

EDUCATOR'S GUIDE

UNITED, BUT DIVERSE

At a Glance

Learning Objective

Build phylogenetic trees and interpret the evolutionary relationships that they represent.

Student Objectives

Construct phylogenetic trees using complementary phenotypic and molecular data.

Use online resources to explore genomic information and molecular phylogenies.

Recognize that uncertainty exists about the true evolutionary relationships among organisms.

Acknowledge that new information continues to improve our understanding of the Tree of Life.

Introduction

This module is designed as a story in which students are applying for an internship at a local college. It is presented in two sections: a “Diagnostic Assessment” and an “Application”.

In the first section, students investigate the relationships among fictitious alien species by comparing shared characteristics using morphological data.

In the second section, students use online resources to gather real DNA sequences on present-day organisms, construct a phylogenetic tree based on this genetic data, and then revise their tree after the addition of a new “Discovery” species.

Targeted Audience:

High school students in grades 11 and 12 (but can be adapted for higher or lower levels)

Duration of Exercise

Three to four class periods (45 minutes each)

Materials Needed

Student handout (One copy per student)

Card Sets A and B (One copy of each per pair)

Discovery Species Cards (Copies dependent on class size)

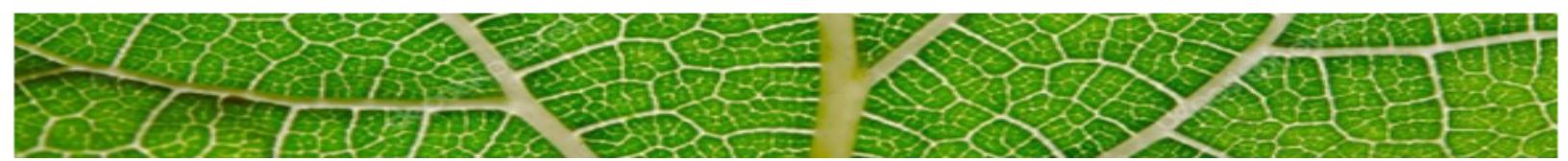
Online Resources #1 and 2 (One copy of each per pair)

Computer/Laptop

Colored Pencils

Scissors





Alignment with Next Generation Science Standards

The activities described in this module align with several Next Generation Science Standards (NGSS). Below, we highlight the NGSS dimensions that are most relevant to this module, and the specific skills that would demonstrate understanding of the core ideas.

Students who demonstrate understanding can:

- HS-LS-1-1** Construct an explanation based on evidence for how the structure of DNA determines the structure of proteins, which carry out the essential functions of life through systems of specialized cells.
- HS-LS-3-2** Make and defend a claim based on evidence that inheritable genetic variations may result from: (1) new genetic combinations through meiosis, (2) viable errors occurring during replication, and/or (3) mutations caused by environmental factors.
- HS-LS-4-1** Communicate scientific information that common ancestry and biological evolution are supported by multiple lines of empirical evidence.
- HS-LS-4-2** Construct an explanation based on evidence that the process of evolution primarily results from four factors: (1) the potential for a species to increase in number, (2) the heritable genetic variation of individuals in a species due to mutation and sexual reproductions, (3) competition for limited resources, and (4) the proliferation of those organisms that are better able to survive and reproduce in the environment.
- HS-LS-4-3** Apply concepts of statistics and probability to support explanations that organisms with an advantageous heritable trait tend to increase in proportion to organisms lacking this trait.
- HS-LS-4-4** Construct an explanation based on evidence for how natural selection leads to adaptation of populations.

Science and Engineering Practices	Disciplinary Core Ideas	Crosscutting Concepts
Developing and using models	Structure and function (LS1.A)	Patterns
Analyzing and interpreting data	Variation of traits (LS3.B)	Systems and system models
Constructing explanations	Evidence of common ancestry and diversity (LS4.A)	Structure and function
Obtaining, evaluating and communicating information	Natural Selection (LS4.B) Adaptation (LS4.C)	Stability and change

Note to the teacher:

If your students are not already familiar with phylogenetic trees, take some time to introduce the concept by using real examples in the biology textbook or pre-made accompanying handouts. You may also want to show a video or include other activities from the following resources:

Evolution NOVA Labs by PBS – Introduces evolution and allows students to explore a phylogenetic tree online

The Origin of Species: Lizards in an Evolutionary Tree by HHMI BioInteractive – Explores the evolution of lizards, their phenotypic traits, and their DNA differences.

Terms to Know

Analogous trait – A character that is similar in structure and function between species, but was not present in the most recent common ancestor. Analogous traits are the result of convergent evolution.

Binomial nomenclature – A formal system of naming species of organisms using a two-part Latin format (genus and species) that was instituted by Carolus Linnaeus in the 18th century. For example, the binomial name, or scientific name, for leopard is *Panthera pardus*.

Clade – A group of organisms that consists of a common ancestor and all of its descendants.

Cladogram – a branching diagram depicting the evolutionary relationships between groups of organisms.

Convergent evolution – the process in which organisms that are not closely related to one another independently evolve similar characteristics due to adaptations to similar environments or ecological niches.

Genotype – The genetic makeup of an organism.

Genus – A taxonomic rank that ranks above species and below family. In the system of binomial nomenclature, genus is the first term used to denote a species of organisms (e.g. *Panthera* for leopard).

Homologous trait – A character that is similar in structure and function between species, and is derived from the same character in the most recent common ancestor.

Most recent common ancestor (or MRCA) – The youngest common ancestor shared by two lineages. On a phylogenetic tree, the node at which two lineages meet represents the MRCA for those taxa.

Outgroup – A species or group of species that diverged *before* the lineage of the group of species that is being studied (the ingroup).

Phenotype – The set of observable characteristics of an organism that results from the interaction of its genotype and the environment.

Phylogenetic tree – A branching diagram that represents the evolutionary history of a group of organisms.

Phylogeny – The evolutionary history of a species or group of species.

Shared derived characteristic (or synapomorphy) – An evolutionary novel characteristic that distinguishes a clade from other organisms. It is present in the most recent common ancestor and then shared among the descendant species.

Species - The basic unit of biological classification and taxonomic rank of an organism. In the system of binomial nomenclature, the species name is the second term used to denote a species of organisms (e.g. *pardus* for leopard), and is also known as the specific epithet.



Educator's Instructional Suggestions

Section 1: Diagnostic Assessment – “Do you have skills to be an intern?”

A checklist of the tasks to complete is found on the first page of the student packet.

Teacher's discretion: student pairs may complete tasks together as a class or at their own pace.

Have Section 2 “Application” handouts and resources ready for pairs who finish quickly.

MATERIALS:

CARD SET A: Alien Species

1. (Optional) Laminate sheets for future use.
2. Before class, cut and organize one deck of alien cards for each pair of students.
3. Student worksheets may be collated together or printed as separate handouts.

