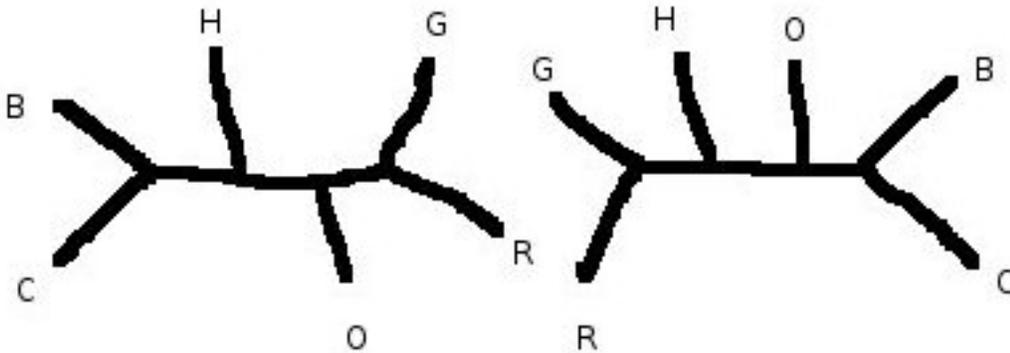


Note: If this homework is turned in by 4:00 pm Thursday December 7, I will grade and return it on December 8 for study purposes. If it is turned in on December 8 you will have to contact me to get it back.

The following species key applies to all trees in this assignment:

- H Human
- B Pygmy Chimpanzee (Bonobo)
- C Common Chimpanzee
- G Gorilla
- O Orangutan
- R Rhesus Monkey

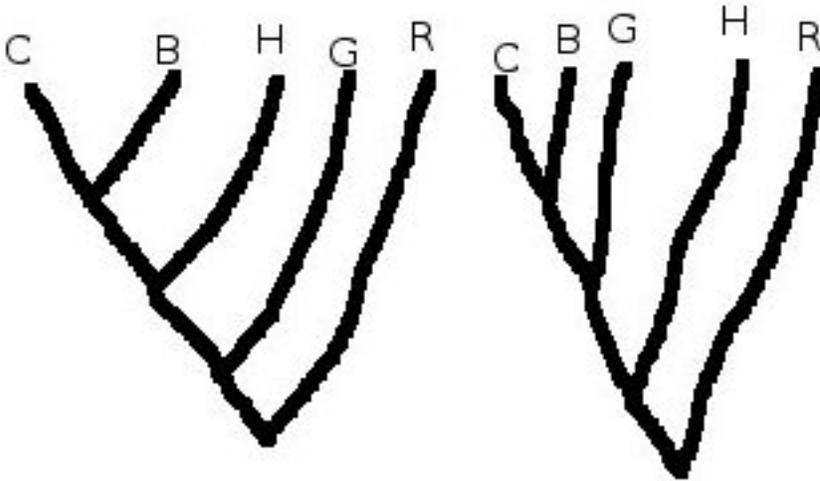
1. Are these two trees the same? If not, what is the significant difference between them?



2. Please draw BIG trees for the following problems:

- (a) Draw a rooted tree which expresses the statement “The two kinds of chimpanzees are most closely related. Humans and the two kinds of chimpanzees have a common ancestor more recently than their common ancestor with gorillas. Orangutans are the outgroup.” Do not include rhesus monkeys.
- (b) Draw an unrooted tree which corresponds to your rooted tree (it expresses the same relationships).
- (c) Starting with your unrooted tree, draw a *different* rooted tree which would also correspond to it. (In other words, show the rooted tree that would be produced if you moved the root to a new location.) Be sure your second tree is genuinely different, not just a different drawing of the same tree.

3. These two trees have been proposed to describe relationships among the great apes:



Tree 1 (“Third Chimpanzee”)

Tree 2 (“Traditional”)

- (a) Chimps, bonobos and gorillas walk on their knuckles. Humans and rhesus monkeys do not, and are genetically ill-equipped to do so (wrong body proportions). What is the minimum number of changes of state (gains or losses of knucklewalking) needed to explain this trait on each tree?
- (b) The following (fictional) mtDNA data were gathered from these species (only variable sites are shown):
- H ATACGAGT  
 B AACCGATT  
 C ATCCGATT  
 G CTCCGTGC  
 R CTCGATGC

For each of the two trees, what is the minimum number of changes needed to explain these data? Mark each change on the tree as a slash. Which tree is preferred by the parsimony criterion on these data?

- (c) Why might the knucklewalking data disagree with the genetic data? (Note that the genetic data are mtDNA, and almost surely have nothing to do with knucklewalking; the genes in mtDNA control basic energy metabolism. Also note that knucklewalking is not a purely behavioral trait; if you try it, you will find that your arms are too short relative to your legs.)
- (d) Create an (uncorrected) distance matrix from these data.
- (e) From your distance matrix, draw a rooted UPGMA tree. Does it agree or disagree with your favored parsimony tree? (Bear in mind that even though the parsimony trees are drawn as rooted, parsimony is an unrooted method: so this question is asking “If you unroot both trees, do they match?”)