Table for Primate Skull Morphology Data Collection

Measurement	Outgroup: Lemur	Alouatta:	Homo:	Macaca:	Pan:	
Dentition					<u></u>	
Total number of teeth (see #4a)	36	36	32	32	32	
General Cranium Shapes						
Development of ear tube	simple	simple	tube-like	tube-like	tube-like	
Post-orbital closure	open	closed	closed	closed	closed	
Skull ridge presence (see #4b)	yes	yes no		yes	yes	
Two skull ridges (see #4c)	yes	yes	no	yes	no	
Size Measurements						
Skull length (cm)	7.5	10	18	11	13.5	
Snout length (cm)	2.2	2.6	0.8	1	0.5	
Cranial capacity (cm³)	14	33	1500	77	460	
Size Ratios						
Snout length ÷ skull length	0.29	0.26	0.04	0.09	0.04	
Cranial capacity ÷ skull length	1.87	3.3	83.3	7	34	
Other		<u></u>			<u> </u>	
Tail?	yes	yes	no	yes	no	

Character Matrix

Write an "A" (for "ancestral") in each box which shares the Lemur data for that character; write a "D" (for "derived") in each box which is different from the lemur data.

See Steps #5 and #6 for instructions; also pay attention to the footnotes below.

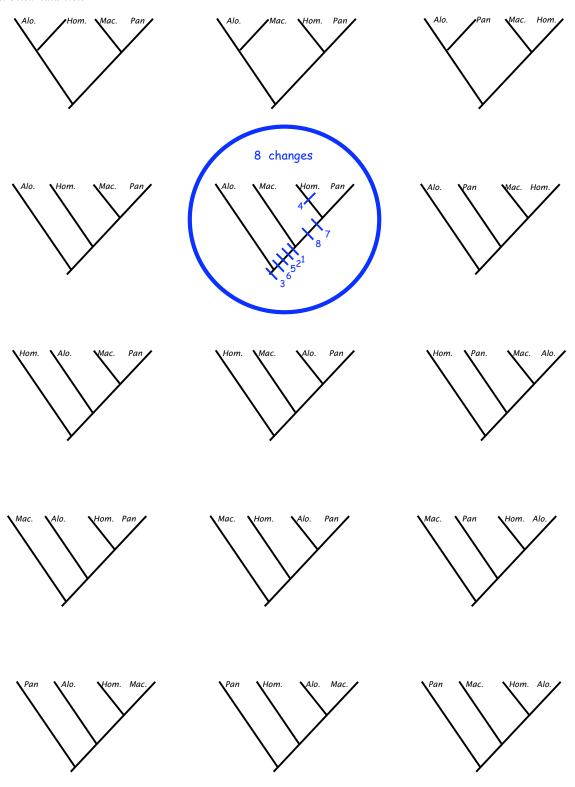
	1. Number of Teeth	2. Development of Ear Tube	3. Post-orbital closure	4. Skull ridge presence	5. Two skull ridges	6. Snout length ratio ¹	7. Cranial capacity ratio ²	8. Tail		
Alouatta:	Α	Α	٥	Α	Α	Α	Α	Α		
Homo:	D	D	D	D	D	D	D	D		
Macaca:	D	D	D	Α	D	D	Α	Α		
Pan:	٥	D	٥	Α	D	D	D	D		

¹ Check each datum to see if it is greater than or less than 0.17; if it is greater than 0.17, like the Lemur, it should be considered ancestral.

² Check each datum to see if it is greater than or less than 12; if it is less than 12, like the Lemur, it should be considered ancestral.

Possible Phylogenetic Relationships

Each time there is a change from A to D or D to A required based on your character matrix and the arrangement of primates on the tree, put a hash mark on the tree and indicate which character must change (you can use the number associated with each character in the character matrix) and what the change is. Count the number of changes required and write it below each tree.



Phylogenetics Assignmen	t
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Name:	KEY	′

Turn in just pages 11 & 12 by Monday, 1 June 2009.

- 1. Complete the phylogenies following the instructions at the top of page 11. Circle the most parsimonious tree (or trees, if necessary).
 - You should have hash marks included on your trees; see the dinosaur practice problem key for examples.
- 2. Which of the 8 characters were informative in helping you determine the most parsimonious tree?
 - 1, 2, 5, 6, 7, 8 (rarely, some variation depending on your character matrix) For most people's trees, characters 1, 2, 5, and 6 allowed you to group *Macaca*, *Pan*, & *Homo* together as having these shared, derived characters. Characters 7 and 8 allowed you to group *Pan* and *Homo* together as sharing the most recent common ancestor because of these shared, derived characters. (Some people found that only *Pan* & *Homo* were derived for trait 5, which moved it up next to 7 and 8 on their tree; this is just due to a difference in how you interpreted the "two skull ridges" character.)
- 3. For each of the characters which were not useful in cladistics, explain why.

Character 3 was not useful because all of the organisms shared the derived trait; it was never going to allow us to group subsets of the organisms based on their shared, derived characters. This hash mark would appear at the very bottom of all 15 possible trees.

Character 4 was not useful because only humans were derived; it wasn't possible to group organisms with the shared, derived character because the derived character wasn't shared! This hash mark would appear on the "Homo" branch (after it split off from the rest of the tree) of all 15 possible trees.