ACTIVITY:

- a) **TASK #1** – Arrange the Alien cards using prior knowledge of Biology to hypothesize the evolutionary relatedness among the species.
- b) Teacher can circulate around the room and question choices made by the students. *Why did you place this alien next to this one?*
- c) **TASK #2** – Complete the character matrix by noting which phenotypic characteristics are present or absent in each alien species.
- d) **TASK #3** – Fill in the phylogenetic tree by labeling the evolution of new (derived) characteristics at the appropriate arrows, and identifying the serial number for each species in the appropriate box.
- e) Announce to students that they should leave room next to serial numbers to fill in the scientific name. (See Task #4)
- f) **TASK #4** – Follow the steps in the dichotomous key to identify the alien species.
- g) **TASK #5** – Answer the analysis questions. (See Educator’s Key for answers and notes)
- h) Debrief answers as a whole class.
- i) Have student pairs submit for “approval” from Dr. Wallace-Darwin. (That’s you!)
- j) Students who finish quickly may work on level-appropriate multiple choice and/or open response questions for homework.

Section 2: Application – “You earned the internship!”

A checklist of the tasks to complete is found on the first page of the Application section (DNA border).

Teacher's discretion: Student pairs may complete tasks together as a class or at their own pace.

Have copies of RESOURCE #1 and RESOURCE #2 ready.



MATERIALS:

CARD SET B: 10 present-day animal species

1. (Optional) Laminate sheets for future use.
2. Before class, cut and organize one deck of animal cards for each pair of students.
3. Student worksheets may be collated together or printed as separate handouts.

DISCOVERY SPECIES CARDS

1. Six Discovery Species are included on the last sheet of CARD SET B.
2. Make as many copies as needed so that each pair of students receives one Discovery Species.
3. (Optional) Place one species in one envelope. Have a student pair select one envelope from your stack for their Discovery Species. *For example, 15 pairs of students (30 in total) should have at least 15 envelopes from which to select.*

ACTIVITY:

- a) **TASK #1** – Arrange the species cards using prior knowledge of Biology to hypothesize the evolutionary relatedness among the ten animals.
- b) **TASK #2** – In the box for Tree A, draw a phylogenetic tree that depicts the predicted evolutionary relationships.
- c) **TASK #3** – Computers with internet access are needed. Before using this module in the classroom, check that your school has access to the National Center for Biotechnology Information website (www.ncbi.nlm.nih.gov). See your school administrator or technology specialist if necessary.

If students are searching the database for DNA sequences:

- Students must read RESOURCE #1 carefully and not skip any steps.
- With this resource, students will use the NCBI website to look up the DNA sequence for the hemoglobin alpha protein for each species.
- Open a Word Doc or Google Doc to paste all 10 species' sequences.
- Do not close any tabs. You may need them later.

If educator is distributing DNA sequences:

- Educators can distribute the DNA sequences of the ten species to the students directly if the task of collecting DNA sequence from the NCBI website may be too challenging.
- A file with the DNA sequences of hemoglobin alpha for all 10 species can be found in the supplementary materials.
- The educator should email the DNA file to each student pair for them to input in TASK #4.



d) TASK #4 - Computers with internet access are needed. Prior to use in the classroom, check that your school has access to phylogenetic alignment and analysis website Phylogeny.fr. See your school administrator or technology specialist if necessary.

STUDENTS: Must read RESOURCE #2 carefully. Students will build a computer-generated phylogenetic tree by inputting the collected FASTA files from NCBI and compare it to their predicted phylogeny (Tree A).

EDUCATOR: Practice using Phylogeny.fr prior to administering in class for easier troubleshooting during the exercise. Feel free to contact the corresponding author (Erin McCullough) if needed.

e) TASK #5 – Students copy the generated tree into the box for TREE B.

Note: The branch lengths and red numbers indicate confidence estimates, but are not important for Tree B analysis.

- Students answer the accompanying analysis questions. (See Educator's Key for answers.)

f) TASK #6 – Announce to pairs that an 11th species has been discovered!

- Have each student pair select an envelope containing a discovery species.
- Write the species on the line provided in the student packet.
- PREDICT the phylogenetic position of the 11th species in relation to the original ten species, and draw a new branch for this species in TREE B using a colored pencil.

g) TASK #7 – Students should:

- Use RESOURCE #1 to find the DNA sequence for the discovery species on NCBI.
- Add the DNA sequence for the 11th species to the existing DNA sequence file.
- Follow the instructions on the second page of RESOURCE #2 to add the name and DNA sequence for the 11th species.
- Click "SUBMIT" to generate an updated phylogenetic tree

h) TASK #8 – Answer the analysis questions. (See Educator's Key for answers and notes.)

Beyond the Module – Extensions of Learning

1) Create a three-dimensional phylogenetic tree mobile

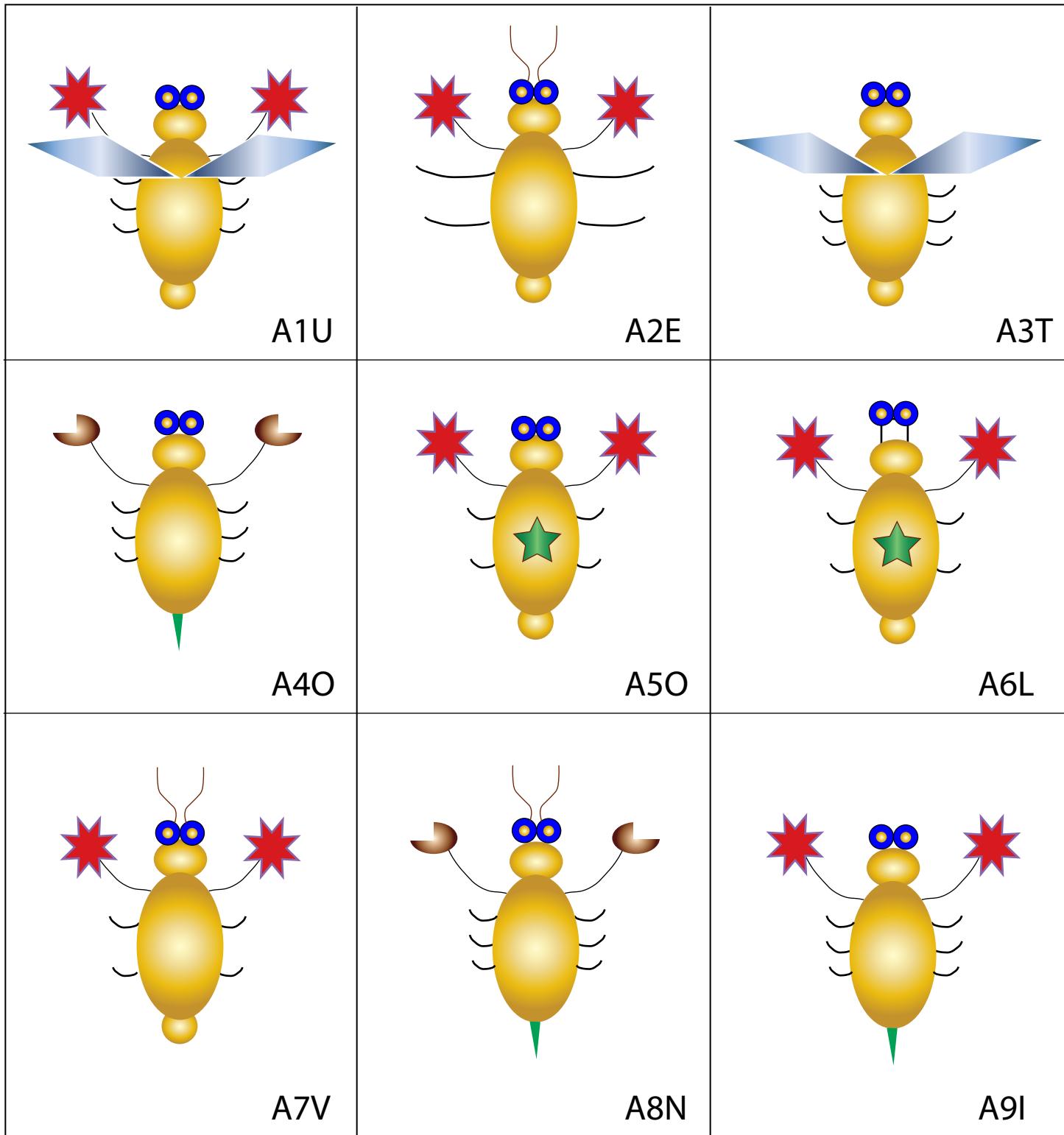
This activity tackles the misconception of relatedness that two-dimensional trees may convey. This extension allows students to physically pivot the character nodes to see the relationships more clearly.

