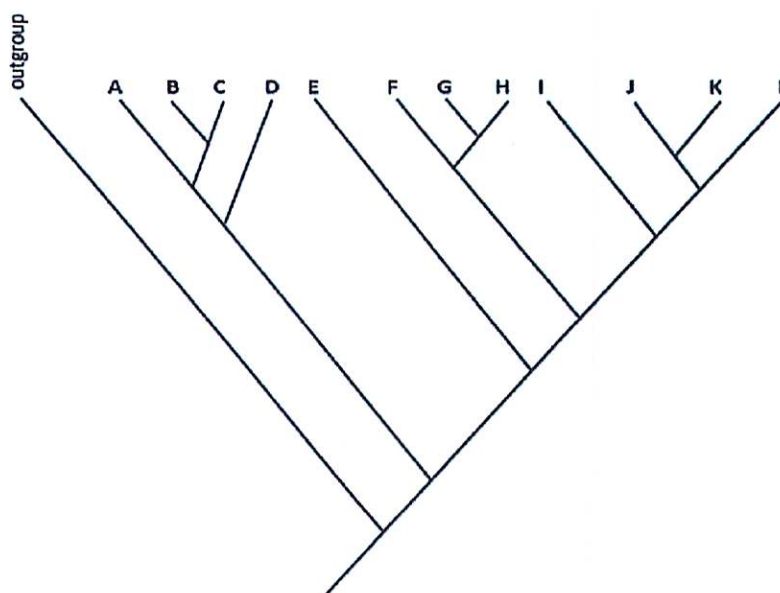


EEB 2245/2245W Spring 2019
Working with phylogenetic trees and characters

1. Answer questions a through i below using the tree provided below.
 - a. Identify the taxon (or taxa if there is more than one) that is the sister group of J?
K
 - b. Identify the taxon (or taxa if there is more than one) that is the sister group of E?
F+G+H+I+J+K+L
 - c. Circle the node that represents the most recent common ancestor of A and L.
At node that joins branch A, B, C, D with branch E, F, G, H, I, J, K, L
 - d. Circle the node that represents the most recent common ancestor of E and G.
At node that joins branch of E with branch F, G, H, I, J, K, L
 - e. List all taxa that are more closely related to C than they are to D.
A, B
 - f. List all taxa that are more closely related to K than they are to H.
I, J, L
 - g. List four monophyletic groups that include K.
Examples: K+J, K+J+L, I+J+K+L, F+G+H+I+J+K+L.
(Obviously more are possible)
 - h. Identify a paraphyletic group that includes F.
As long as you leave out a descendant of the most recent common ancestor of a group that also includes F, you are correct. For example: A+C+D (leaving out B) gives you a paraphyletic group.
 - i. Identify a paraphyletic group that includes L.
Example, H+I+J+K+L. (You would need to also include G and F for this to be a monophyletic group.)



2. Answer questions a through e using the tree provided below.

a. Circle a node that represents a dichotomy.

Examples include: node that joins A+G, or node that joins A+G+F+E, or node that joins D+H+B+C, etc.

b. Circle a node that represents a polytomy.

Node that joins the branches of H+B+C

c. Circle the root of the tree.

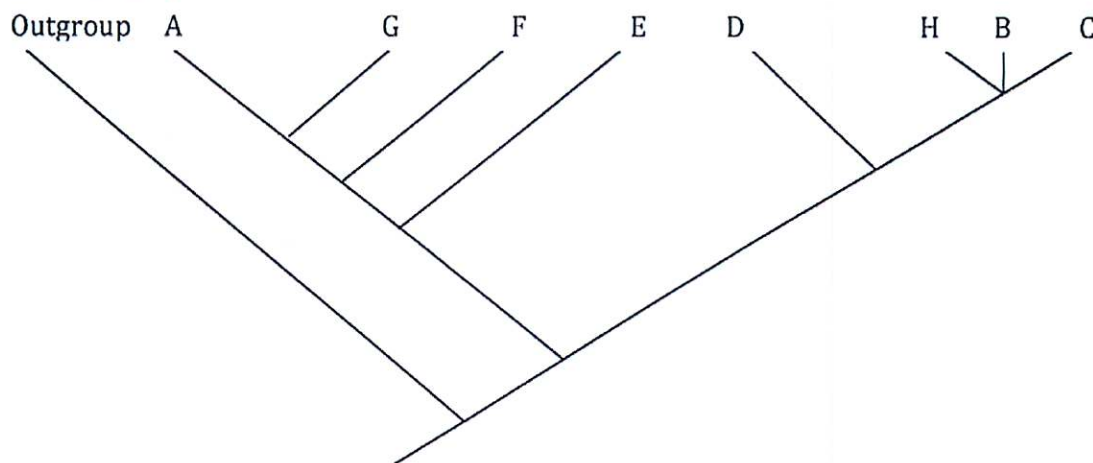
Node that joins the Outgroup branch with that of the clade that consists of A through C

d. Identify the taxon (or taxa if there is more than one) that is most closely related to B.

