

Homework 4

Michael Li

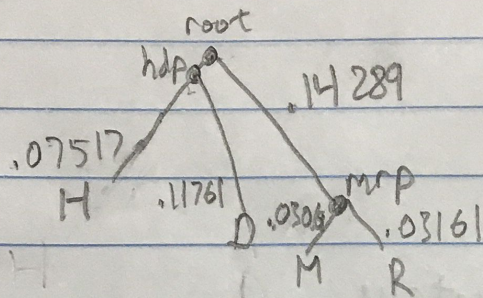
1. (a) Code submitted separately

(i) log likelihoods: topology 1 = -1556.07

topology 2 = -1651.54

topology 3 = -1651.54

Since topology 1 has the largest log likelihood, the maximum likelihood tree represented by topology 1 is



(ii) A shorter branch length for branch 5 compared to the other branches would be more similar to topologies B and C where the maximum likelihood estimates are 0 vs. topology A, where branch 5's estimate is larger than the others. So I would expect the likelihood for B and C to increase while A's would decrease. This would mean the difference between likelihoods would be smaller, so you would be less sure of your estimated topology due to the likelihoods being less distinct.

(iii) To improve confidence I would implement random sampling based on the model and then run the algorithm again many times to improve confidence. I can quantitatively measure my confidence in the reported phylogeny by looking at the differences/changes in the phylogeny, for example just counting the number of different bases.

(b) Code submitted separately

Checked output for test file provided vs the correct output, and sequence is the same

(c) Code submitted separately

Output for test file is same as correct sequence given

2. (a) Code submitted separately

Output for test-dst3 file matches the correct tree provided.

(b) Newick tree:

((Gorilla:0.008964,(Orangutan:0.01894,(Gibbon:0.0227,
(Green-monkey:0.027,(Baboon:0.008042,(Rhesus:0.004991,
Grub-eating-macaque:0.004991):0.003):0.01961):0.02204)
:0.003471):0.009693):0.0005,(Bonobo:0.0074,(Human:0.00655,
Chimp:0.00684):0.00122):0.0005));


```
[Michael-MacBook-Pro:CS4775 michaeli$ python HW4Q2a.py -f dist10.txt  
( (Gorilla:0.008964, (Orangutan:0.01894, (Gibbon:0.02227, (Green_monkey:0.027, (Baboon:0.008042,  
  (Rhesus:0.004991, Crab_eating_macaque:0.004991):0.003):0.01961):0.02204):0.003471):0.009693):0  
.0005, (Bonobo:0.00784, (Human:0.00655, Chimp:0.00684):0.00122):0.0005);
```