2) Research: What sorts of information can be extracted from molecular data (i.e. DNA sequences)? Medical? Genetic? Historical?

3) Brainstorm: What are some other applications for phylogenetic trees?

Instructors may want to discuss how phylogenetics has become an important tool in a number of diverse disciplines, including Conservation biology (illegal whale hunting), Medicine (disease transmission events), and Agriculture (pesticide sensitivity).

SET A - Alien Insects



Card Set B:
10-Card Set:

Tiger, Dog, Polar Bear, Mouse,
Macaque, Hamster, Chicken,
Chimpanzee, Rat, Human

Tiger
(Panthera tigris)



Dog
(Canis lupus)



Polar Bear
(Ursus maritimus)



Mouse
(Mus musculus)



Macaque
(Macaca mulatta)



Hamster
(Cricetulus griseus)



Chicken
(Gallus gallus)



Chimpanzee
(Pan troglodytes)



Brown Rat
(Rattus norvegicus)



Human
(Homo sapiens)



Discovery Species 6-Card Set:
**Hedgehog, Tarsier, Whale,
Platypus, Bat, Walrus**

DISCOVERY SPECIES

Walrus
(Odobenus rosmarus)



Tarsier
(Carlito syrichta)



Platypus
(Ornithorhynchus anatinus)



Hedgehog
(Erinaceus europaeu)



Killer Whale
(Orcinus orca)



Bat
(Myotis lucifugus)



Phylogenetic Trees: United, but Diverse

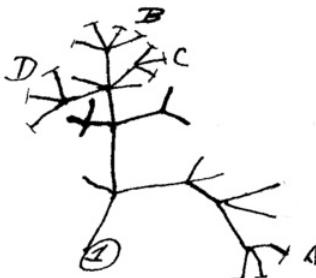


Illustration from Charles Darwin's notebook (1837)

SCENARIO: The Biology Department at your local college is looking to hire paid interns who will assist in the development of the Evolutionary Relationships course (Bio 327). You and your lab partners are definitely interested in this opportunity and attend the information session.

You meet Dr. Wallace-Darwin, a Science Education research fellow, who is screening potential applicants for intern positions. She states that only applicants who successfully complete an initial diagnostic assessment will be offered one of the internships. Still interested, you request the assessment materials.

Section 1: Diagnostic Assessment – Alien Phylogenetics

Using CARD SET A, complete the following tasks and submit them for approval to Dr. Wallace-Darwin. Good Luck!

- Task #1 – Arrange the cards based on shared characters to establish a hypothesis about the relationships between these species.
- Task #2 – Complete Character Matrix 
- Task #3 – Complete Phylogenetic Tree 
- Task #4 – Complete Dichotomous Key 
- Task #5 – Complete Analysis Questions
- Request Teacher Feedback. Approved _____ Revised _____
- Submit completed files for Dr. Wallace-Darwin's approval.



= Indicates that a worksheet is needed

Name: _____

Character Matrix

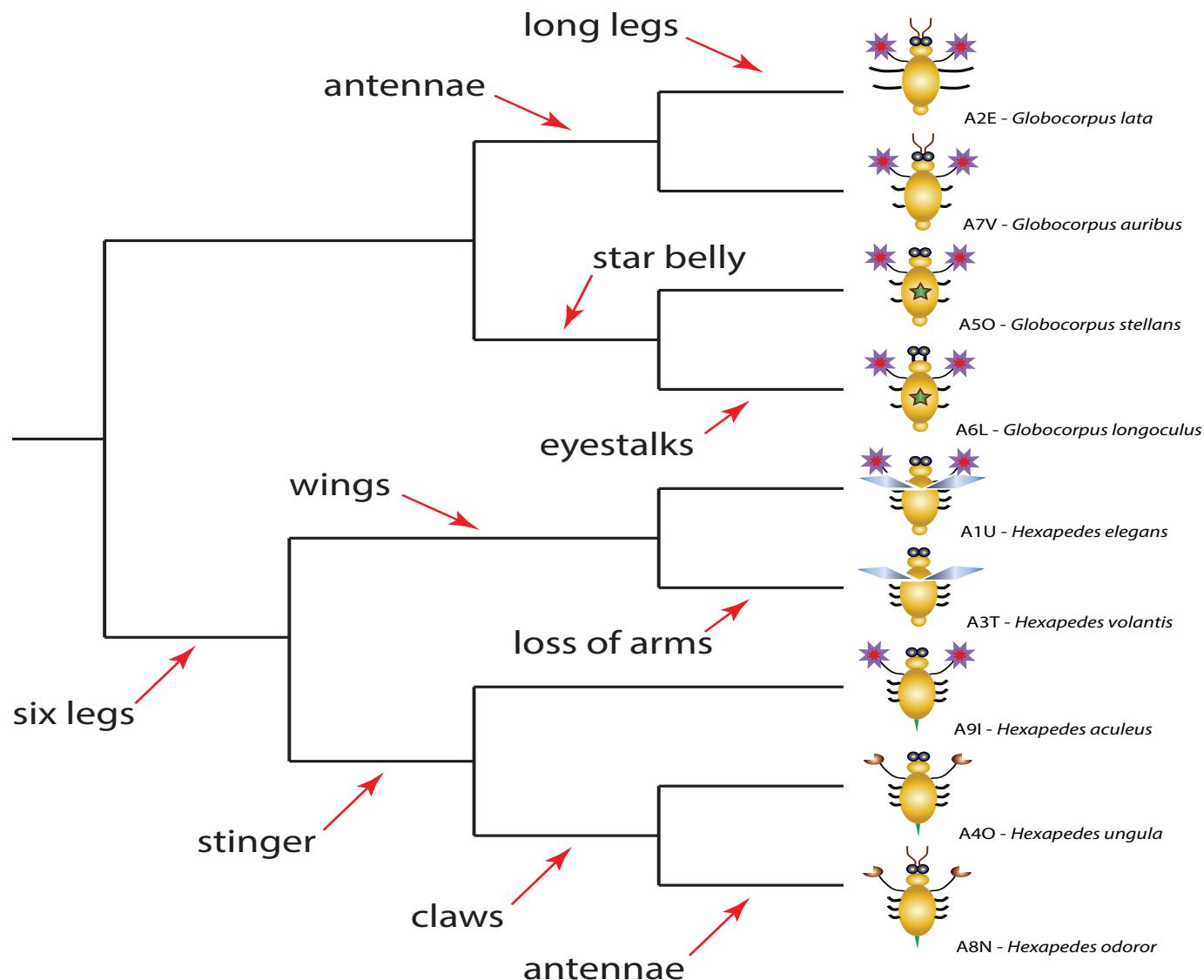
Instructions: For each species, mark an “X” for each character present. Using the information in this matrix, arrange the species based on their shared characters to fill in the phylogenetic tree below.