Both H and C

e. Identify the taxon (or taxa if there is more than one) that is the sister group of D.

H+B+C



3. Answer questions a through d using the character matrix provided below.

a. What are the character states for number of toes?

1, 3, and 4

b. What is the ancestral character state for spots?

Absent

c. Does Taxon C exhibit the ancestral or derived character state for coloration?

Derived

d. Identify the taxon (or taxa if there is more than one) that has the apomorphic state for tail.

B and D

	Number of Toes	Spots	Tail	Color
Outgroup	4	Absent	Present	Brown
Taxon A	4	Absent	Present	Green
Taxon B	3	Present	Absent	Blue
Taxon C	1	Absent	Present	Green
Taxon D	3	Absent	Absent	Blue

4. Hyliid frogs (true “tree” frogs) in Australia consist of three genera: *Nyctimystes*, *Cyclorana*, and *Litoria*, and a total of about 70 species (apparently, the skin of one species smells like curry!). The phylogenetic tree showing the relationships among the *Litoria* species from the state of Queensland (denoted A-H) is shown below, along with information about two characters in these frogs: (1) Pupil Pattern and (2) Predominant Skin Color. Using the tree and distribution of character states of each of these characters shown on the tree, which you should assume represents the correct topology, answer the following questions.

a. What is the ancestral state for Pupil Pattern?

Cross-shaped

b. What is the derived state for Skin Color?

Green

c. Identify an instance of homoplasy; what type of homoplasy is represented by the example you have chosen?

Brown skin in G: transition from brown to green in ancestor of group C through H but reverts to brown in G (=reversal)

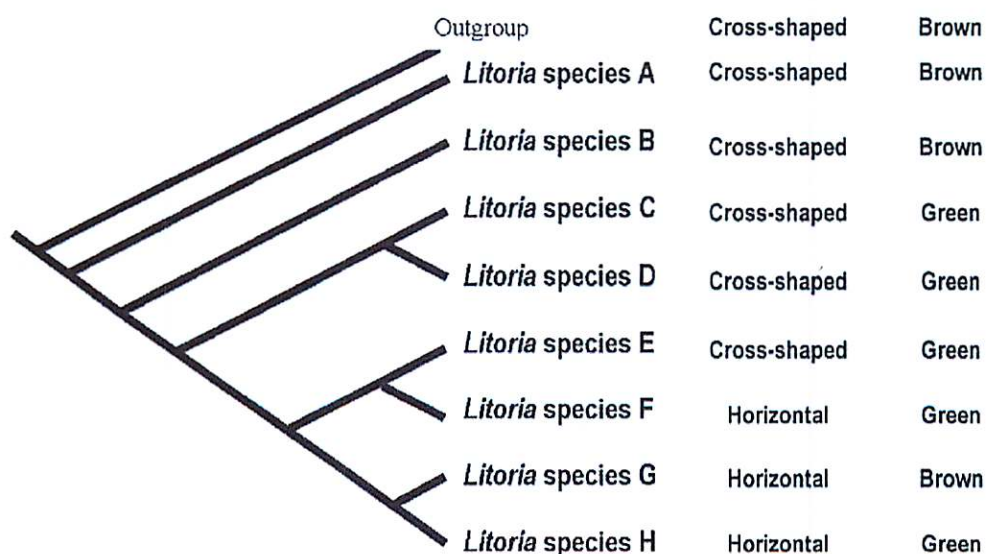
Transition to horizontal pupils in ancestor of group E through H but reverts to cross-shaped pupils in E (= reversal); or transition from Cross-shaped to horizontal in F and the ancestor of the group G+H (=parallelism, rather than convergence because this is within a family)

d. Do the *Litoria* species that have horizontal pupils represent a paraphyletic or a monophyletic group? Justify your answer.

