

Title: “When did I lose my legs? A limbless lizard tale”

Author(s):

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Abstract:

The anatomical record can lie. It's a fact of evolutionary biology. Through the use of models created by the oVERT project, students will examine models of extant traditional lizards, snakes and limbless lizards. Students will classify the organisms and create cladograms based on their traits. Students will then use sequence data from these species to create phylogenies showing the relationship between these species based on the more reliable molecular record. Through the use of OneZoom, the relative timing of a common ancestor between the three groups can be determined. Based on this activity, students should be able to determine the best source in determining relatedness. This activity can easily be branched into discussions of convergence/divergence and the principles of natural selection.

Subject, Grade, Level:

This activity is targeted for high school Biology courses at all levels.

Learning objectives:

Students will be able to:

1. Analyze similarities/differences between species
2. Create a cladogram with multiple organisms
3. Evaluate the use of comparative anatomy and molecular data in determining evolutionary relationships
4. Interpret phylogenetic trees.

Science Standards:

- HS-LS4-1. Communicate scientific information that common ancestry and biological evolution are supported by multiple lines of empirical evidence.
- SC.912.L.15.1 Explain how the scientific theory of evolution is supported by the fossil record, comparative anatomy, comparative embryology, biogeography, molecular biology, and observed evolutionary change
- SC.912.L.15.4 Describe how and why organisms are hierarchically classified and based on evolutionary relationships.
- SC.912.L.15.5 Explain the reasons for changes in how organisms are classified.

Timeframe:

Instructor prep time is minimal. Two 50 minute periods

List of materials:

- Electronic device/internet access per two students
- Student worksheets in google doc form or printed one per student

Procedure and general instructions (for instructor):

1. Distribute technology/student worksheet to all students
2. Have students work on pre-activity question as bellringer
3. Pose the question: How do we organize life?
 - a. Record student answers/discussion
4. Introduce the student student activity and sketchfab the models.
 - a. Model how to manipulate 3D models
5. Allow students to manipulate models and work on Part 1 through step 3
6. Whole group discussion (What characteristics did each group use to classify them? Why did you choose that? Reaffirm that there is more than one correct answer to classifying life and that is the challenge in taxonomy)
7. Irrelevant of their choices in the first part, have students group the organisms by presence of limbs.
8. Allow students to work on Part 1 through step 5.
9. Whole group discussion (What characteristics did each group use to classify them? Why did you choose that? Reaffirm that there is more than one correct answer)
10. Model the steps required for Part 2 and the phylogeny website.
11. Allow students to continue working on the rest of the activity while walking around and monitoring their recorded responses.
12. The end of Part 2 can be a natural stopping point if the period is ending.
13. At the end of the activity, have students share out answers to the last question.

Procedure and general instructions (for students):

Name: _____

When did I lose my legs?

Pre-activity question: List ways in which we classify and attempt to organize life.

Part 1: Classifying Life

1. Navigate to the sketchfab collection of images (to come)
2. Spend a few minutes manipulating the models and observing them.

Record any observations:

3. Classify the organisms into two groups based on a chosen characteristic and record.

Characteristic used to classify organisms:

Group A:

Group B:

Wait for instructor before continuing.

4. Observe the legless organisms models
5. Group these organisms into two classes and record the characteristic you chose and list the species under each class.

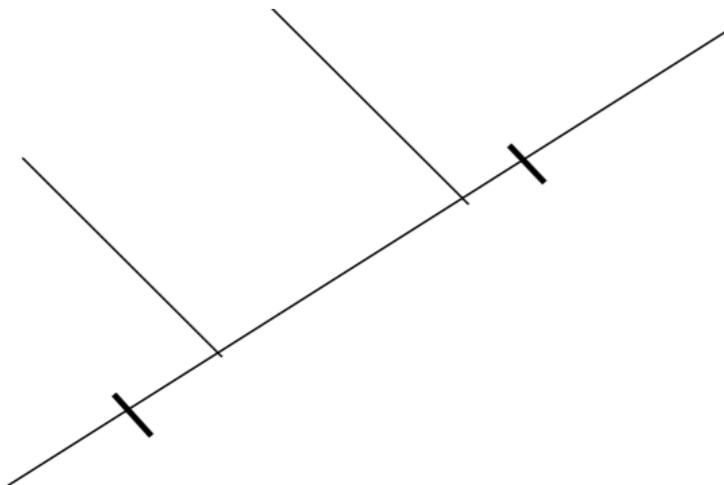
Characteristics used to classify organisms:

Group 1:

Group 2:

Wait for instructor before continuing.