CHARACTER	A2E	A7V	A4O	A6L	A1U	A3T	A9I	A5O	A8N
SIX LEGS			X		X	X	X		X
WINGS					X	X			
STINGER			X				X		X
STAR BELLY				X				X	
CLAWS			X						X
LONG LEGS	X								
LOSS OF ARMS						X			
EYE STALKS				X					
ANTENNAE	X	X							X

NAME: _____

PHYLOGENETIC TREE

Instructions: Using the information from your character matrix, arrange the alien species based on their shared characters. Identify the evolution of new (derived) characters and label them at the appropriate branch on the tree. At the tip of each branch, identify the species using the dichotomous key provided.





Name: _____

Dichotomous Key

Instructions: A dichotomous key is an organized set of couplets of mutually exclusive characteristics that is used to identify biological organisms. Use the key below to identify each alien species. Write the genus species by the appropriate serial number at the end of this key.

1a – Has 4 legs.....**Go to STEP 2**
1b – Has 6 legs.....**Go to STEP 5**

2a – Has antennae.....**Go to STEP 3**
2b – Has no antennae.....**Go to STEP 4**

3a – Has long legs.....*Globocorpus lata*
3b – Has short legs.....*Globocorpus auribus*

4a – Has star belly and no eye stalks.....*Globocorpus stellans*
4b – Has star belly and eye stalks.....*Globocorpus longoculus*

5a – Has wings.....**Go to STEP 6**
5b – Has a stinger.....**Go to Step 7**

6a – Has arms.....*Hexapedes elegans*
6b – Has no arms.....*Hexapedes volantis*

7a – Has claws.....**Go to Step 8**
7b – Has no claws.....*Hexapedes aculeus*

8a – Has antennae.....*Hexapedes odoror*
8b – Has no antennae.....*Hexapedes unguila*

A1U: *Hexapedes elegans*

A6L: *Globocorpus longoculus*

A2E: *Globocorpus lata*

A7V: *Globocorpus auribus*

A3T: *Hexapedes volantis*

A8N: *Hexapedes odoror*

A4O: *Hexapedes unguila*

A9I: *Hexapedes aculeus*

A5O: *Globocorpus stellans*

Analysis Questions of Diagnostic Assessment

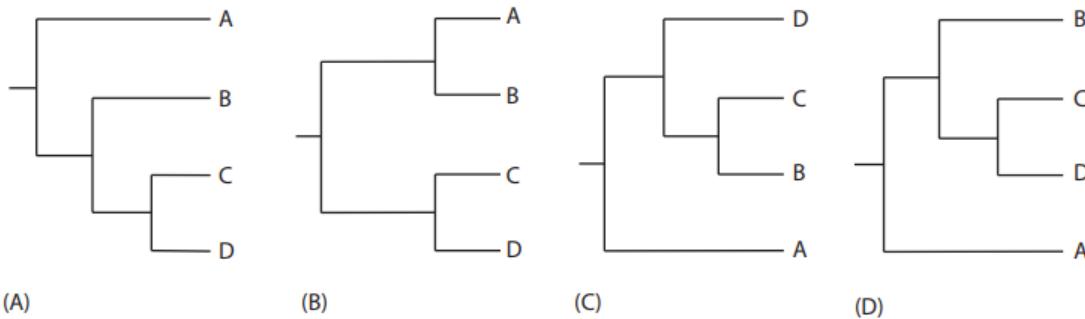
1. The phylogenetic tree that you completed in the lab investigation is also known as a:

- A) cladogram
- B) evolutionary diagram
- C) flow chart
- D) genetic map
- E) morphological diagram

2. Which of the following best explains what a cladogram is?

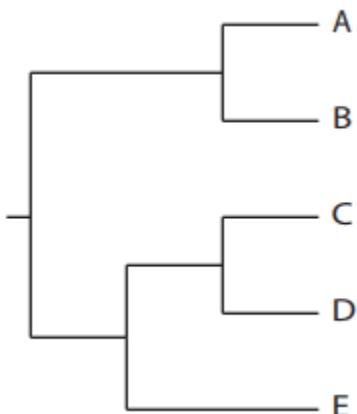
- A) a map showing the geographical location of species
- B) a visualization of the chromosomal similarities between species
- C) a diagram of the analogous similarities between species
- D) a diagram of the evolutionary relatedness of species with branches not drawn to scale
- E) a visualization of the location of genes on chromosomes

3. Which two phylogenetic trees (cladograms) depict the same evolutionary relationships between species A, B, C and D? Explain your answer.

