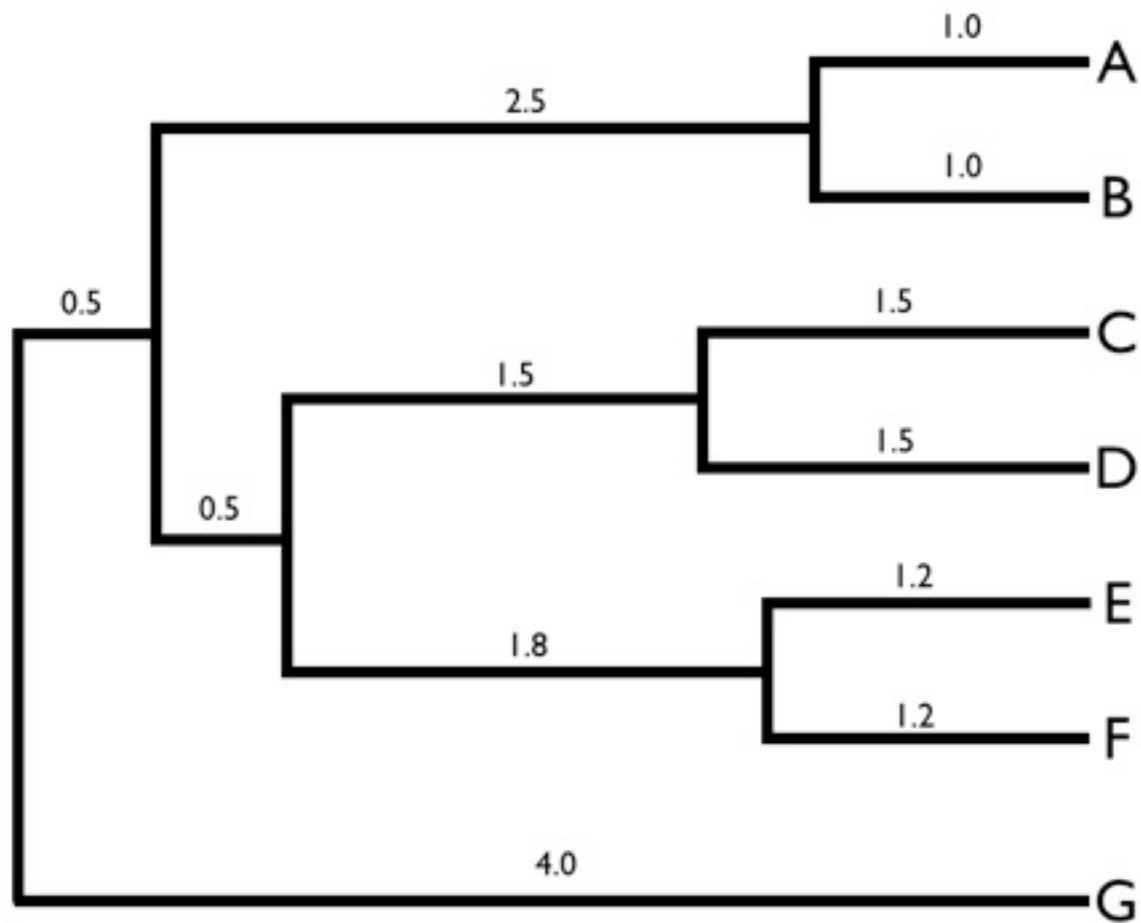


1. There is a seven-species phylogeny with branch lengths below.



a. What is the probability of obtaining the (1,6) split at the base of this tree under an ERM model?

b. What are the other possible splits one could have at the base of a seven-taxon tree? Which of these is the most likely?

2. What is an AIC score? How are these scores interpreted? What can we use them for in comparative biology?

3. We discussed a common model for growing phylogenetic trees, the birth-death model.

a. How many parameters does the birth-death model have? What are these parameters?

b. If you are growing trees under a birth-death model, from what distribution are the waiting times drawn?

c. If $b > d$, how will the number of species change through time under a birth-death model?

4. What is “phylogenetic signal?” What can we learn by measuring it?

5. You collect data on two discrete characters for the species you study: whether or not they have hairy ears (0=no, 1=yes), and whether or not they yodel (0=no, 1=yes). You suspect that there is a relationship across species between having hairy ears and yodeling, because the hair protects females from having to listen to that nonsense all day long.

To address this problem, you fit three models to the data. For model 1, both characters evolve independently under an Mk model. For model 2, both characters evolve independently but each character can have a separate forward (q_{01}) and backward (q_{10}) rate. Model 3 is a dependent model where both forward and backward rates can depend on the state of the other character.

Model	lnL
1	-120.4
2	-114.2
3	-70.3

Carry out a model selection procedure on these results. What do you conclude?