Name: _____   Date: _____

Student Exploration: Cladograms

Vocabulary: adaptation, amino acid, amnion, artiodactyla, bipedal, clade, cladistics, cladogram, convergent evolution, evolution, flower, mammary glands, molecular, morphological, multicellular, parsimony, sagittal crest, phloem, selenodont teeth, SNP, xylem

Prior Knowledge Questions (Do these BEFORE using the Gizmo.)

1. Look at the images below. Which two organisms do you think are most closely related?

Worm   Deer   Turtle
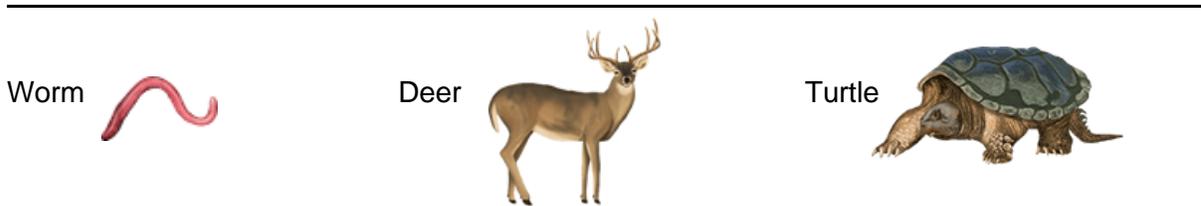
2. Why do you think so? _____

_____

Gizmo Warm-up

Cladistics is a method of hypothesizing the **evolutionary** relationships between species. A **cladogram** is a branching diagram that illustrates these relationships. For example, the cladogram on the right shows that deer are more closely related to turtles than to worms. In the *Cladograms* Gizmo, you will use **morphological** (physical characteristics) and **molecular** data to create cladograms.

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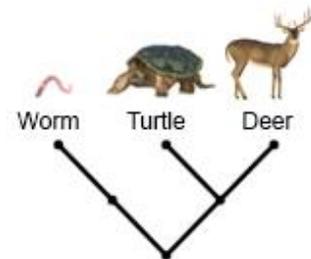
To begin, make sure **Plants** is selected for the **Organism group** and **Morphological** is selected for the **Data** type. Click on one of the characteristics to the left of the table on the TABLE tab. Information about the characteristic will be shown on the ORGANISM tab.

Using the information on the ORGANISM tab, describe each of the characteristics below.

- **Xylem** and **phloem**: _____

  _____

- **Flowers**: _____

- **Multicellularity**: _____

Activity A: **Morphological cladogram**	Get the Gizmo ready: • 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?

1. Fill in: Using what you learned in the warm-up, fill in the table. Clicking one of the boxes of the table will add a check mark to indicate the presence of a characteristic. Then, select **Check table** and adjust any of the boxes you may have filled in incorrectly.

   Which organism has the fewest shared characteristics? _____

2. Organize: Now you are ready to organize the table.

   A. How many characteristics (check marks) does each organism have?

   Algae: _____   Arabidopsis: _____   Cycad: _____   Moss: _____

   Drag the arrows (↔) below the table to order the organism columns from fewest characteristics on the left to most on the right.

   B. How many organisms have each characteristic?

   Multicellularity: _____   Xylem and phloem: _____   Flowers: _____

   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. Build: 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 organism is most distantly related from the other three? _____

(Activity A continued on next page)

Activity A (continued from previous page)

4. <u>Analyze:</u> On a completed cladogram, the orange dot that connects two branches represents a common ancestor. In the cladogram to the right, organisms B and C descended from a common ancestor (D) that was more recent than the common ancestor (E) of organisms A, B, and C.
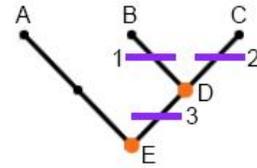
   Describe how the organisms in your cladogram are related through common ancestors.

   _____

   _____

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 either gained or lost characteristic 1 after diverging from organism C.