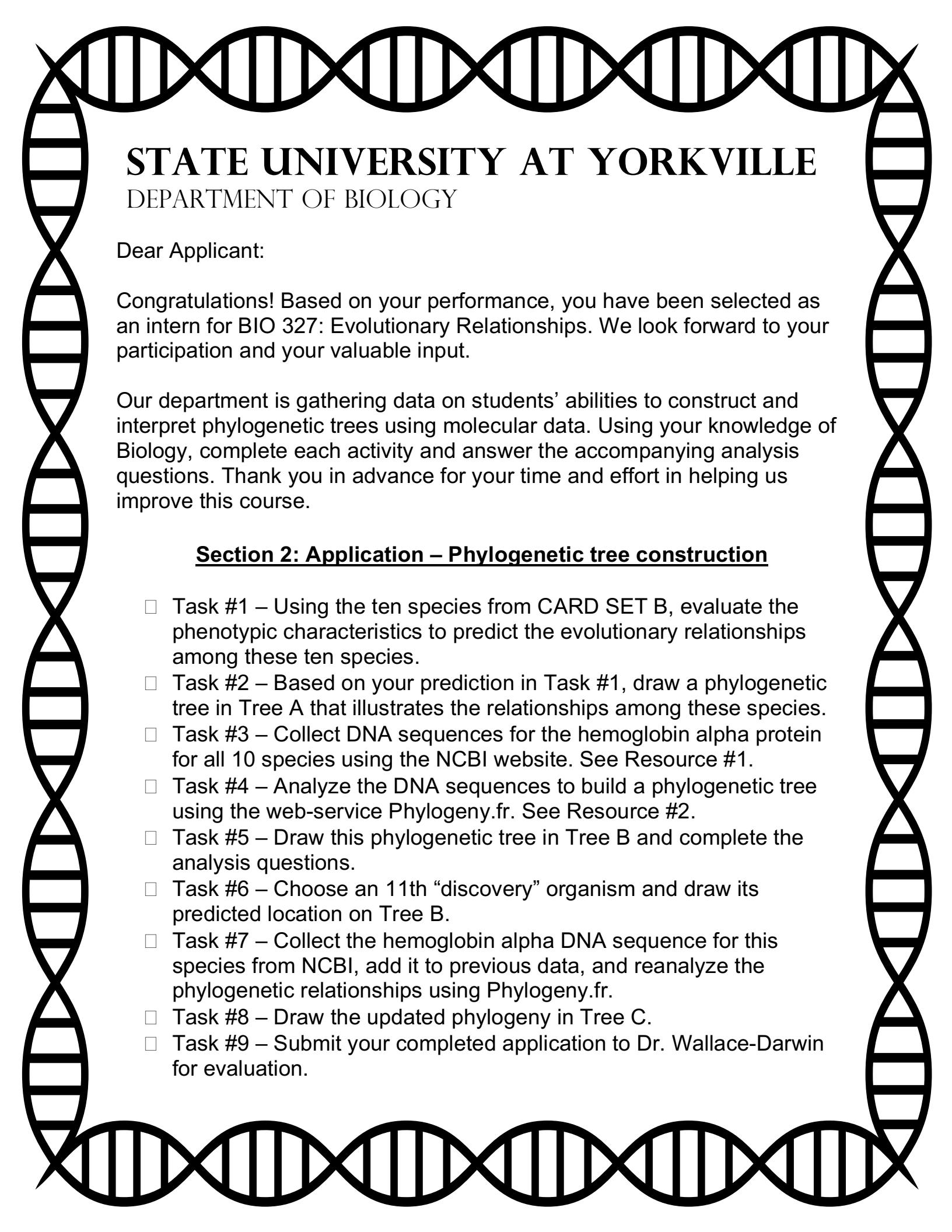


A and D, because they have the same relative branching pattern.

4. Draw a new phylogenetic tree that depicts the same evolutionary relationships as the tree below. Your new tree must change the order of species in at least two positions.



Multiple examples exist as long as the relative branching pattern is the same.



STATE UNIVERSITY AT YORKVILLE

DEPARTMENT OF BIOLOGY

Dear Applicant:

Congratulations! Based on your performance, you have been selected as an intern for BIO 327: Evolutionary Relationships. We look forward to your participation and your valuable input.

Our department is gathering data on students' abilities to construct and interpret phylogenetic trees using molecular data. Using your knowledge of Biology, complete each activity and answer the accompanying analysis questions. Thank you in advance for your time and effort in helping us improve this course.

Section 2: Application – Phylogenetic tree construction

- Task #1 – Using the ten species from CARD SET B, evaluate the phenotypic characteristics to predict the evolutionary relationships among these ten species.
- Task #2 – Based on your prediction in Task #1, draw a phylogenetic tree in Tree A that illustrates the relationships among these species.
- Task #3 – Collect DNA sequences for the hemoglobin alpha protein for all 10 species using the NCBI website. See Resource #1.
- Task #4 – Analyze the DNA sequences to build a phylogenetic tree using the web-service Phylogeny.fr. See Resource #2.
- Task #5 – Draw this phylogenetic tree in Tree B and complete the analysis questions.
- Task #6 – Choose an 11th “discovery” organism and draw its predicted location on Tree B.
- Task #7 – Collect the hemoglobin alpha DNA sequence for this species from NCBI, add it to previous data, and reanalyze the phylogenetic relationships using Phylogeny.fr.
- Task #8 – Draw the updated phylogeny in Tree C.
- Task #9 – Submit your completed application to Dr. Wallace-Darwin for evaluation.

NAME: _____

Phenotypic vs. Molecular Data

Tree A: Construct a phylogenetic tree for 10 species based on phenotypic characteristics.



Student answers will vary. Students may correctly group the nine mammalian species according to their order (primates, rodents, and carnivores) and may also identify the chicken as the outgroup.

Tree A Analysis Questions:

a) Identify at least three characteristics that all 10 species have in common.

All of the animals are vertebrates, so it may be useful to discuss key, shared characteristics among vertebrates, including, but not limited to:

Bilateral symmetry, head, amniotic egg, hinged jaw, forelimbs and hind limbs, vertebrae

b) Explain how shared, derived characteristics are used to infer evolutionary relationships.

Recently evolved characteristics that are shared among organisms are one piece of evidence that suggest they have evolved from a common ancestor. These similarities can be used to group based on their evolutionary relatedness.

c) Select a group of closely related species from your phylogenetic tree and explain why you have grouped them together.

The main purpose of this question is to encourage students to identify specific characteristics as evidence for their hypothesized groupings. The species contained in this exercise contain species from three mammalian orders (primates, carnivores, and rodents) and one evolutionary outgroup (birds), so students may also successfully identify species that belong to the same order, and describe some of the shared characteristics for that order.

d) Select two species that are distantly related on your phylogenetic tree and describe at least two phenotypic characteristics that distinguish them from one another.

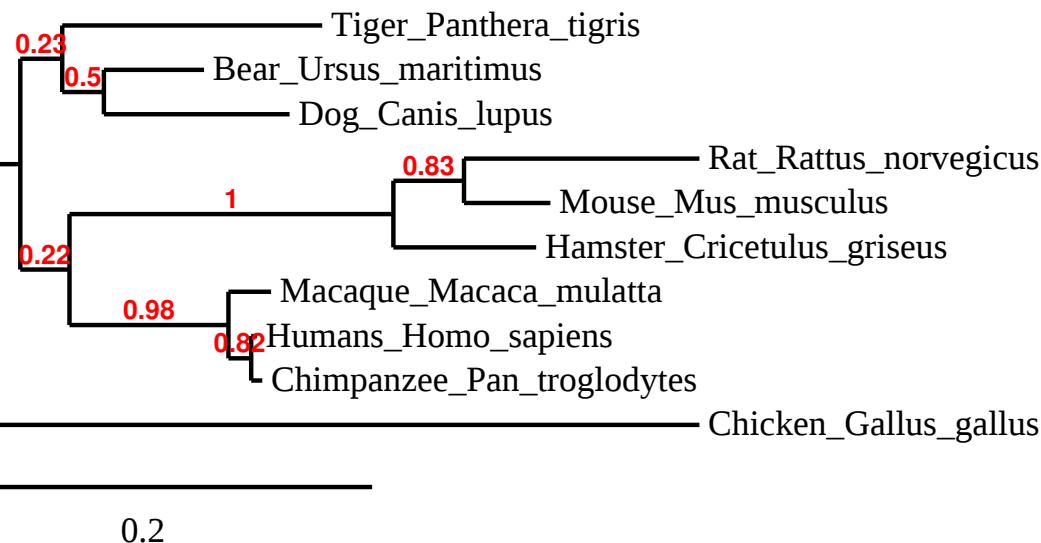
As above, the purpose of this question is to encourage students to identify specific characteristics that differ between the species in their hypothesized phylogenetic tree.

e) What additional data could be incorporated to strengthen your hypothesis about the evolutionary relationships between these species?

The purpose of this question is to highlight that additional pieces of information improve our understanding of evolutionary relationships. Some examples include molecular data (DNA/protein sequences), fossil evidence, geographical distributions, and developmental patterns.

Tree B: Draw the phylogenetic tree for the 10 species generated by Phylogeny.fr based on DNA sequences. Your tree should reflect the correct branching order of these species.

Note: The branch lengths and red numbers that indicate confidence estimates are *not* important for Tree B analysis. However, these data points may be needed in the future.



