Phylogenetic Mana-trees

Using Genomic Data to Evaluate Evolutionary Relationships

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Grade Level	9th – 12th Grade	**Time Frame**	200 minutes
Subject	Science	**Duration**	3-4 class periods
Course	Biology		

Essential Question

How do molecular data and morphological data compare when predicting phylogenetic relationships? How are molecular and morphological data used to determine manatees' evolutionary relationships?

Summary

In this lesson, students will develop cladograms and phylogenetic trees to predict manatees' evolutionary relationships to several other mammals. By comparing trees based on morphological characteristics with trees made from protein sequences, students will deepen their understanding of why scientists use multiple lines of evidence to determine relationships among organisms. This lesson includes the use of UniProt, a free online database, as a tool to collect and analyze protein sequences.

Snapshot

Engage

Students draw cladograms to predict how manatees are classified.

Explore

Students analyze protein sequence data from the UniProt online database to determine phylogenetic relationships among several organisms of their choice.

Explain

Students synthesize what they learned from the Explore investigation and discuss the value of using molecular and morphological data for classifying organisms and their evolutionary relationships.

Extend

Students use UniProt to construct a phylogenetic tree for manatees and compare it with their previous prediction(s), as well as recently published phylogenetic trees.

Evaluate

Using the tree comparisons from the Extend section, students explain how genetic and morphological data serve as evidence for manatees' evolutionary relationships.

Standards

ACT College and Career Readiness Standards - Science (6-12)

IOD202: Identify basic features of a table, graph, or diagram (e.g., units of measurement)
IOD304: Determine how the values of variables change as the value of another variable changes in a simple data presentation
IOD403: Translate information into a table, graph, or diagram
IOD505: Analyze presented information when given new, simple information
SIN201: Find basic information in text that describes a simple experiment
SIN404: Identify similarities and differences between experiments
SIN502: Predict the results of an additional trial or measurement in an experiment
SIN702: Predict the effects of modifying the design or methods of an experiment
EMI301: Identify implications in a model
EMI401: Determine which simple hypothesis, prediction, or conclusion is, or is not, consistent with a data presentation, model, or piece of information in text
EMI402: Identify key assumptions in a model
EMI403: Determine which models imply certain information
EMI502: Determine whether presented information, or new information, supports or contradicts a simple hypothesis or conclusion, and why
EMI504: Determine which models are supported or weakened by new information
EMI505: Determine which experimental results or models support or contradict a hypothesis, prediction, or conclusion
EMI603: Use new information to make a prediction based on a model

Next Generation Science Standards (Grades 9, 10, 11, 12)

HS-LS4-1: Communicate scientific information that common ancestry and biological evolution are supported by multiple lines of empirical evidence.

Oklahoma Academic Standards (Biology)

B.LS4.1: Communicate scientific information that common ancestry and biological evolution are supported by multiple lines of empirical evidence.
B.LS4.1.1: Genetic information provides evidence of common ancestry and diversity. DNA sequences vary among species, but there are many overlaps; in fact, the ongoing branching that produces multiple lines of descent can be inferred by comparing the DNA sequences of different organisms. Such information is also derivable from the similarities and differences in amino acid sequences and from anatomical and embryological evidence.

Attachments

- Lesson-Slides-Phylogenetic-Mana-trees.pptx
- Protein-Alignment-Notation-Phylogenetic-Mana-trees.pdf
- Student-Slides-Phylogenetic-Mana-trees - Spanish.pptx
- Student-Slides-Phylogenetic-Mana-trees.pptx

Materials

- Lesson Slides (attached)
- Student Slides (attached and linked)
- Protein Alignment Notation handout (attached; optional)
- Chromebooks or laptops
- Internet access
- Uniprot.org

15 minutes

Engage

Teacher’s Note: Prerequisite Knowledge

To successfully complete this lesson, students should already have a working knowledge of what cladograms and phylogenetic trees are and how they are used (found in the same standard as this lesson’s, HS-LS4-1) and the general process of how proteins are produced from genetic code (HS-LS3-1). If students need more practice with phylogenetic tree basics, the Evolution Lab from NOVA is a good tool to explore.

Additionally, the College Board's AP Biology curriculum provides a student investigation of DNA sequences and evolutionary relationships using the BLAST tool from NCBI. That investigation may be a useful prerequisite activity.

Teacher’s Note: Maintain Curiosity

Manatees’ closest relatives are elephants and hyraxes. However, do *not* give this information to students yet! Throughout the lesson, the goal is for students to use their phylogenetic trees to investigate this relationship themselves.

Begin the lesson using the attached **Lesson Slides**. Display **lesson slide 3** to share the lesson’s essential questions. Display **lesson slide 4** to go over the lesson’s learning objectives. Review these slides with students to the extent you feel necessary.

