

## EEB 2245/2245W Spring 2014: exercises working with phylogenetic trees and characters

### 1. Answer questions a through i below using the tree provided below.

- a. The sister group of J.

**K**

- b. The sister group of E.

**F+G+H+I+J+K+L**

- c. 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. 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. All taxa that are more closely related to C than they are to D.

**A and B**

- f. All taxa that are more closely related to K than they are to H.

**I, J, L**

- g. Four monophyletic groups that include K (you can list these).

**Examples (Obviously more are possible):**

**K + J**

**K + J + L**

**I + J + K + L**

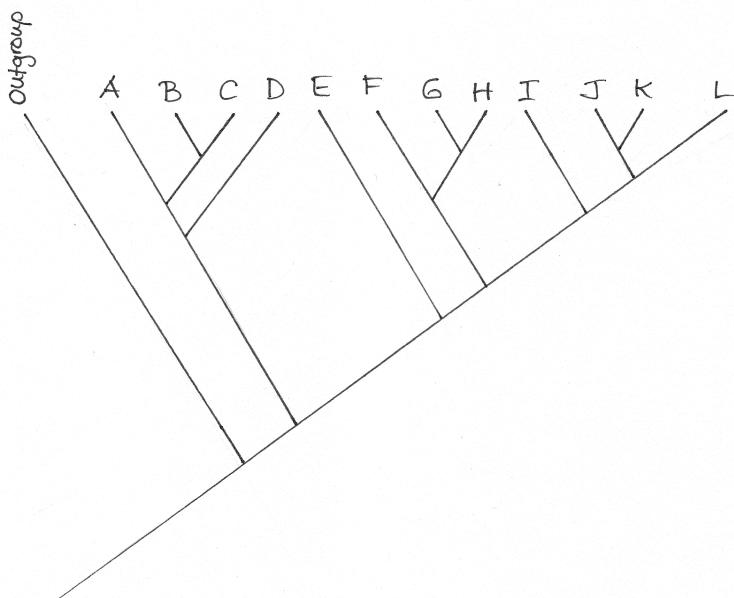
**F + G + H + I + J + K + L**

- h. A paraphyletic group that includes F.

**As long as you leave out a descendant of an ancestor of a group that also includes F, you have it. For example: H + F + E (leaving out G, I, J, I and L); there are many others.**

- i. A paraphyletic group that includes L.

**Again, as long as you leave out a descendant of an ancestor of a group that also includes L, you have it. e.g., or K + L (leaving out J) OR L + K + J + I + H (leaving out G, F).**



2. Hylid 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 of the relationships among the *Litoria* species from the state of Victoria (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 & distribution of character states of each of these features 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 (i.e., the state found in the outgroup).**

- b. What is the derived state for Skin Color?

**Green (the state Brown is found in the outgroup and is thus plesiomorphic; this is a binary character, thus, the alternate state is the derived state)**

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

**Skin colour reverts to the ancestral condition (i.e., Brown) from the derived state of Green in *Litoria* species G. This is an example of a reversal.**

**Also, one of the most parsimonious mappings of Pupil Pattern would have this character transforming from Cross-shaped to Horizontal in the ancestor of E + F + G + H, and then reverting to the ancestral condition of Cross-shaped in species E, which also be an example of a reversal (Note: alternatively, it could be mapped as a parallelism with the transformation from Cross-shaped to Horizontal occurring both in species F and also in the ancestor of G and H)**

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

**Paraphyletic; F, G, and H have horizontal pupils; their most recent common ancestor is at the node from which species E also descended, but species E does not possess horizontal pupils.**

	<u>Pupil Pattern</u>	<u>Skin Color</u>
Outgroup	Cross-shaped	Brown
<i>Litoria</i> species A	Cross-shaped	Brown
<i>Litoria</i> species B	Cross-shaped	Brown
<i>Litoria</i> species C	Cross-shaped	Green
<i>Litoria</i> species D	Cross-shaped	Green
<i>Litoria</i> species E	Cross-shaped	Green
<i>Litoria</i> species F	Horizontal	Green
<i>Litoria</i> species G	Horizontal	Brown
<i>Litoria</i> species H	Horizontal	Green

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graph LR
    Root --- Outgroup
    Root --- LitoriaA
    Root --- LitoriaB
    Root --- LitoriaC
    Outgroup --- LitoriaA
    Outgroup --- LitoriaB
    Outgroup --- LitoriaC
    LitoriaA --- LitoriaD
    LitoriaB --- LitoriaD
    LitoriaC --- LitoriaD
    LitoriaD --- LitoriaE
    LitoriaD --- LitoriaF
    LitoriaD --- LitoriaG
    LitoriaD --- LitoriaH
    LitoriaE --- LitoriaF
    LitoriaE --- LitoriaG
    LitoriaE --- LitoriaH
  
