

Parsimony Exercise

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```
library(phangorn)
```

```
## Loading required package: ape
```

```
primate <- read.delim("exampleData.txt")
```

```
primate
```

```
##           species char1 char2 char3 char4 char5 char6 char7 char8 char9 char10
## 1 chimpanzee      1      1      1      2      2      2      2      3      1      1
## 2 howler_monkey    0      1      0      3      1      3      2      2      2      2
## 3 rhesus_monkey     1      1      1      2      2      2      2      1      1      1
## 4 gorilla          1      1      1      2      3      3      3      3      1      1
## 5 ring_tail_lemur   0      1      0      2      1      1      1      1      2      2
## 6 gibbon           0      1      1      1      2      1      1      2      1      1
## 7 human            0      0      0      3      3      2      3      3      1      1
## char11 char12 char13 char14 char15
## 1      1      1      2      2      2
## 2      1      1      1      2      2
## 3      1      1      2      3      3
## 4      1      1      3      1      3
## 5      0      1      1      1      1
## 6      0      0      2      3      1
## 7      0      0      3      2      2
```

```
primate_df <- data.frame(primate[,2:11], row.names = primate[,1])
primate.mat <- as.matrix(primate_df)
levels <- c("0", "1", "2", "3")
primate.phy <- phyDat(primate.mat, type = "USER", levels = levels)
primate.phy
```

```
## 7 sequences with 10 character and 9 different site patterns.
## The states are 0 1 2 3
```

```
dm <- dist.hamming(primate.phy)
treeUPGMA <- upgma(dm)
```

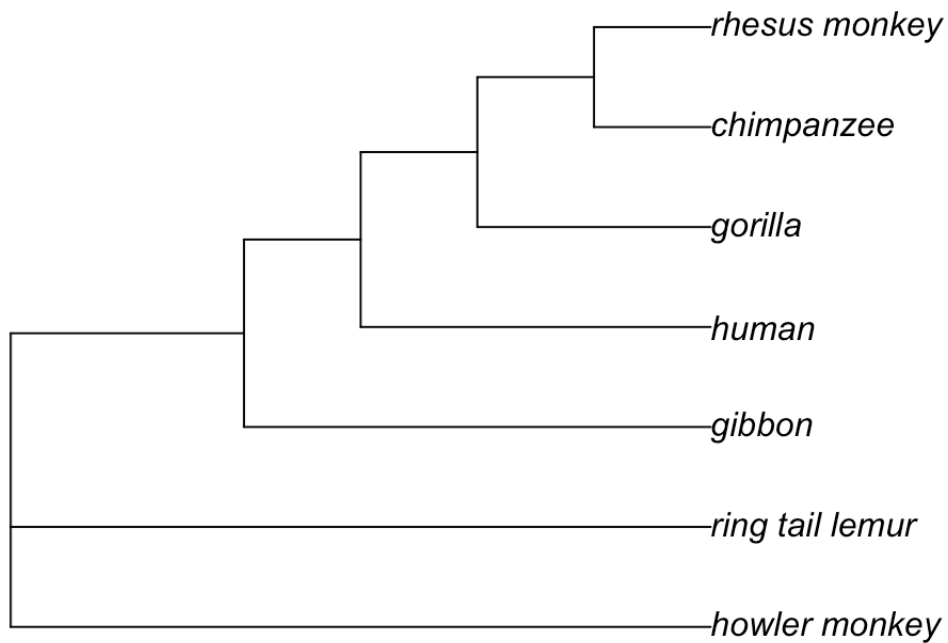


```
tree_parsimony <- optim.parsimony(treeUPGMA, primate.phy)
```

```
## Final p-score 21 after 1 nni operations
```

Question 1: It runs very quickly (< 1 second). Returns a p-score of 21 after 1 nni operation.

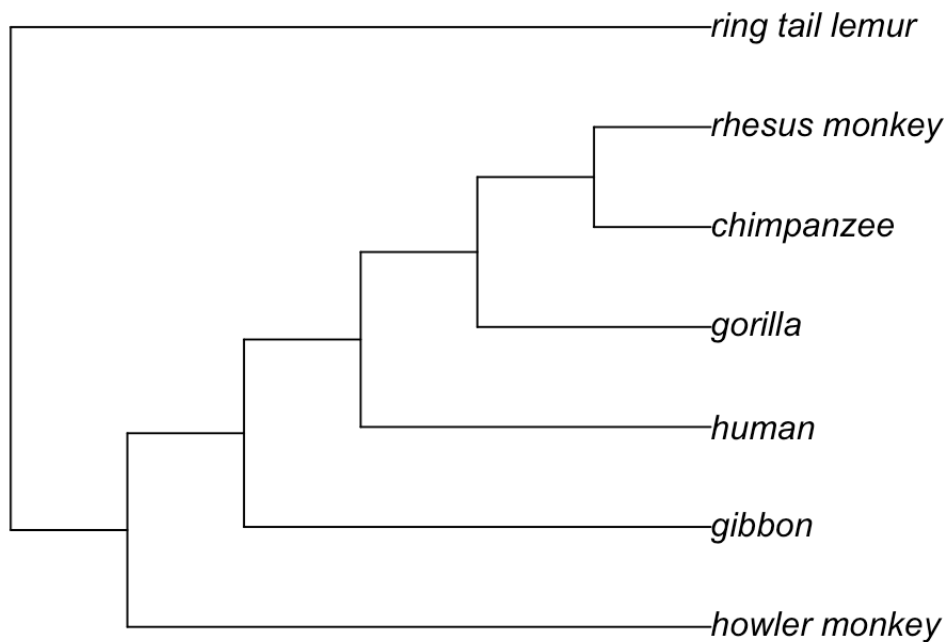
```
plot.phylo(tree_parsimony)
```



Question 3: The root taxon has three branches (it is not properly bifurcated).

```
tree_parsimony <- root(tree_parsimony,  
                        outgroup = "ring_tail_lemur",  
                        resolve.root = TRUE)
```

```
plot.phylo(tree_parsimony)
```

Question 5: Rhesus monkey + chimpanzee + gorilla form a monophyletic clade. All the organisms in this group have:

- a protruding jaw, elongated canines, a prominent orbital ridge/crest, a bony step-off at the back of the skull
- a similar number of cranial vein holes in their skull
- orbital diameter
- number of teeth and pointy molars

Among these traits, the ones that are not shared by other organisms (suggesting a synapomorphy) include the protruding jaw.