

Due: April 15, 2014

Total points: 25

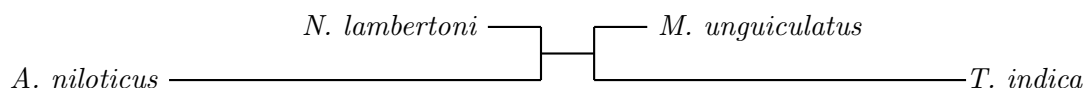
1. (25pts) (A) Use the tree and branch lengths shown below, and the Jukes-Cantor model of sequence evolution to calculate the likelihood of the following two characters:

Taxon	Character #	
	1	2
<i>Nesomys lambertoni</i>	A	T
<i>Arvicanthis niloticus</i>	C	T
<i>Tatera indica</i>	C	G
<i>Meriones unguiculatus</i>	A	G
Likelihood:		

See the slides on calculating a likelihood for the formulae needed. The slides give you the a formula for a A→A event and an A→G event across a branch of length ν . Recall that in the Jukes-Cantor model all character states are considered be interchangeable. Therefore:

- The probability for a C→C event, a G→G event, or a T→T event can each be calculated using the same formula as the A→A event.
- The probability of any particular character-state-changing event can be calculated using the formula given for the A→G event.
- For the probability of drawing any base at the root of the tree, you can simply use 0.25

The unrooted tree to use:



The branch lengths to use:

- The three short branches: $\nu_S = 0.02$ expected changes per site.
- The two long branches: $\nu_L = 0.23$ expected changes per site.

Many of the factors in the probability calculations will be re-occur as you solve this problem. You can save **a lot** of work by watching out for cases in which the same calculation will occur multiple times (and just reusing the number that you calculated). I **strongly** recommend using a spreadsheet or some other computer-based method of helping you perform these calculations. Show your work (or email us your spreadsheet).

(B) What do the probabilities imply about using parsimony to infer a tree of this shape?