

**GEOL431
Spring 2017**

Spuds

Deriving a cladogram using a phylogenetic analysis

The following items refer to the specimens spread around the room. These may look like Mr. Potatohead, but NO. They are specimens of four separate **taxa** of strange creatures from another planet! Your task is to figure out their evolutionary relationships using the phylogenetic methods we have described.

Outgroup choice: For all of these exercises, assume that taxon A represents the most ancestral form (we find fossil spudheads that confirm this). It should be our outgroup for all analyses.

1) Examine the four specimens to identify **characters** - anatomical ways in which they are different from one another. For example, you might see that in some, a hat is present and in others it is absent. You ought to be able to identify seven of these. List them here:

2). Record the **character state** - i.e. the presence or absence of each character you identified - in taxon - character matrix 1, on the accompanying page. (You may code these as "Y" for "present" and "N" for "absent.")

Taxon - Character Matrix

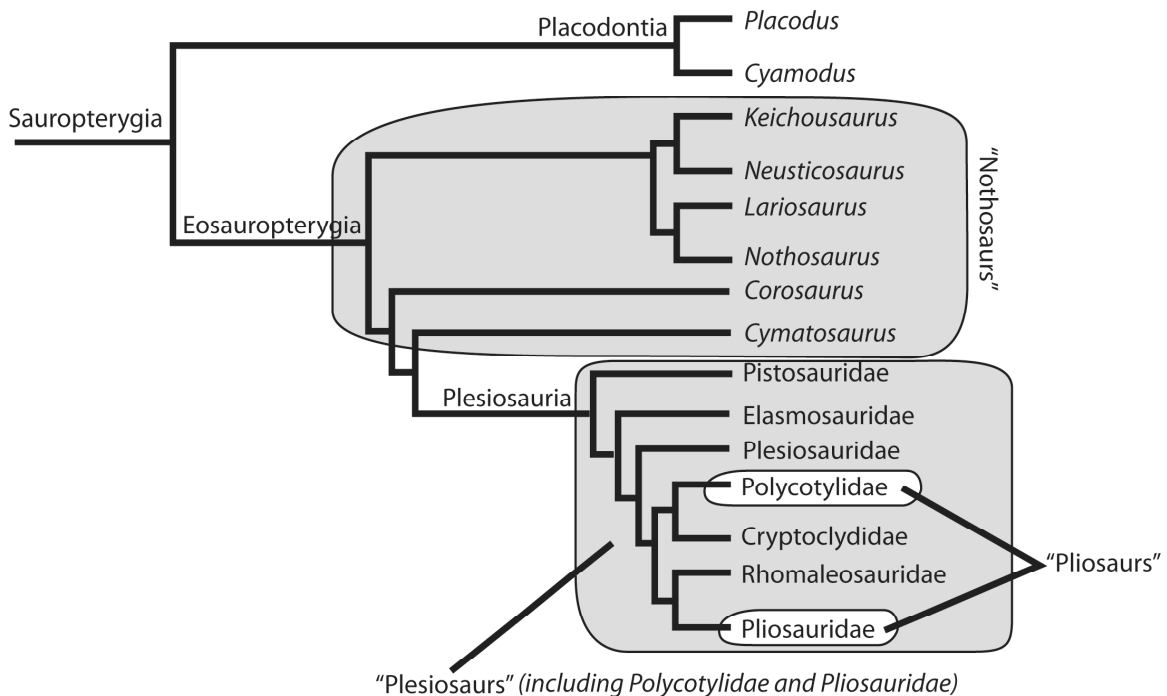
	Character						
Taxon	1	2	3	4	5	6	7
A							
B							
C							
D							

3) For each character in the matrix, decide which character state is ancestral and which is derived. Do this by referring to the outgroup. Whatever state it shows, by definition, is ancestral. (Note! in some cases, the absence of a feature may be derived!) For each character, draw a circle around the cells of the matrix in which the derived state is observed.

4) For each of the possible trees of the first tree page, map the appearance of the derived state onto the tree in a way that minimizes the number of state changes. (For example, if a derived state is seen in taxa B, C, and D, it is simpler to assume that it appeared just before their last common ancestor than to assume that it appeared three separate times in the critters immediate ancestors.)

5) For each tree, count the number of state changes you mapped. This will be the "most parsimonious tree" and our preferred hypothesis of the critter's evolutionary history. Record the number of changes here, and say which tree is most parsimonious.

Part II: Types of groups.