Teacher’s Note: Student Slides

The investigation handout for this lesson is the **Student Slides**, provided as a PowerPoint file (attached) and as a Google Slides presentation (linked here). The Google Slides presentation has been the most effective way for students to collaborate on the work. Use of the PowerPoint version is not preferred, but the slides can be printed out as student handouts for use as they are or in science notebooks, if necessary.

The Student Slides contain screenshot images from the UniProt website and align with placeholders in the Lesson Slides. Students can follow along with their slides as you walk through the demonstration, and the screenshots can serve as a point of reference to revisit later.

Display **lesson slide 5 (student slide 2)** and review cladogram structure as a formative assessment before continuing. Revisit this in greater detail in the Explain section if students struggle to remember the relationships illustrated in a cladogram or need more practice interpreting the models.

Display **lesson slide 6**. Share with students the list of organisms (manatee, seal, hyrax, narwhal, elephant) that they will investigate later in the lesson. Ask students to create their own cladograms based on how these five organisms look and what they know about these organisms on **lesson slide 7 (student slide 3)**. Students should be able to defend with evidence why they placed each organism where they did.

Go to **lesson slide 8**. Discuss why students’ cladograms look different from one another even though they have the same organisms. Using the strategy Partner Speaks, have students give their reasoning for placing organisms where they did. Ask students what they could do to see which cladogram is most accurate, or how they could make a more accurate one.

Student Answers

All of the questions that students answer in this section will be addressed later in the lesson, so the correct answers should *not* be given at this point. This can be used as a formative assessment.

90 minutes

Explore

Before students begin the UniProt investigation, display **lesson slide 9.** Take some time to discuss the information on the slide so students have context for their work and a basic understanding of the UniProt database. Go to **lesson slide 10 (student slide 5)** to help students prepare their setup for the activities.

Go to **lesson slide 11 (student slide 6).** In partners or in small groups, have students select five organisms to investigate. Each animal should be in the same class (e.g., Mammalia, Amphibia, etc.). Once students have selected their animals, have students read the directions on **student slide 7**. Then, demonstrate how to use the UniProt database for Part 1 using **lesson slides 12–13 (student slide 8)**.

Part 1: Collecting Sequences

Students should search the UniProt database for "hemoglobin subunit alpha" (HBA) sequences from each of their five organisms. They should copy the FASTA sequence for each organism and paste it in their data table on **student slide 9**.

See the attached **Protein Alignment Notation** handout as a reference for how to interpret protein sequences. Feel free to pass it out to students if you feel they are ready for the additional information. Otherwise, it is not a necessary handout for students if you feel it might confuse them or distract from the lesson.

Go to **lesson slide 14 (student slide 10)**. Before moving on to the next activity, student groups should predict what they think the cladogram for their organisms will look like based on the HBA sequences.

Part 2: Comparing Sequences

Have students read the directions on **student slide 11**. Once again, show students how to complete the steps for Part 2 within the UniProt database using **lesson slides 15–16 (student slides 12–13)**. Once the procedure has been demonstrated, give students time to complete their comparisons and fill out the table on **student slide 14**.

Part 3: Analyzing Sequences

Before continuing, display **lesson slide 18** and take a moment to address the differences between cladograms and phylogenetic trees. At this point, inform students they will use phylogenetic trees for the rest of the lesson.

Have students read the directions on **student slide 15**. Then, go to **lesson slide 19 (student slide 16)**. Based on the comparisons of what percentage of the sequences are identical (% similarity data), ask students to create another predicted phylogenetic tree for their organisms. Have students answer the questions on **lesson slide 20 (student slide 17)**.

Using the procedural steps outlined on **student slide 18**, students should put all five HBA sequences into the UniProt alignment tool used in Part 2, which will generate a phylogenetic tree from the data. Go to **lesson slide 21 (student slide 19)**. Students should either take a screenshot of the UniProt tree or redraw it themselves to include with their predicted tree(s).

40 minutes

Explain

Display **lesson slide 22**. Have student groups share out their findings from the investigation. They should specifically address how well their predicted tree and molecular protein tree align and why there are (presumably) differences between them.

Teacher's Note: Revisiting Prior Knowledge

If students lack sufficient prior knowledge about phylogenetic trees, **lesson slide 23** is an ideal place to take some time to address the elements of phylogenies and how they are used for analysis. Lean on student knowledge as much as possible. Ask them to identify and explain the information before resorting to direct lecture.

Display **lesson slide 24**. Provide students with some background information about conserved sequences (HBA) and why scientists might prefer them over other molecular data for these analyses. It is assumed that students already understand the relationship between DNA and protein synthesis (HS-LS3-1), concepts which are necessary for students to understand before the upcoming discussions.