   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?

   _____

6. <u>Score:</u> The **parsimony** principle states that the most likely solution is usually the simplest. In general, biologists try to create cladograms that require the fewest evolutionary changes. For example, it is more likely that xylem and phloem evolved once rather than multiple times. The "parsimony score" calculates how many changes occur in a given cladogram.

   A. How many changes (purple lines) occurred in your cladogram? _____

   B. Select **Show parsimony score**. What is the score of your cladogram? _____

   C. Select **Show best possible parsimony score**. Have you created a cladogram with

   the least number of possible characteristic changes? _____

7. <u>Revise:</u> If you have not created a cladogram with the lowest possible parsimony score, adjust the cladogram until you do. Make sure that the organisms are ordered from fewest shared characteristics on the left to most shared characteristics on the right.

   Select **Show accepted cladogram.** Does your cladogram match the scientifically accepted

   cladogram? _____

   Click the camera (📷) to take a snapshot of your cladogram. Right click the image, select **Copy**, and then paste the image into a blank document that you will turn in with this sheet.

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

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

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

1. <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, take a snapshot of the cladogram and save it in your document.

   What is the lowest possible parsimony score? _____

   Which two insects are most closely related? _____

2. <u>Build</u>: Create cladograms for the **Primates** and **Animals** groups (skip the Artiodactyla for now). These cladograms are a little more complex, and you may have to include multiple branches at the same level, such as in the example shown at the right. When you have built cladograms with the lowest possible parsimony score, compare them to the accepted cladogram.
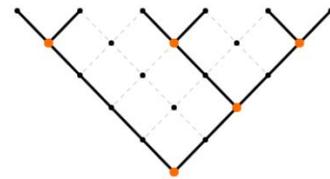
   Take snapshots of the finished cladograms and save them in your document.

3. <u>Observe</u>: Sometimes a trait can evolve separately in different groups. For example, both bats and birds have wings, but their common ancestor did not have wings.

   In the **Animals** cladogram, which trait evolved two different times? _____

4. <u>Think and discuss</u>: What could cause similar traits to evolve independently in different species?

   _____

   _____

   _____

   Species that live in the same environment or face similar threats may need to develop traits that help them adapt to their situations. For example, hedgehogs and porcupines independently evolved prickly spines to protect themselves from predators. This process is called **convergent evolution,** where similar characteristics evolved in species of different lineages.

Activity C:	Get the Gizmo ready:	
Molecular cladograms	• Select the ORGANISMS tab, **Plants**, and **Molecular** data.	

Introduction: The creation of cladograms has been improved with the advent of protein and DNA sequencing. A protein is a sequence of hundreds of **amino acids**. 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?

1. Collect data: On the ORGANISMS tab, the amino acid sequences for the protein cytochrome c oxidase in four plant species are listed. Select the top organism name on the table. Compare the amino acids in that species to the amino acids in the other three species. If an amino acid does NOT match the amino acid in the top row, click the box to turn it orange. Mark all of the differences in the entire sequence as you scroll to the right. Use this data to fill in the table on the TABLE tab.

   Press **Reset**. Select the organism in the second row. Compare the amino acids in this organism to the other two 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. Organize: Look at your table.

   A. Which two organisms have the fewest differences? _____

      Use the arrows to the right of the table to drag those two species to the bottom rows.

   B. Which organism is most similar to the two organisms in part A above? _____

      Drag this organism to the second row of the table.

   C. Which organism is the most different compared to the other three? _____

      This organism should be positioned at the top of the table.

3. Build: Select the ORGANISMS tab. If you have organized the table correctly, the species should be organized from least-related on the left to most-related on the right.

   Build a cladogram as you did when **Morphological** was selected. Draw it in the space provided on the right.

   (Activity C continued on next page)

Activity C (continued from previous page)

4. <u>Score</u>: Select **Parsimony score** and **Best possible parsimony** score. Did you create the

   best possible cladogram? _____ If so, take a snapshot and add it to your document.