Paraphyletic because that group of species does not include E.

Pupil Pattern
Color

Skin



5. Answer questions a through d using the matrix and trees below.

a. Circle the most parsimonious and correct tree for the given matrix.

Tree at upper left.

b. Using the matrix and your selected tree, identify a taxon (or taxa if there is more than one) that has the apomorphic state for pupil shape.

C and D

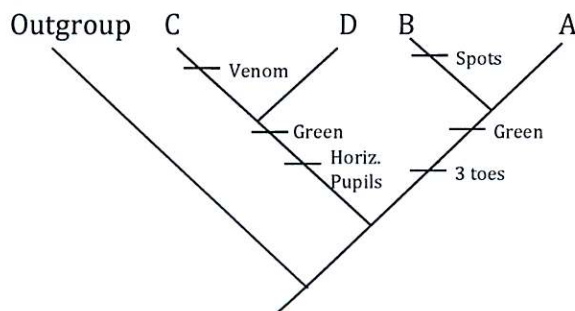
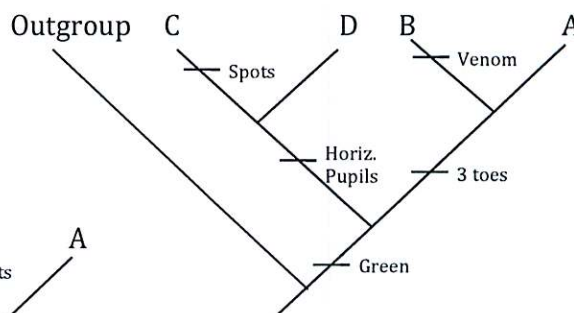
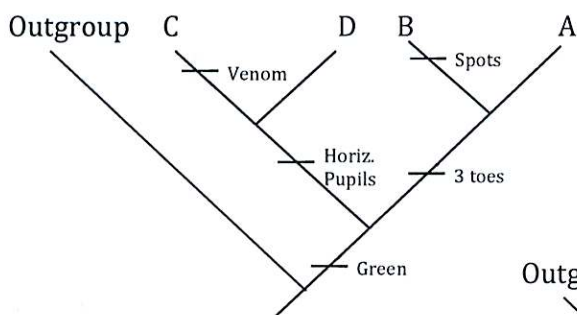
c. Using the matrix and your selected tree, identify a taxon (or taxa if there is more than one) that has the plesiomorphic state for spots.

A, C, and D

d. Using the matrix and your selected tree, identify a taxon (or taxa if there is more than one) for which 4 toes is symplesiomorphic.

C and D

	Color	Number of Toes	Pupil Shape	Spots	Venom
Outgroup	Brown	4	Cross	Absent	Absent
Taxon A	Green	3	Cross	Absent	Absent
Taxon B	Green	3	Cross	Present	Absent
Taxon C	Green	4	Horizontal	Absent	Present
Taxon D	Green	4	Horizontal	Absent	Absent



6. Imagine that you have recently found fossils of a lineage of extinct proboscideans (i.e., elephants & their relatives) from fossil beds in the extreme north of Siberia; and further, that these fossils are dated to approximately the early Oligocene. It is determined that the fossils represent 13 distinct species in the same family, and that within this family four different lineages have independently acquired the prominent forward-facing tusks as seen in *Mammuthus* sp. (i.e., the woolly mammoth).

a. What type of homoplasy is characterized by the occurrence of these similar morphologies across the 13 species? How do you know this? Justify your answer.

Forward-facing tusks are stated to have occurred independently in the four lineages and is thus homoplasious; these lineages are all within the same family and thus this is an example of parallelism

b. Is this case of homoplasy an example of the same type of homoplasy as illustrated by the placental, monotreme, and marsupial anteater species example given in lecture? Explain your answer.

No. Placental, monotreme, and marsupial anteaters belong to different higher taxa of Mammals (i.e., this homoplasy has occurred in a taxon well above the level of family—in this case above the level of order)

7. Answer questions a through e using the tree provided below.

a. Identify the taxon (or taxa if there is more than one) that have bothridia.

B, A, C, D, and E

b. Identify the taxon (or taxa if there is more than one) that have loculi.

C and D

c. If you were to group the taxa that have suckers together, would you have a monophyletic group?