This is the tree that phylogeny.fr should produce using the DNA sequences for the hemoglobin alpha protein provided in the educators' guide. The exact branching order may differ depending on the exact sequences the students download from NCBI. Students should be instructed to focus on the relative branching pattern, *not* the branch lengths or confidence estimates for the nodes (indicated in red).

If questions arise and the students are interested, the instructor can discuss that this tree also provides information about the relative molecular divergence of the hemoglobin alpha protein across lineages, which is reflected in the branch lengths. Additionally, it may be informative to remind students that this tree is based upon molecular evidence from a single protein, so our confidence of the true branching patterns at some nodes is relatively poor (see below). This discussion can be used as an opportunity to highlight the importance of re-evaluating hypotheses using larger and more diverse datasets.

Tree B Analysis Questions:

a) Hemoglobin is an oxygen-transport protein that is found in the red blood cells of almost all vertebrates. It has four subunits: two alpha subunits and two beta subunits. Explain how this protein is produced from the DNA sequences you just collected.

The purpose of this question is to review the basic processes of transcription and translation

b) Identify the similarities and differences between the phenotypic phylogeny (Tree A) and molecular phylogeny (Tree B)?

The purpose of this question is to encourage students to re-examine their original hypothesis after the introduction of new, complementary data. It may be common for students to successfully group the species within their correct mammal orders. However, students may not consider different degrees of relatedness between orders or amongst species within a particular order, or correctly position the chicken as the evolutionary outgroup. Additionally, the phylogenies may differ because the students mistakenly include information about biological “complexity” in deciding how to structure their tree.

c) The phylogeny you built using molecular data correctly assigns the nine mammalian species to their respective orders (i.e., primates, carnivores, and rodents), and identifies the chicken as an evolutionarily distant outgroup. Are the specific branching patterns within these three orders the same as your original predictions in Tree A? Are the species in these orders equally related to one another? Explain.

The purpose of this question is to encourage students to interpret the phylogenetic tree as a set of nested hierarchies. For example, amongst rodents, the mouse and rat are more closely related to each other than either is to the hamster.



Now choose a Discovery Species _____
Using a colored pencil, predict where the Discovery Species
would fit in Tree B. Draw it in.

d) Explain your reasoning for placing the Discovery Species in this phylogenetic position.

The purpose of this question is to encourage students to identify specific characteristics that justify the hypothesized placement of the Discovery species.

Tree C: Draw the revised phylogenetic tree generated by Phylogeny.fr after adding the DNA sequence of the 11th species.

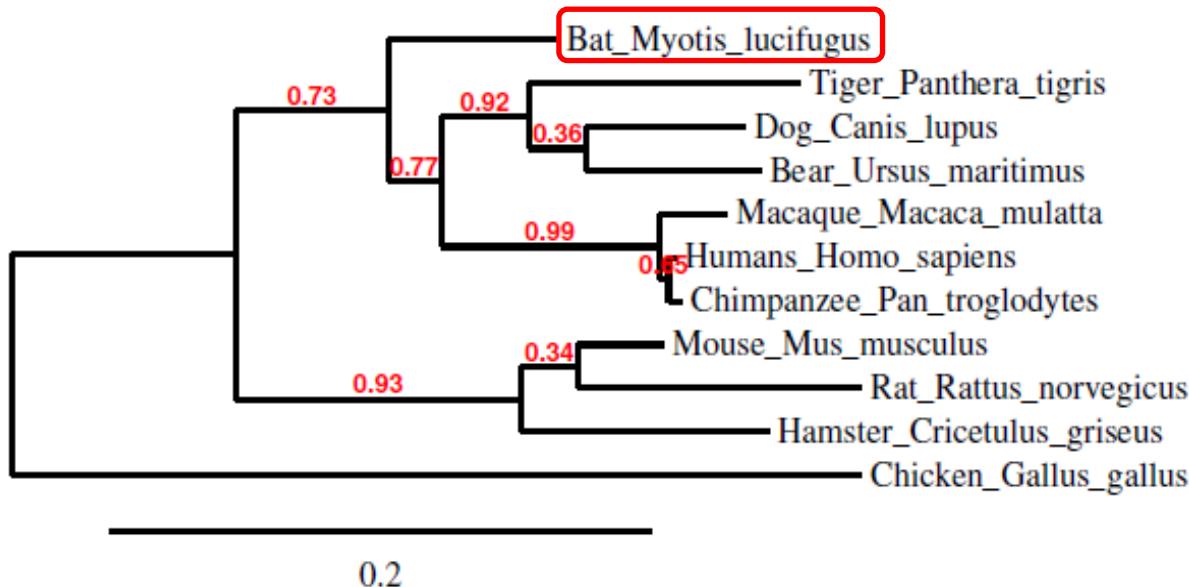
For this analysis, consider the confidence estimates for each node, which are indicated in red.

These are the six trees that phylogeny.fr should produce after the inclusion of DNA sequences for the hemoglobin alpha protein from the six discovery species provided in the resources.

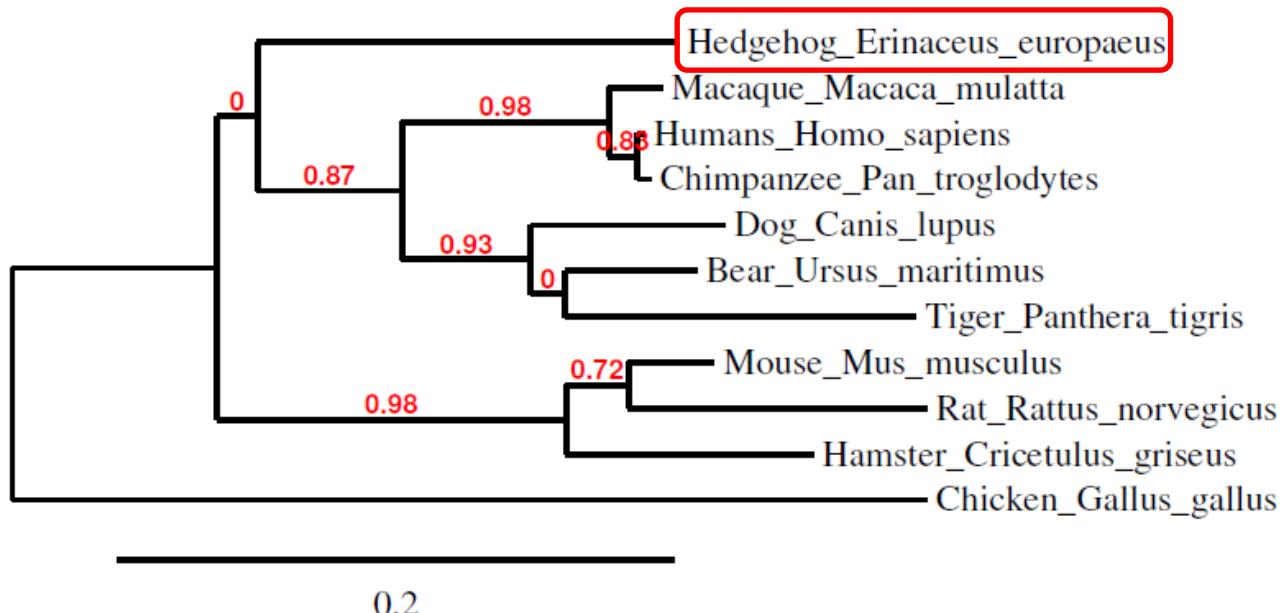


Note: because this phylogeny is based on the DNA sequences of a single protein, inclusion of more than one discovery species may alter the structure of the resulting tree.