Display **lesson slides 25–26**. Using the Roundabout Conversations strategy, have students answer the following questions one at a time through movement and discussion:

- How do we know which of our phylogenetic trees is most likely to be accurate?
- What steps could we take to find more evidence to support the tree(s) we have constructed or to improve the accuracy of our tree(s)?
- Why is analyzing protein sequences a useful way to classify organisms or to determine organisms' evolutionary relationships?
- Is a tree made from molecular data (e.g., DNA or protein sequences) more or less reliable than one made from derived (i.e., morphological) characteristics? Why?

Before moving on to the next activity, have a whole-class discussion to validate the information that students shared in their small groups and address any knowledge gaps or misconceptions that came up.

From their conversations, students should conclude that there is value in using both morphological and molecular data, but molecular data is more reliable. Additionally, students should recognize that protein sequences are useful for classification since proteins are what give organisms their characteristics. This detail may not be immediately obvious to them.

Display **lesson slide 27**. To transition to the Extend section of the lesson, remind students they have constructed a morphological tree for manatees' evolutionary relationships. Ask students what their next step would be if they were scientists trying to improve or support their original manatee trees.

40 minutes

Extend

Display **lesson slide 28 (student slide 20)**. Ask students to return their focus to manatees and the other four organisms from the Engage section. Using **student slides 21–24**, students should repeat the same processes from the Explore investigation to collect HBA sequences and construct a phylogenetic tree for the manatee.

Go to **lesson slide 29 (student slide 25).** Once students have the HBA tree from UniProt, ask them to compare it with the cladogram they made in the Engage section using morphological characteristics. They should identify similarities and differences between their predicted morphological cladogram and the molecular protein tree.

Finally, provide students with a simplified version of the manatee's phylogenetic tree on **lesson slide 30** to compare it with the other two.

Teacher's Note: Manatee Phylogenetic Tree

The manatee's phylogenetic tree provided in the Lesson Slides is based on numerous trees that have been published since 2010. The provided tree represents the most common relationship supported by a variety of morphological and molecular evidence across these publications. However, it is *highly simplified* for this lesson and does not reflect the complexity of mammalian evolution.

Be sure to share this detail with students so they recognize the tree is an incomplete representation. For a more concrete representation, it may be helpful to search Google Images for pictures of other manatee phylogenetic trees to show students.

Display **lesson slide 31.** Facilitate a group discussion addressing the following:

1. What patterns did you notice among your three phylogenetic trees?
2. What did your group find interesting or surprising?
3. What patterns did you notice across all groups' observations of their trees?

For the first two questions, have student groups share out the similarities and differences they noticed among the three manatee phylogenetic trees and what they found interesting or surprising. For the third question, have students participate in a whole-class discussion to identify patterns across all groups' observations.

Go to **lesson slide 32** and pose the following question: *How is it possible for scientists to get different trees for the same organisms?* After students have shared their thoughts, provide a summary of the major ideas from the discussion. This should reinforce what students have just discussed, but it also is an opportunity to clarify alternative conceptions or fill gaps in students' knowledge.

Go to **lesson slides 33–34.** Based on these conversations, facilitate consensus-building for the class to determine manatees' closest living relative(s). Conclude the discussion by asking students to explain why having different "*mana-trees*" contributes to our understanding of evolution broadly.

15 minutes

Evaluate

Display **lesson slide 35**. Each student should submit two completed trees: the morphological cladogram they created in the Engage section and the HBA molecular tree created in the Extend section using UniProt. If the class consensus tree differs from these, ask students to explicitly identify manatees' closest living relative(s). In addition to the trees, students should include their answers and explanations for the following questions:

1. What evidence did you use and how did you use it to determine manatees' evolutionary relationships?
2. Why do scientists use multiple lines of evidence to determine evolutionary relationships among organisms?

Explanations might be written, oral, or completed as formal class presentations as is appropriate for a given group of students.

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Resources

- AP Central. (n.d.). AP Biology Investigation 3: Comparing DNA Sequences to Understand Evolutionary Relationships with BLAST. College Board. https://apcentral.collegeboard.org/courses/ap-biology/classroom-resources/investigative-labs-comprehensive-links
- Hinkel, D., & U.S. Fish and Wildlife Service. (2012, July 24). Endangered Florida manatee [Photo]. Flickr. https://www.flickr.com/photos/usfwshq/7636816484/in/photostream/
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- K20 Center. (n.d.). Roundabout Conversations. Strategies. https://learn.k20center.ou.edu/strategy/fe96d3de46cfdc1f385aab7e75009704
- NOVA Labs. (n.d.). Evolution Lab. PBS Online by WGBH Educational Foundation. https://www.pbs.org/wgbh/nova/labs/lab/evolution/
- UniProt. (n.d.). UniProt Consortium. https://www.uniprot.org/