Using the derived characteristics create a cladogram using the six species:



What do the nodes represent in a cladogram? Which organisms are most closely related based on this and why based on your diagram? Explain the purpose of the nodes in determining the relationships on this cladogram.

Part 2: Creating Phylogeny using Molecular Record:

In the first part you created a cladogram based on morphology or anatomy (the physical structure of an organism). The molecular record (DNA or amino acid sequences from proteins) is another source which can be used to classify organisms and determine relatedness. We will use amino acid sequences from a protein common to all these species to compare them.

1. Copy the following amino acid sequences into the textbox on

<https://ngphylogeny.fr/workflows/oneclick/>

(Examples only. Actual to follow)

>Corucia zebrata

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LLVMGLMSTSTGGWGLNQTQTRKIMAFSSIAHLGWMATILTLNPNMMLLNLLLYIMMTT
TTFMLMFTSSKTLKDLTTSWTISPPITALMLMLLSLGGPLPLTGFIPKWFILQELTTH
NLPTTAILAISALLSFFYLRLSYVMTLTMFPTSMQTTTHKWRFPKLSITMMSTLLLLSLLLLPLAPMMMY
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>Crotalus cerastes

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MNPPSLMTIMTSFTLSTILXTTTHWLMWACLEINTLSMVPIISKPHHPRATEAATKYF
LTQTLASTAMLFAATMNALNTSNWEINLTTETTMKIITLALMMKMAAAPFFHWLPEVAQ
GATTLTTLTLTWQKIAPLAILIDNHNNTNLILTTSAILSVLVGGVGGGLXQTQLRKLMA
FSSIAHTGWILATITLAPNIXIITFLIYLTTPIFXALNXXXXTTIKDXG
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>Tribolonotus schmidti

HWLLAWIGLELNTLAIIPIIAKQHNPRAEATTKYFLTQAAASAMILFASTINAWSTGTW
DISLMTNQPACTLLTMALSMKLGAPLHFWLPEVLQGTSLKTALIITWQKLAPMALLYM
TYNSMQPAILMTMGLLSTMTGGWGG

>Anelytropsis papillosus

MNPIAMSMILSGLGTGSITMASSHVLIWIGLEINTLAIPIITKHHHPRSTEAAATKYF
LTQAAASALILFSSVNAWHSGQWDITQLTYEPACITITMALAMKLGAPLHFWLPEVMQ
GTTLTTALLITWQKLAPMALIYLTSNQLSTPTMLMMGLTSTMIGGWGGLNQTQLRKVMA
FSSIAHLGWMATIATIPNIMLLNLIYITMTIPVFFSLIFSSKTIKDLGNSWTMSMTT
TTLMMLTLMSLGGPPMTGFMPKWILQEMANQQLTPLATTLAISALLSLFFYMRLAYTM
TLTSPNTMNTKCNWRFKPTMKTTMISMSLILALCMLPMTPLIT

1. Click submit and allow to run until finished.
2. Look at step 12 and click the far right  button to view the phylogeny.
3. Copy the tree below

Based on the phylogenetic tree, which organisms appear to be more closely related? Does this match the cladogram you made in part 1?

Which do you think would be a more accurate model of their relatedness? Could you think of two other animals that might look physically similar or have similar traits but would probably have relatively different DNA or amino acid sequences?

Part 3: Using multiple lines of evidence:

Science is not using one piece of evidence from one source to support a claim. Multiple (and sometimes conflicting) information must be combined and woven together to produce an explanation which can support challenge. You will now view a phylogeny that has been produced based on multiple sources and attempts to show the relatedness of all extant (not extinct) species.

1. Navigate to



<https://www.onezoom.org/life/@Amniota=229560#x852,y-313,w1.5257>

2. On the top right click
3. Type in the following species (insert a limbless lizard and snake species name here)
4. The site should navigate to the most recent common ancestor (if not, click the “common ancestor” button)

Record when the common ancestor existed:

5. Redo this but trace the path between (insert a limbless lizard and limbed lizard species name here)

Record when the common ancestor existed:

Based on when the common ancestor existed, which organisms are more closely related?

Which model (from Part A or B) does this support and how? Based on this information,

which source (anatomical or molecular data) provided a more accurate representation of relatedness between the organisms? Justify your answer