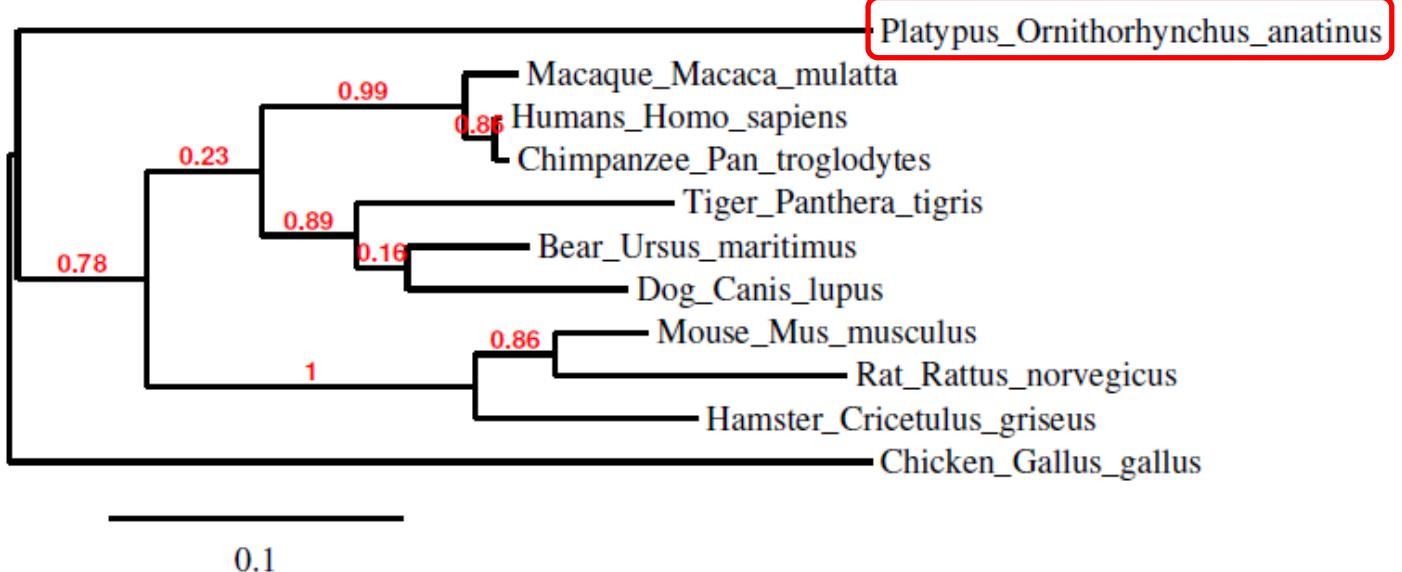
Discovery species: Bat



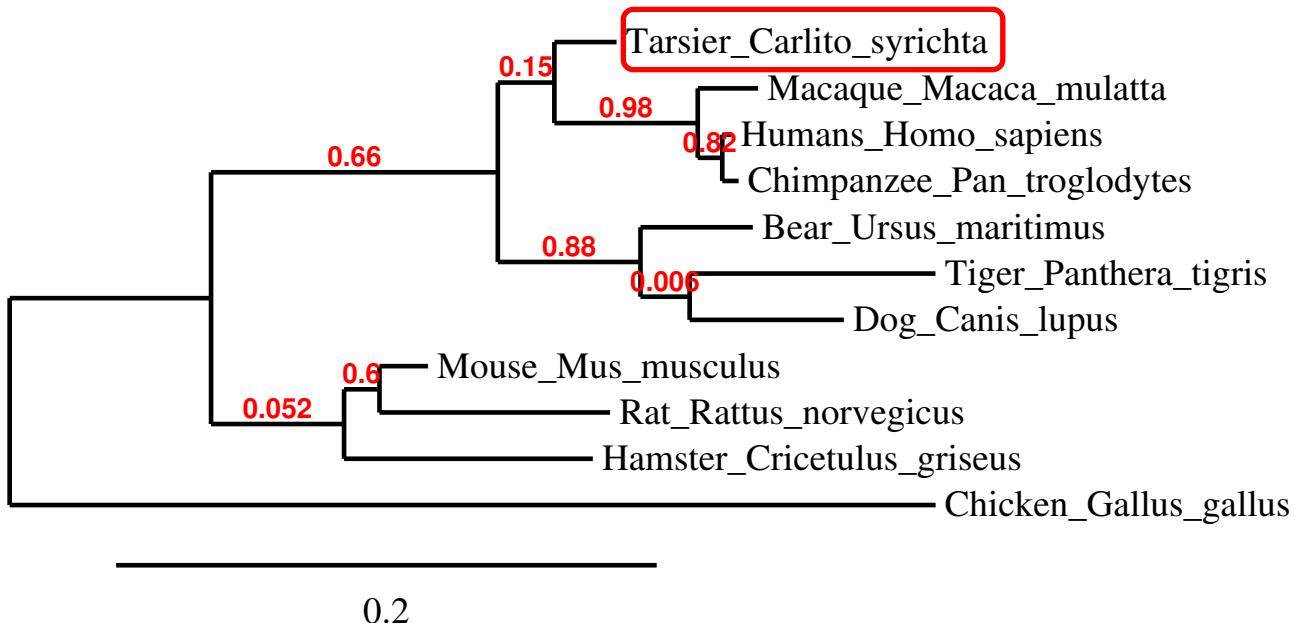
Discovery Species: Hedgehog



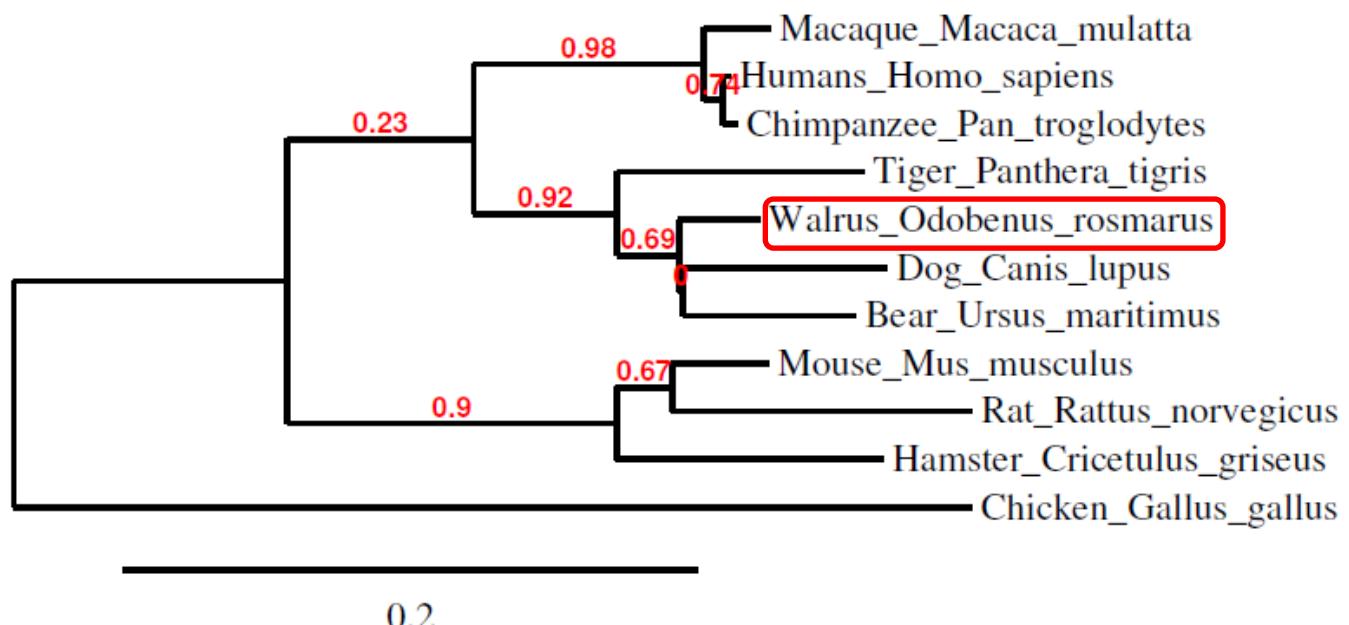
Discovery Species: Platypus



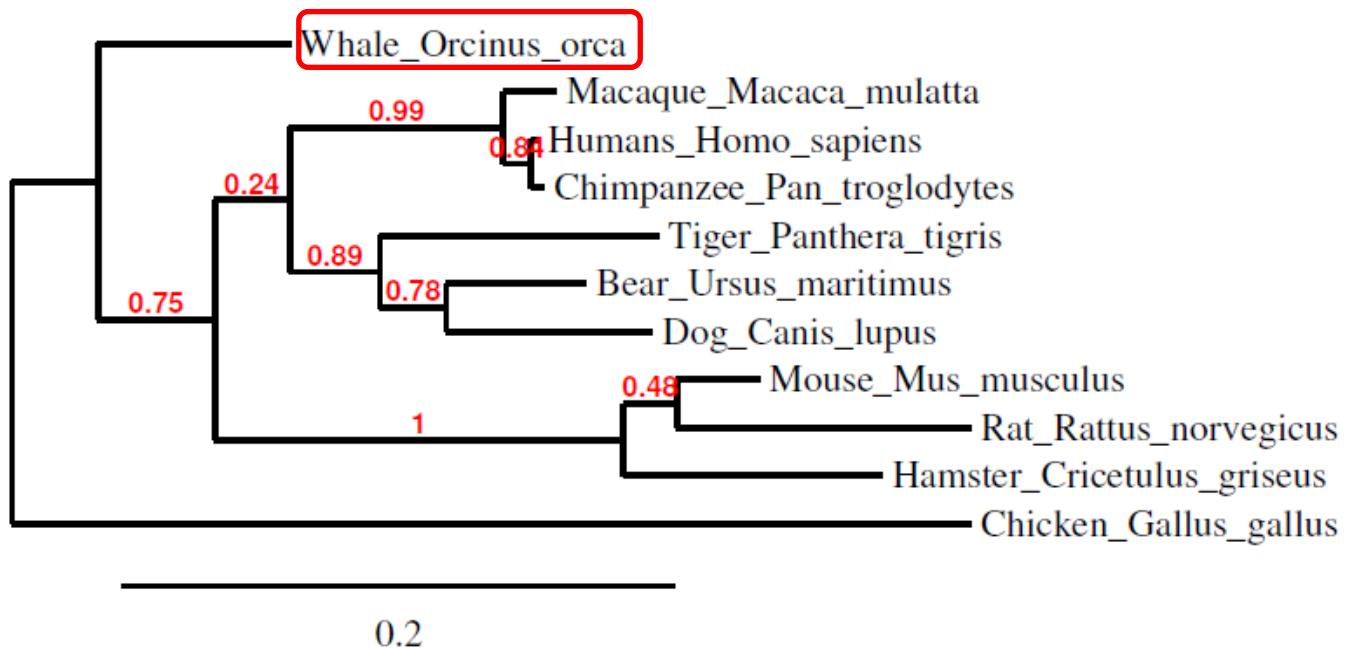
Discovery Species: Tarsier



Discovery Species: Walrus



Discovery Species: Whale



Tree C Analysis Questions:

a) Is the phylogenetic placement of your Discovery species consistent with your original prediction? If not, identify an additional phenotypic characteristic(s) that supports the updated molecular phylogeny.

We intentionally selected six discovery species that would be more difficult for students to position correctly on the mammalian phylogeny using phenotypic characteristics alone. In some cases, the students may be surprised by the results of the updated tree. This may challenge their prior knowledge of the evolutionary relationships among the eleven species, and encourage them to reassess their initial prediction based on new information.

Note: Students may notice that the confidence estimates at some nodes are different in Tree C than in Tree B. The addition of a new species changes the composition of the data, and therefore changes our certainty about the relative branching pattern.

b) On the Phylogeny.fr screen, click on the 3. Alignment tab.

What information is presented? How is it relevant to understanding the evolutionary relationships between species?



The alignment tab presents the nucleotide sequence alignments and highlights the nucleotide positions based on the extent to which they are shared across species. Like phenotypic traits, shared DNA sequences are evidence that species have evolved from a common ancestor and can be used to infer degrees of relatedness.

c) Today, you compared the evolutionary relationships among species using the DNA sequence for the hemoglobin alpha protein. If we repeated this analysis using the DNA sequence of another protein, would you predict the evolutionary relationships to stay the same? Why or why not?

The evolutionary relationships may or may not stay the same depending on the specific protein that is chosen. The purpose of this question is to encourage students to evaluate why the DNA sequences for some proteins might be more informative than others.

