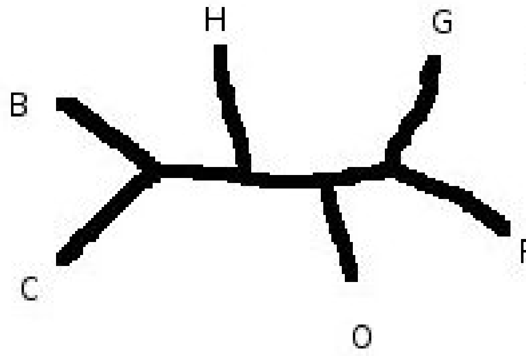
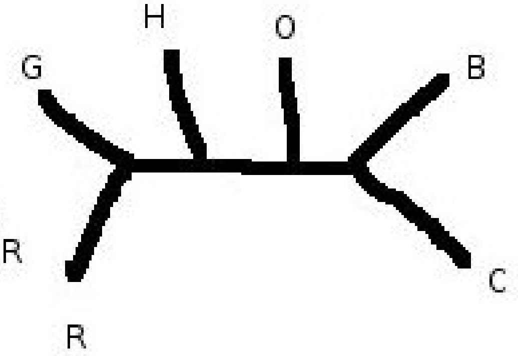
The following species key applies to all trees in this assignment:

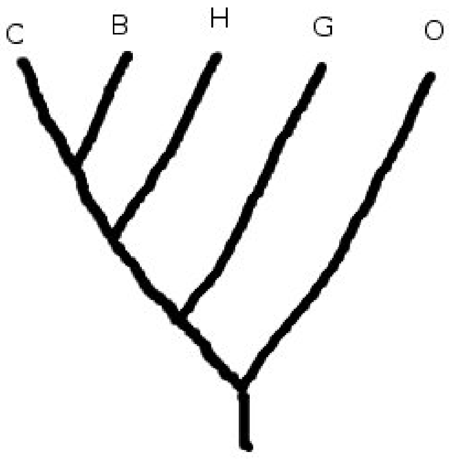
H	Human
B	Pygmy Chimpanzee (Bonobo)
C	Common Chimpanzee
G	Gorilla
O	Orangutan
R	Rhesus Monkey

1. (1 pt) Are these two trees the same? If not, what is the significant difference between them? *They are not. The first tree has orangutan closer to gorilla and rhesus than human is; the second tree has human closer to gorilla and rhesus. None of the other differences are meaningful (left-right orientation, top-bottom orientation, etc.) The best way to see this is to pick an arbitrary tip at the root, then trace through both trees noting the order in which you encounter the other species. No matter what root you pick, this will not give the same order in these two trees, which demonstrates that they are not the same tree.*

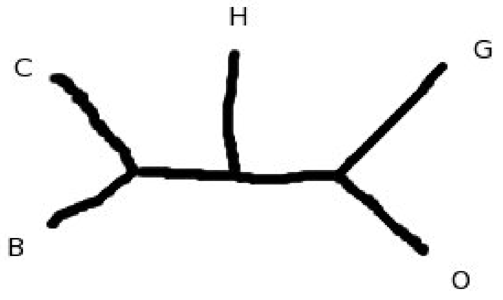




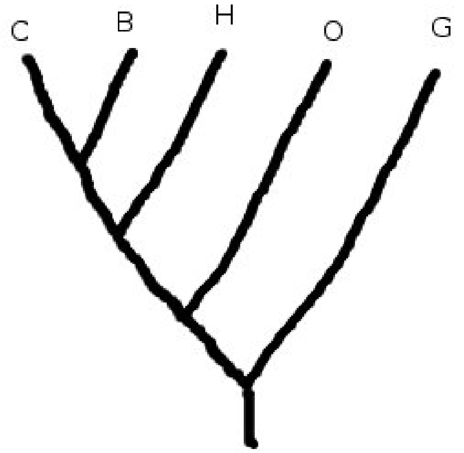
   (a) (2 pts) Draw a rooted tree which expresses the statement "The two kinds of chimpanzees are most closely related. Humans and the two kinds of chimpanzees have a common ancestor more recently than their common ancestor with gorillas. Orangutans are the outgroup." Do not include rhesus monkeys.