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**3. Imagine that you have recently found fossils of a lineage of extinct proboscidians (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 a group of 13 closely-related species, and within that group, four lineages had *independently acquired* the prominent forward-facing tusks as seen in *Mammuthus* sp., the woolly mammoth.**

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

**This is an example of parallelism, one of three types of homoplasy. The hints here were “closely-related” and “independently-acquired”.**

- b. Is this case of homoplasy an example of the same type of homoplasy as was illustrated in the placental (*Canis*) and marsupial (*Thylacinus*) “wolf” species example in lecture? Explain your answer.

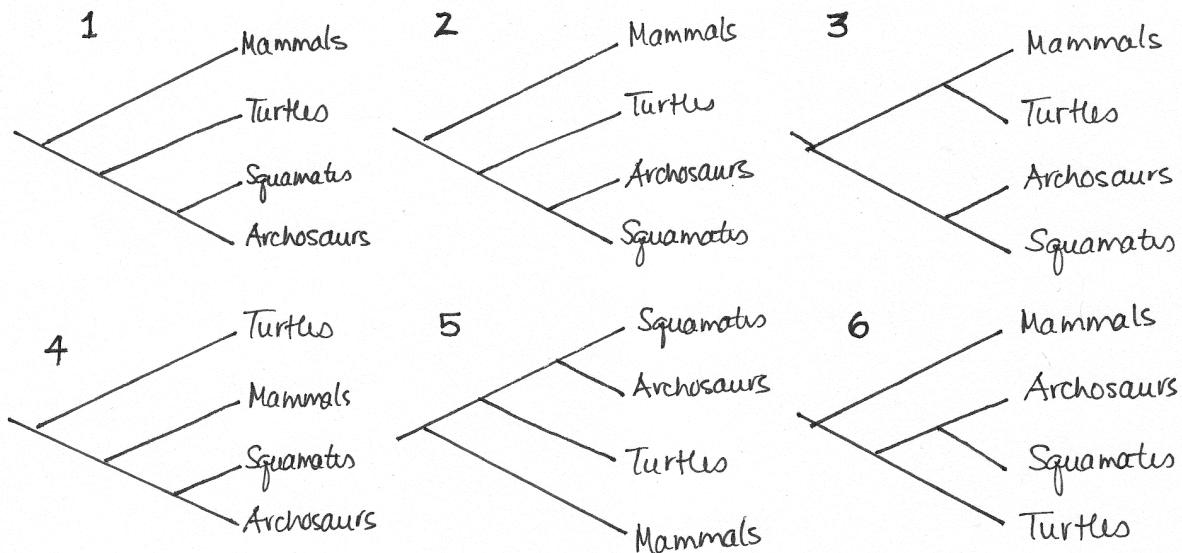
**The above example is different than the marsupial vs. placental example. Whereas the former (part a.) occurs within a relatively closely related group of taxa, the latter example (part b.) occurs within relatively distantly related suite of taxa, thus whereas the former is an example of a parallelism, the latter is an example of convergence.**

- 4. a. Which of the 6 trees shown below illustrate the same phylogeny (i.e., the same topology) as tree 1?**

**2, 5 & 6 are identical to 1.**

- b. Which tree topology is most parsimonious?

**You CANNOT tell without the characters!**



5. Use the tree of the relationships among 9 species (A through I) in the bird family Xiidae to answer the following questions.

- a. Identify a homoplasious character.

**Characters 2, 9, 6 and 3 are all homoplasious.**

- b. Identify a reversal.