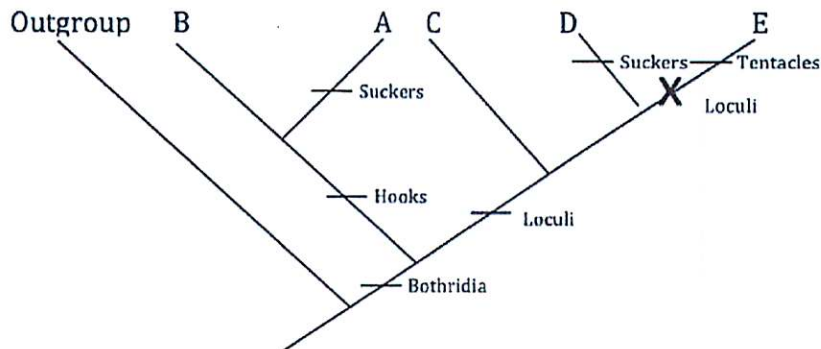
No, you would be missing three decendents of the common ancestor of A and D (i.e., B, C, and E)

d. Is the presence of hooks an ancestral or derived state?

derived

e. Identify an instance of a reversal.

Loss of loculi in E.



8. Answer questions a through c using the trees provided below.

a. Which of the 6 trees shown illustrate the same set of phylogenetic relationships?

