## TOPIC: BUILDING PHYLOGENETIC TREES
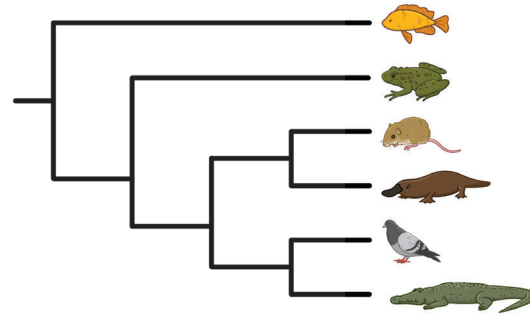
### Shared Derived Characters

◆ Phylogenetic trees are built by looking at _____ or "characters".

  ‣ To build a tree, _____ characters suggest that organisms are more closely related.

> **Shared derived character:** trait present in more than one taxon that evolved _____ the tree.
> ◆ Shared derived characters are used to build trees. (E.g., mammary glands & hair in mammals)

> **Shared ancestral character:** trait that was present at the _____ of the tree. (E.g., bones, egg-laying)



◆ Most shared characters are homologous – inherited from a _____ ancestor.

◆ Some shared characters may be analogous – _____ inherited from a common ancestor.

  ‣ Using _____ characters helps us build better trees.

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### EXAMPLE

Use your knowledge of the organisms on the tree below to decide if the following characters are shared derived characters (SD), shared ancestral characters (SA), or neither (N).

_____ Having 4 limbs.

_____ Presence of gills.

_____ Having feathers.

_____ Having lungs.

_____ Laying eggs.

_____ Terrestrial reproduction.

_____ Producing milk.

_____ Teeth.
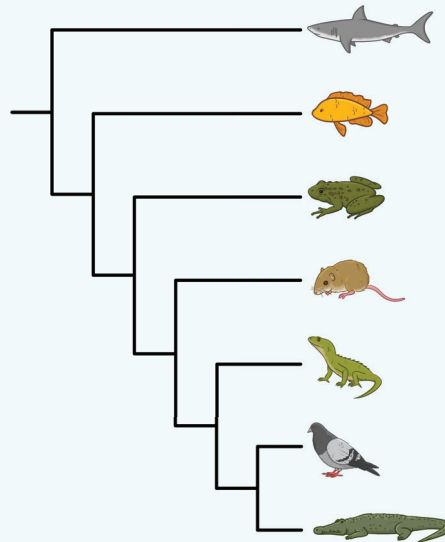
## TOPIC: BUILDING PHYLOGENETIC TREES

Which of the following statements are true regarding shared derived characters?

    I)   Shared derived characters are examples of analogies.

    II)  Shared derived characters are traits shared by multiple taxa within a tree.

    III) Shared derived characters are used to establish evolutionary relationships.

a)  I & II.             b)  I & III.             c)  II & III.             d)  I, II, & III.

The following table shows an inferred ancestral sequence for five DNA nucleotides. Then it shows the sequence for the same five nucleotides in taxa X, Y, & Z. If you wanted to build a phylogenetic tree for taxa X, Y, & Z, which nucleotide would be the most informative?

a)  Nucleotide 1.

b)  Nucleotide 2.

c)  Nucleotide 3.

d)  Nucleotide 4.

e)  Nucleotide 5.

| Nucleotide | 1 | 2 | 3 | 4 | 5 |
|---|---|---|---|---|---|
| Ancestral Sequence | A | T | C | C | A |
| Taxon X: | A | G | T | C | C |
| Taxon Y: | A | G | T | C | T |
| Taxon Z: | T | G | C | C | G |

## TOPIC: BUILDING PHYLOGENETIC TREES

### Ingroups, Outgroups, & the Character Matrix

◆ Character Matrix: used to identify shared _____ characters.

◆ Ingroup: the taxa we wish to _____ in our phylogenetic tree.

◆ Outgroup: _____ taxon that we know is more _____ related than anything in the ingroup.

  ▪ Used to identify _____ derived characters & correctly place the _____ on the tree.

| | Lays Eggs | 4 limbs | Amnion | Mammary Glands | Gizzard |
|---|---|---|---|---|---|
| Fish | 1 | 0 | 0 | 0 | 0 |
| Frog | 1 | 1 | 0 | 0 | 0 |
| Mouse | 0 | 1 | 1 | 1 | 0 |
| Platypus | 1 | 1 | 1 | 1 | 0 |
| Bird | 1 | 1 | 1 | 0 | 1 |
| Crocodile | 1 | 1 | 1 | 0 | 1 |

Filling in a character matrix:
  Write a "1" if the taxon has that character;
  Write a "0" if it does not.

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### EXAMPLE

Based on the data below, which two species do you think are sister taxa?