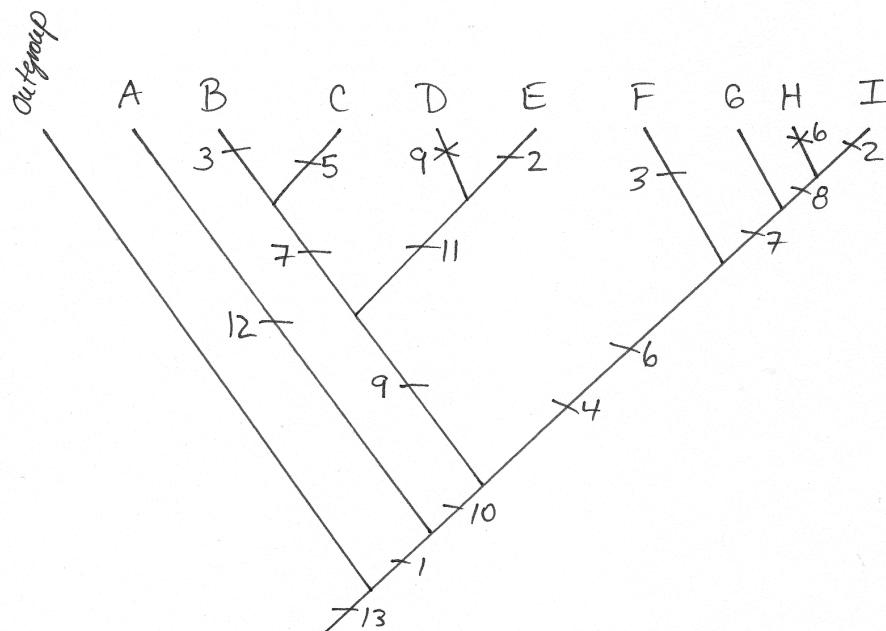
**Characters 6 and 9 are reversals.**

- c. Identify a convergent character.

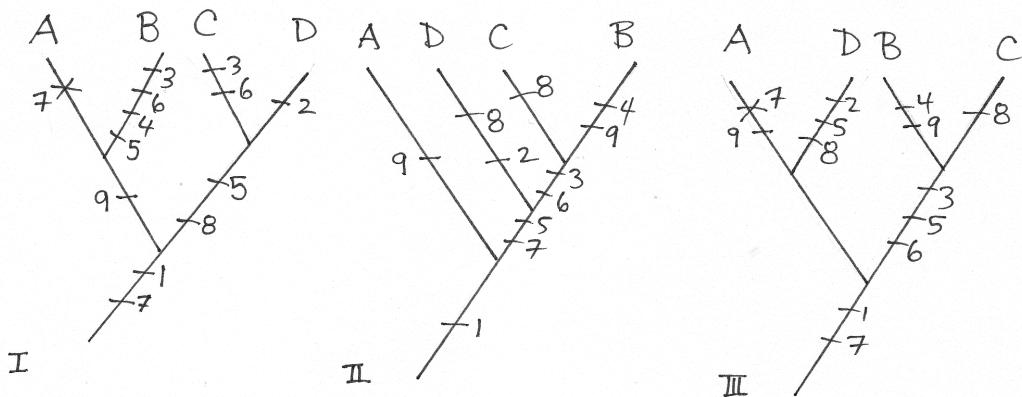
**There are NO convergent characters on this tree as it is a phylogeny for a FAMILY; thus the taxa involved are relatively closely related.**

- d. Identify a parallelism.

**Characters 2 and 3 are examples of parallelisms.**



6. Which of the following phylogenetic trees is the MOST parsimonious?

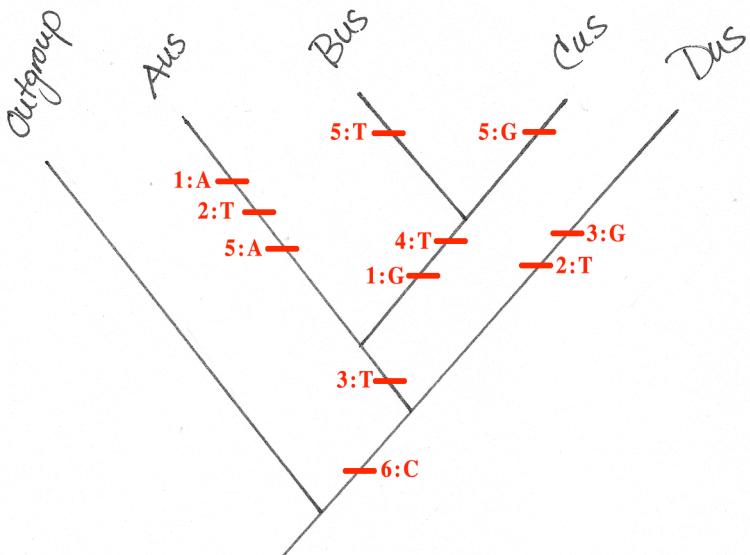


Tree II is MOST parsimonious; it is 11 steps long, whereas the other 2 trees are each 13 steps long.

7. Use the data matrix of molecular characters and the corresponding tree provided below to answer the following questions.

