Continue this process until the table is complete. Select **Check table** to make sure the table was filled in correctly.

- 2. <u>Organize</u>: Look at your table. Which two organisms have the fewest differences? Drag those two species to the bottom two rows. Of the remaining four species, use the right-most row of the table to order the species from fewest differences at the bottom to most differences at the top.
- 3. <u>Build</u>: Build a primates cladogram with the best possible parsimony score. When you are done, sketch your cladogram in the space to the right.



The woolly and howler monkeys are very different from the human and chimp, so they appear at the other side of the cladogram, but they are very similar to each other so they likely share a more recent common ancestor. (Both woolly and howler monkeys are "New World" monkeys native to South America.)

4. <u>Build</u>: Using the same method, create a molecular cladogram for the **animals** group. When you are done, sketch your cladogram in the space to the right.