5. <u>Organize data</u>: Select **Primates**. Turn on the **Show differences** check box and select the top organism in the table. This will automatically highlight the differences between the other organisms and the one selected, which will allow you to complete the table more quickly.

   Fill in the table. Which two species 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.

6. <u>Build</u>: Build a primates cladogram with the best possible parsimony score. Take a picture of the cladogram and add it to your document. Select **Show accepted cladogram**.

   Does your cladogram match the accepted cladogram? _____

   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.)

7. <u>Build</u>: Using the same method, create a molecular cladogram for the animals group. When you are done, take a snapshot and save it in your document.

8. Compare: Compare the molecular cladograms for plants, primates, and animals to the morphological cladograms. Do these cladograms match? Explain.

   _____

   _____

9. <u>Discuss</u>: How does the molecular data help reinforce the evolutionary relationships you

   inferred from the morphological data? _____

   _____

   _____

| **Activity D:** **Rewriting history** | Get the Gizmo ready:

• Select **Artyodactyla** and **Morphological** data.
• Select the ORGANISMS tab. | |
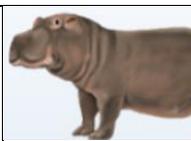
Introduction: In some cases, molecular data can give insight into relatedness that morphological data cannot. That was true for the Artiodactyla, a group of even toed mammals.

Question: Can molecular data to create cladograms that are more accurate?

1. Form a hypothesis: Which data type, morphological or molecular, do you think will allow you

   to create a more accurate cladogram? Explain. _____

   _____

   _____

2. Build: Create the best possible cladogram using the morphological data. Paste a picture of the cladogram in your separate document.

    A. Based on this cladogram, which organism is most closely related to cow and deer?

       _____ Why? _____

       _____

    B. Which organism shares the fewest traits with the others? _____

3. Build: Switch to the Molecular data type. Notice that the molecular data used here are **SNPs**, or single-nucleotide polymorphisms. A SNP is a difference in a nucleotide in a specific location of an organisms DNA that varies among individuals. Create the best possible cladogram. Paste a picture of the cladogram in your separate document.

    A. Is this cladogram the same as the molecular cladogram? _____

    B. How do the two cladograms differ? _____

       _____

       _____

4. Compare: Select **Show accepted cladogram.** Do either of your cladograms match the

   accepted cladogram? _____

(Activity D continued on next page)

Activity D (continued from previous page)

5. <u>Discuss</u>: Where does the whale appear in the molecular cladogram? Is that surprising?

    _____

    _____

    Until recently, scientists used a cladogram based on morphological characteristics similar to the one you created. A parsimonious morphological cladogram can be created if you assume that **selenodont** teeth and three-part stomachs evolved only once.

    This is not, however, consistent with the molecular data. Based on this data, whales and hippos are related. Camels are distantly related to the other artiodactyls and must have evolved multi-part stomachs and selenodont teeth independently. While it is based on a wealth of molecular data, this new view of Artiodactyla is still new and somewhat controversial.

6. <u>Create</u>: Select **Insects** for the **Organism group** and **Molecular** for the **Data** type. As you have done previously, use the Gizmo to create a parsimonious cladogram.

    Is your cladogram equivalent to the accepted cladogram? _____

    In this case, it is ok if your cladogram does not match the accepted cladogram. This Gizmo uses small numbers of characteristics and short molecular sequences to allow for manageable data analysis. In this case, the limited amount of molecular data is not enough to sort out a relationship between the different insect groups.

    Scientists must consider many traits and large molecular data sets to create an accurate picture of evolutionary history. They also must weigh the significance of major evolutionary changes, like skeleton development, versus less significant changes, like skin color.

7. <u>Discuss</u>: Are molecular or morphological data more useful when creating cladograms?

    Explain. _____

    _____

    _____

8. <u>Think and discuss</u>: What can a scientist do to improve the accuracy of their cladograms?

    _____

    _____

    _____