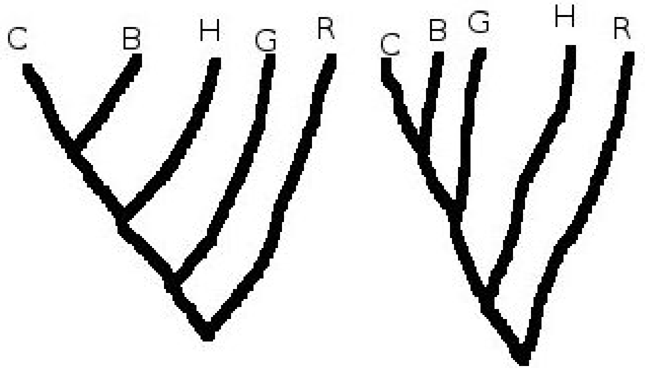
(b) (2 pts) Draw an unrooted tree which corresponds to your rooted tree.



(c) (2 pts) 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. *Here is one of several possible trees. Note that any tree where you can flip the left-right orientation of tip pairs and get your previous tree is NOT a different tree. To get a new tree, move the root to a new location.*



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



(a) (1 pt) 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? *Tree 1, 2 changes; tree 2, 1 change.*

(b) (4 pts) The following (fictional) mtDNA data were gathered from these species (only variable sites are shown):

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H  ATACGAGT
B  AACCGATT
C  ATCCGATT
G  CTCCGTGC
R  CTCGATGC
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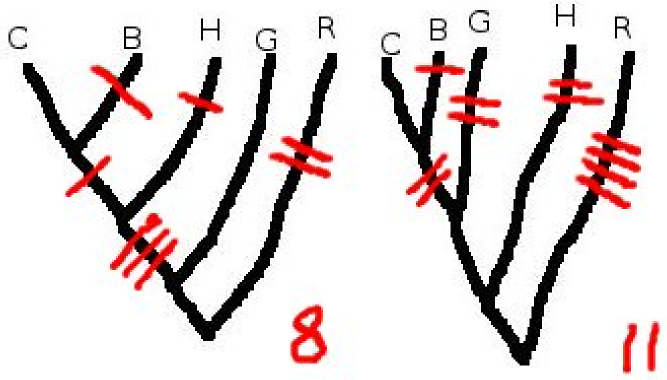
For each of the two trees, what is the minimum number of changes needed to explain these data? Mark each change on the tree. Which tree is preferred by the parsimony criterion on these data? (Please make your trees large and clear!) *Tree 1 is preferred with 8 changes as opposed to 11 for tree 2. The diagram below shows one of many possible labellings.*



(c) (2 pts) 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 small details of morphology or behavior such as knucklewalking; the genes in mtDNA control basic energy metabolism.) *Knucklewalking might have evolved in parallel in gorillas and chimpanzees as an adaptation to their common environment. Alternatively, it might have been present in the common ancestor of humans, chimps and gorillas, but been lost in humans due to adaptation to ground living. In any case, it is a single trait only, and its evolution might not have been parsimonious. On the other hand, there are only a few informative sites in the mtDNA data (sites 2, 3, 4 and 5 are not helpful as they would have the same score on any tree) and those might not be parsimonious either. More data are needed. (In molecular data sets tree 1 has generally been favored, and it is currently accepted as best. Prior to genetic data, tree 2 was favored; scientists may have been over-impressed by the knucklewalking trait.)*

We should also consider the chance the gene tree of mtDNA does not match the species tree perfectly; this can happen with young species. In other words, the common ancestor of all human mtDNA could theoretically have been *in the common ancestral species of humans, chimps and gorillas, making mtDNA uninformative about speciation order. This particular explanation doesn't work here because the human mtDNA ancestor is known to be very recent, but it's an important possibility in general.*

(d) (2 pts) Create an (uncorrected) distance matrix from these data.

	H	*B*	*C*	*G*	*R*
H	–	*3*	*2*	*4*	*6*
B		–	*1*	*5*	*7*
C			–	*4*	*6*
G				–	*2*
R					–

(e) (4 pts) 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?")

Group B and C with a distance of 0.5 to their ancestor, then G and R with a distance of 1.0 to their ancestor, then BC with H with a distance of 1.25, then the BCH and GR groups with a distance of 2.625 (1.375 on the branch to BCH, 1.625 on the branch to GR).

This is, when unrooted, the same as the best parsimony tree.