_____

| Nucleotide | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
|---|---|---|---|---|---|---|---|---|---|---|
| Outgroup: | C | A | G | C | A | T | G | A | C | A |
| Taxon Q: | A | G | C | C | C | G | C | C | T | T |
| Taxon R: | G | G | C | G | C | G | C | T | C | T |
| Taxon S: | T | G | G | G | A | G | G | G | T | A |

_____

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### PRACTICE

You are constructing a phylogenetic tree of all species in the family Bovidae, which includes all cattle, sheep, goats, antelope, bison, and buffalo. What do you think would be a good outgroup?

a)  A moose.          b)  A domestic cow.          c)  A fish.          d)  An oak tree.

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You are constructing a phylogenetic tree of the oak trees, and you include one species of chestnut tree as an out-group. Why would you include the chestnut species?

a)  To test if oak trees are a monophyletic group or if some may be more closely related to chestnut.

b)  Adding the chestnut will help establish branch lengths for the oak species.

c)  The chestnut will help establish which derived characters are homologous and which are analogous.

d)  The chestnut species will help add the correct root to the tree as it helps to establish ancestral traits.

Based on the following character matrix, which of the following organisms would you predict to be sister taxa?

|  | Tail | Prehensile tail | Full trichromatic vision | Arboreal | Downward facing nostrils | Post orbital closure |
|---|---|---|---|---|---|---|
| Lemurs (outgroup) | 1 | 0 | 0 | 1 | 0 | 0 |
| Apes | 0 | 0 | 1 | 1 | 1 | 1 |
| New World monkeys | 1 | 1 | 0 | 1 | 0 | 1 |
| Old World monkeys | 1 | 0 | 1 | 1 | 1 | 1 |

a)  New and Old World monkeys.

b)  New World monkeys and apes.

c)  Lemurs and New World monkeys.

d)  Old World monkeys and apes.

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### Parsimony

◆ Phylogenetic trees are built using the concept of _____.

**Parsimony:** the concept that the _____ explanation is probably correct;  AKA "Occam's _____".

Maximum Parsimony: a tree that represents the _____ number of evolutionary changes is most likely.

☐ Eggs
☐ Four Limbs
☐ Amnion
☐ Gizzard
☐ Mammary Glands

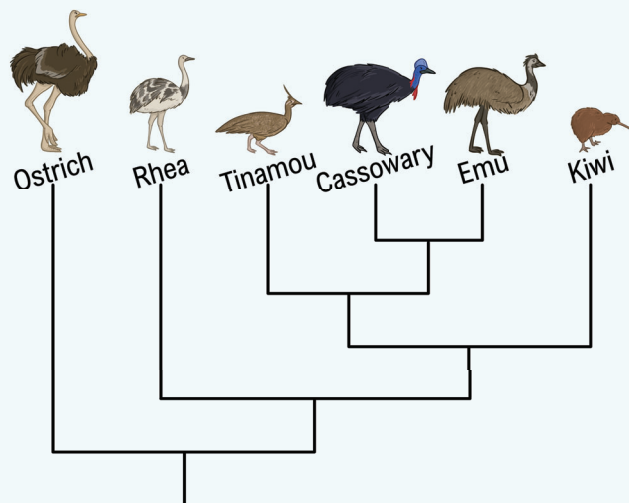| Number of evolutionary changes: | _____ | _____ |
|---|---|---|
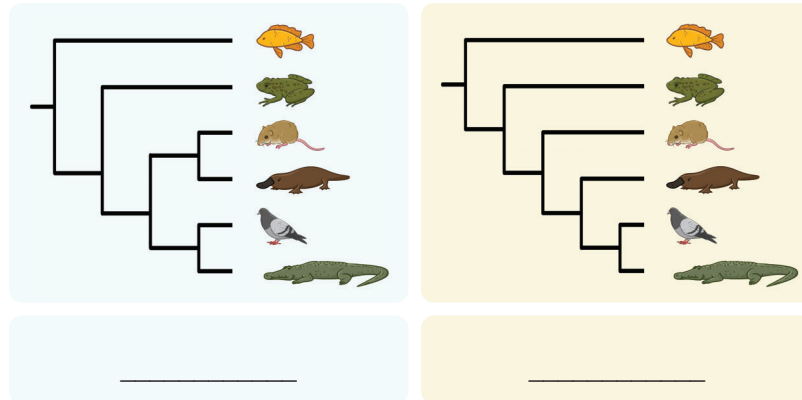
▪ Maximum Likelihood: recognizes that some changes are more _____ than others.

- E.g., certain _____ are more likely.

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In the tree below, the tinamous are the only birds that can fly; all other birds on the tree are flightless. To analyze this tree, you will consider the character of flight. There are two character states for flight: flighted and flightless.

a) Circle the ancestral state that would make the most parsimonious tree possible: flighted / flightless

b) Fewest number of changes:

_____

c) Assume that tinamous are the only birds that retained the *ancestral* state. What is the most parsimonious explanation for how many evolutionary transitions occurred on this tree for the character of flight? _____

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**PRACTICE**

What does it mean to apply the concept of parsimony to an evolutionary tree?

a) A tree should consider both the number of evolutionary steps and the likelihood of each step.

b) A tree should clearly display which evolutionary changes occurred within each lineage.

c) A tree that has the fewest evolutionary changes is usually the correct interpretation.

d) A tree should have as few branch points (nodes) as possible.