The cladogram above synthesizes Sauropterygia, a monophyletic group close to Merck’s heart. The group includes some classic fossil marine reptiles like *Plesiosaurus* and *Liopleurodon*. Note: the format shown is typical of what you would see in a technical publication, with the cladogram rotated 90 degrees from what you have seen before.

Three traditional taxonomic groups are circled:

- “Plesiosaurs” – the familiar long-necked, paddle-flipped marine reptiles
- “Nothosaurs” – primitive relatives of plesiosaurs “Plesiosaurs,” and
- “Pliosaurus” – “short-necked” plesiosaurs.

Indicate what type of group they represent (monophyletic, paraphyletic, or

polyphyletic).

6. Nothosaurs:

7. Plesiosaurs:

8. Pliosaurus:

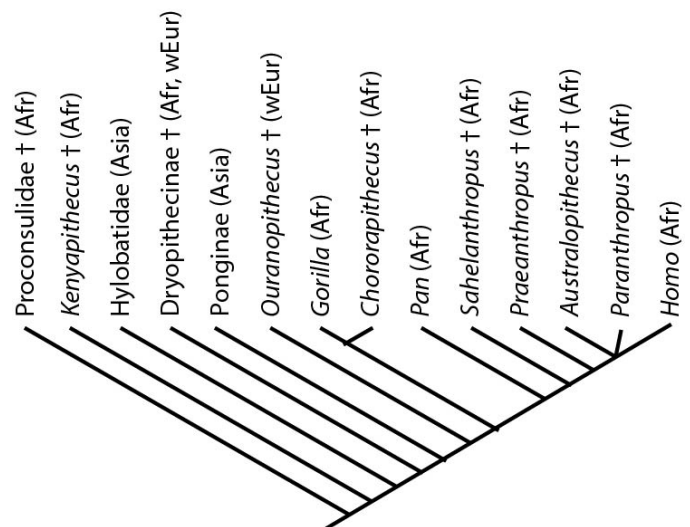
9. Several nodes have been labeled with monophyletic group names. Which of these is the least inclusive (smallest) monophyletic group to include all of the traditional nothosaurs?

Total groups, Node-based groups, and Crown groups:

Let's move closer to home. To the right is a cladogram of the Hominoidea: the apes, including humans. In this cladogram we indicate whether the clade is extinct (†) and the region in which they are found. Afr = sub-Saharan Africa; wEur = western Eurasia (Europe & western Asia). Hylobatidae are the gibbons; Ponginae is *Pongo* (the orangutan and extinct relatives); *Gorilla* is the gorilla (duh!); *Pan* is the chimps and bonobos; *Homo* is modern and extinct members of our genus.

10) Hominoidea is defined as *Homo* and all taxa closer to *Homo* than to the Cercopithecoidea (the Old World monkeys, which are the sister taxon to the entire clade here. Identify the node from which the crown of Hominoidea is descended.

Is there any taxon on here that is a member of the stem of Hominoidea (that is, outside the crown group?)



8) Homininae is defined as *Homo* and all taxa closer to *Homo* than to Ponginae. List all stem-hominines.

Our last thing we'll look at is the minimum divergence times for Hominini. First occurrence ages for each hominine taxon are:

Pan - 0.5 ma
Sahelanthropus - 7 ma
Praeanthropus - 3.9 ma
Australopithecus - 3.3 ma
Paranthropus - 2.7 ma
Homo - 2.1 ma

What are the minimum divergence ages for:

9) Homimini

10) *Sahelanthropus* - *Homo*:

11) *Praeanthropus* - *Homo*:

12) *Australopithecus* - *Homo*:

13) *Paranthropus* - *Homo*:

14) Which taxon has the longest **ghost lineage**: that is, the longest time of missing record between the minimum divergence with its sister taxon and its FAD?

Extant Phylogenetic Bracket:

We have good evidence that members of *Praeanthropus*, *Australopithecus*, *Paranthropus*, and *Homo* all walked upright, and we know that chimpanzees typically don't.

15.) *Paranthropus aethiopicus* is only known from a skull, however based on cranial characters, it is nested within *Paranthropus*. What kind of inference of the extant phylogenetic bracket allows us to infer that it stood upright? How secure would this be?

16) *Sahelanthropus*, is known only from a skull. What kind of inference of the extant phylogenetic bracket allows us to infer that it stood upright? How secure would this be?

17) Suppose we find a fossil skull that is clearly related to chimpanzees. What kind of inference of the extant phylogenetic bracket allows us to infer that it stood upright? How secure would this be?