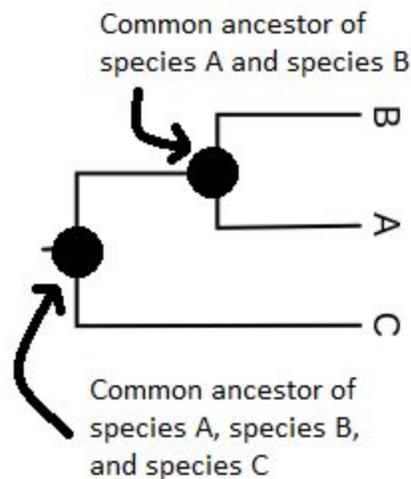




## Activity: Molecular genetics and phylogenetic tree

### Background:

Scientists want to understand the evolutionary relationship among species. One model that scientists use to show evolutionary relationships is a phylogenetic tree.



The phylogenetic tree is a visual representation of the relationships among species showing traits and common ancestors. The species are located on top or side of the “tree” and the lines represent the relationship from one species to another. Phylogenetic trees were originally based on morphological characteristics, which are features that are observed, such as shape, size color, etc. However this do not always accurately show evolutionary relationships. Even if two species look nothing alike, they could be very closely related on the genetic level. For instance, poison ivy, mangos, and cashews all look different, but DNA sequencing shows that they are very closely related.

### Directions:

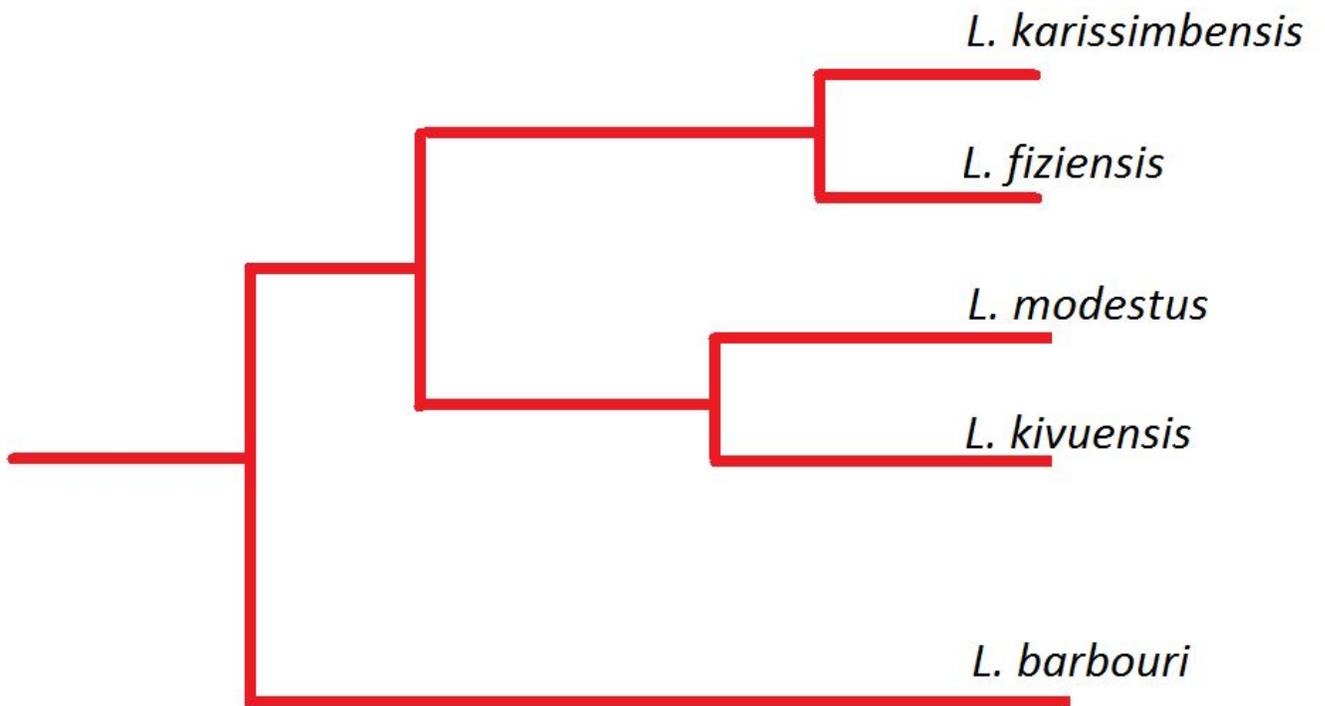
1. Compare the DNA sequences of the five amphibians species below. Do this by counting the number of differences in the code between two of the species of frogs. (Ex: *L. barbouri* and *L. kivuensis* have 9 differences). Record the differences in the DNA matrix.
2. Look through the DNA matrix and find the smallest value. That value represents the two most closely related DNA sequences. Draw a branch between these two species.
3. Find the next smallest value in the matrix and draw a branch between the species. Repeat this step until all species are shown on your phylogenetic tree.

	<i>Leptoelis</i> species	DNA Sequences
 <p>Photo Credit: Klemens Bottig</p>	<i>L. barbouri</i>	CATTCGGCAAATTCG
 <p>© 2008 by Eli Greenbaum. All rights reserved.</p>	<i>L. kivuensis</i>	GAATAGCGGCTTATG
 <p>Photo Credit: Paul Freed</p>	<i>L. modestus</i>	GAACAGCGGCTTACC
 <p>© 2008 by Eli Greenbaum. All rights reserved.</p>	<i>L. karissimbensis</i>	TTCGAGCGGCTGATT
 <p>© 2011 by Eli Greenbaum. All rights reserved.</p>	<i>L. fiziensis</i>	TTCCTGCGGCTGATT

## DNA Matrix:

	<i>L. barbouri</i>	<i>L. kivuensis</i>	<i>L. modestus</i>	<i>L. karissimbensis</i>	<i>L. fiziensis</i>
<i>L. barbouri</i>	—				
<i>L. kivuensis</i>	9	—			
<i>L. modestus</i>	11	3	—		
<i>L. karissimbensis</i>	14	6	7	—	
<i>L. fiziensis</i>	14	7	6	2	—

Draw your Phylogenetic Tree here



## Analysis Questions:

1. Which two species on your phylogenetic tree share the most recent common ancestor? Which two species would share the oldest common ancestor? Explain your reasoning based on the data.

*L. karissinbensis* and *L. fiziensis* share the most recent common ancestor because their DNA is the most similar of all species. Their lack of differences in their DNA sequence would mean that less time would have passed since each species diverged. *L. karissinbensis* and *L. baurbori* would have had the oldest common ancestor because their DNA sequences had the most differences between them.

2. Why would a phylogenetic tree based on DNA comparisons be more accurate than one based on anatomical features?

Using DNA sequences is a more accurate way to show evolutionary relationships because some physical traits are shared by two species with an unrelated common ancestor. For exam, bats and birds both have wings, however bats are mammals and much more closely related to humans, even though we do not have wings. By using DNA, we can see exactly how much of the sequence each species has in common and build evolutionary relationships based on these patterns.