**Taxon**                   **base position**

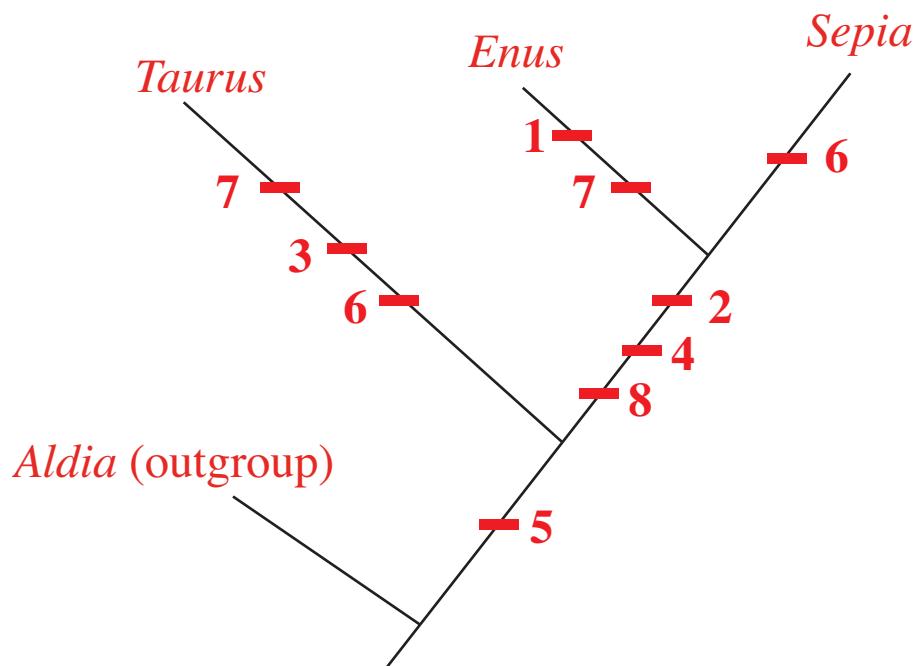
	1	2	3	4	5	6
<i>Aus</i>	A	T	T	A	A	C
<i>Bus</i>	G	C	T	T	T	C
<i>Cus</i>	G	C	T	T	G	C
<i>Dus</i>	T	T	G	A	C	C
<i>Eus</i> (outgroup)	T	C	A	A	C	G



- Map the characters provided in the above data matrix onto the tree topology provided in the most parsimonious way possible. (i.e., avoid postulating homoplasy unless that is the only option.)  
**The characters and their derived states are mapped onto the tree above; this is the most parsimonious mapping of these characters; if your mapping consists of more than 11 character state changes OR it does not accurately reflect the data in the matrix it is incorrect. An alternative correct mapping would be as above, but with Character 2 state T arising in the ancestor of *Aus* + *Bus* + *Cus* + *Dus* and then reverting to condition C in the ancestor of *Bus* + *Cus*.**
- Identify a synapomorphy for the group *Bus* + *Cus*.  
**There are two, Character 1: state G and Character 4: state T**
- Identify a character that is homoplasious on the tree topology provided.  
**There is only one: Character 2: state T arose twice, once in *Aus* and once in *Dus*. (This character could also have been mapped as a reversal i.e., with state T in the ancestor of *Aus* + *Bus* + *Cus* + *Dus*, and then reverting to state C in the ancestor of *Bus* and *Cus*- but that is not how it is mapped on this tree.)**
- Identify a binary character in this matrix.  
**Characters 2, 4, and 6 (they are each represented by only 2 states in this matrix)**
- Identify a synapomorphy for the ingroup taxa. **Character 6: state C**

7. Based on the character matrix provided below, draw the most parsimonious tree topology (i.e., set of relationships) for taxa *Enus*, *Taurus*, and *Sepia*. On that tree provide the most parsimonious mapping of the 8 characters represented in the matrix.

	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>	<b>8</b>
<i>Enus</i>	1	0	1	0	1	0	1	1
<i>Taurus</i>	0	1	0	1	1	1	1	0
<i>Sepia</i>	0	0	1	0	1	1	0	1
<i>Aldia</i> (outgroup)	0	1	1	1	0	0	0	0



FROM CLASS Thursday, February 28<sup>th</sup> (other tree mappings)  
 Nucleotide position

Taxon	1	2	3	4	5	6
birds	T	G	A	C	A	G
crocodiles	T	C	A	C	G	G
lizards	T	G	T	C	A	A
turtles (outgroup)	A	G	G	C	G	A