d) You constructed a phylogenetic tree based on molecular data for a single protein. Would it be beneficial to repeat this analysis using molecular data from more than one protein? If so, why?

In general, more information should lead to more accurate predictions about true evolutionary relationships. In this case, using molecular data from multiple proteins should result in a phylogeny with stronger support, particularly among closely-related species or poorly-resolved nodes.

e) The numbers in red indicate the confidence estimates for each node. If you repeated the analysis using multiple proteins, would you predict most of the values to increase or decrease? Why?

The purpose of this question is to highlight that the results from phylogeny.fr include a measure of our confidence in the relative branching pattern at each node. In general, we predict that the confidence estimates will increase with the inclusion of more molecular data.

f) Two species are that are distantly related based on the analysis of multiple DNA sequences also share a set of very similar phenotypic characteristics, such as the presence of wings in both bats and chickens. Consider and discuss what evolutionary process could lead to this pattern?

Species that are distantly related that experience similar selective forces can independently evolve similar phenotypic characteristics. This process is known as convergent evolution. Convergent evolution can challenge our understanding of evolutionary relationships because similar phenotypic characteristics may be mistaken as shared ancestral traits. Although students may not be familiar with the term “convergent evolution”, this question encourages students to consider how similar environments and lifestyles may lead to the evolution of similar phenotypic characteristics.

f) In this activity, you used several analyses and types of data to explain the evolutionary relationships among a set of present-day species. How do these activities model the process of science?

Science is an iterative process that involves re-evaluation of hypotheses using improved analytical approaches and new data. The goal of this question is for students to reflect upon the analyses they conducted, and highlight that the study of evolution also follows this process.