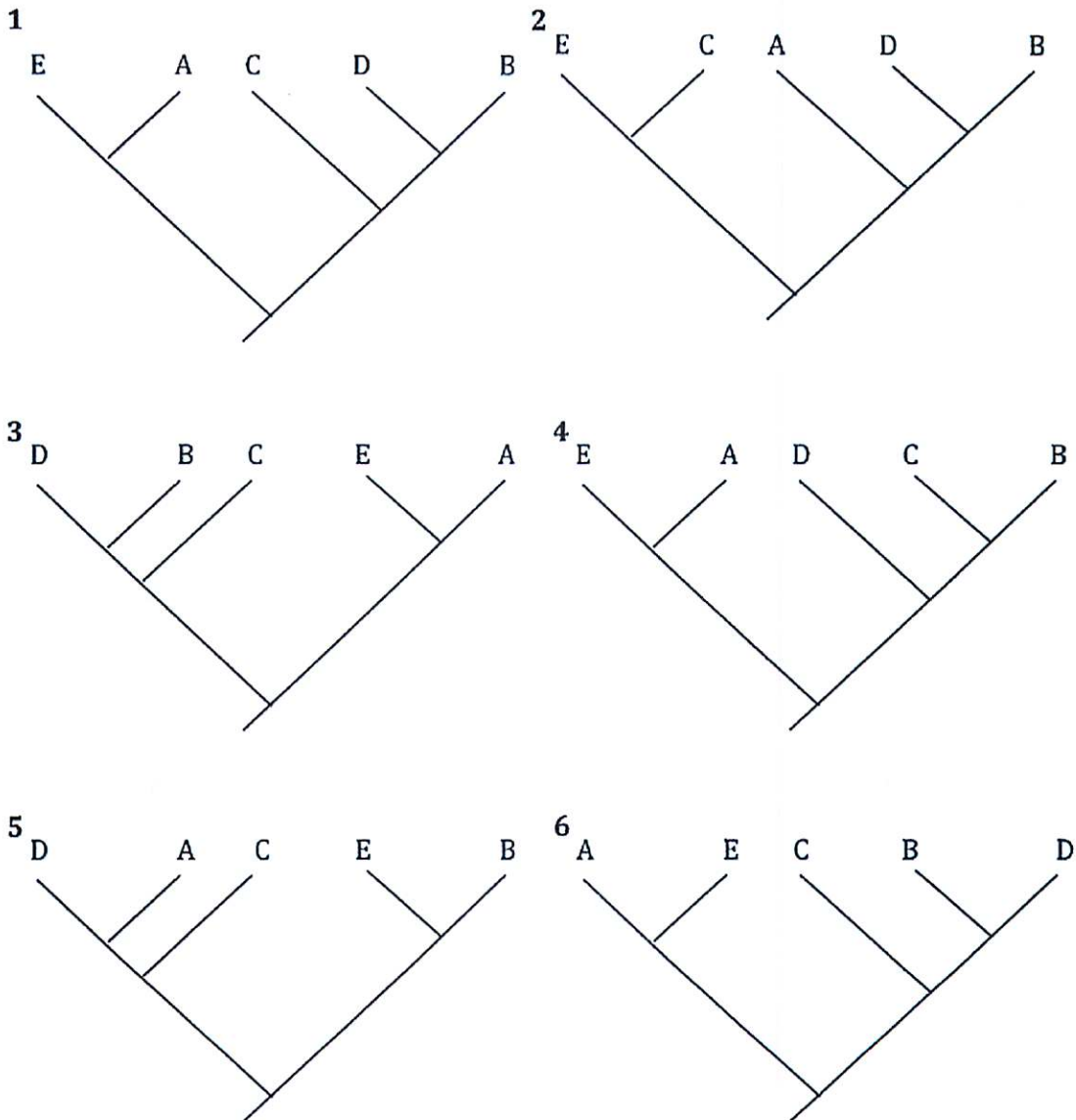
1, 3, and 6

b. Identify the tree(s), if any, in which grouping just D and A together would form a monophyletic group.

5

c. Identify the tree(s) in which grouping just D and B together would form a paraphyletic group.

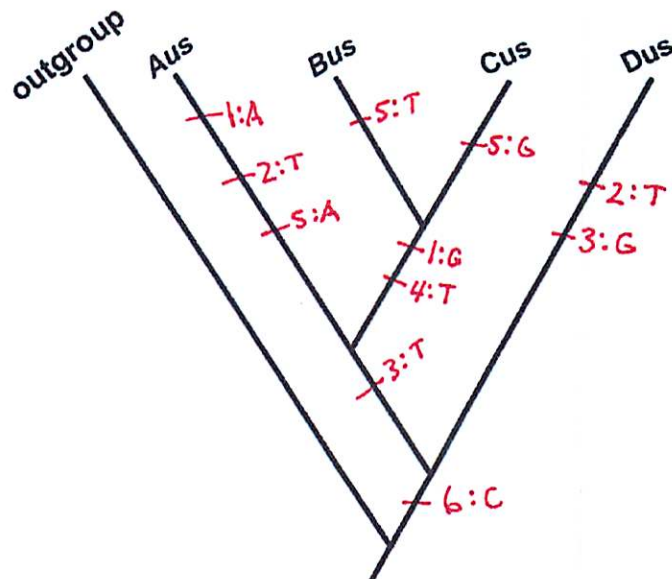
4 and 5



11. Use the data matrix of molecular characters and the corresponding tree provided below to answer the following questions. **Remember that in the cases of multi-state characters you must include both the character and its relevant state.**

- Map all of the characters and their states in the data matrix below onto the tree topology below in the most parsimonious way possible. (i.e., avoid postulating homoplasy unless that is the only option.)
- Identify a synapomorphy for the group Bus + Cus.
1:G, 4:T
- Identify a character that is homoplasious on the tree topology provided.
2:T
- Identify a binary character in this matrix.
2, 4, and 6
- Identify a synapomorphy for the ingroup taxa. 6:C

Taxon	Base Position					
	1	2	3	4	5	6
<i>Aus</i>	A	T	T	A	A	C
<i>Bus</i>	G	C	T	T	T	C
<i>Cus</i>	G	C	T	T	G	C
<i>Dus</i>	T	T	G	A	C	C
<i>Eus</i> (outgroup)	T	C	A	A	C	G



NOW TO REALLY TEST YOUR UNDERSTANDING OF GENERATING PHYLOGENETIC TREES...

12. Based on the tapeworm data matrix provided below do the following.

a. Draw the most parsimonious tree topology for the relationships among these tapeworms. **Two different topologies are equally parsimonious (see below)!**

b. Illustrate the most parsimonious mapping of the character states in the matrix on the most parsimonious tree. **Both are mapped below ... are there other options?**

c. What is the length of the most parsimonious tree? **9 steps**

d. Are any of the characters in this matrix multi-state characters? **No**

Taxon	Character						
	Scolex hooks	Uterus condition	Cirrus armature	Testes number	Ovary shape	Larval type	Vitelline form
<i>Toanium orbita</i>	present	lobate	spined	2	tetralobed	cysticercus	follicular
<i>Toanium itera</i>	absent	lobate	naked	2	tetralobed	cysticercus	compact
<i>Toanium arctos</i>	present	branched	naked	10	bilobed	cysticercus	compact
<i>Toanium littum</i>	present	branched	spined	10	bilobed	cysticercus	compact
<i>Endopium equus</i> (outgroup)	present	lobate	naked	10	tetralobed	hydatid cyst	follicular

