

Feedback — Quiz 3: Computation of Likelihood (manual)

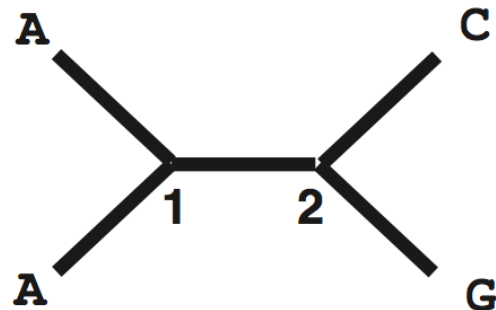
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You submitted this quiz on **Fri 19 Jul 2013 10:46 PM PDT**. You got a score of **1.00** out of **1.00**.

Below is an alignment of four DNA sequences. In this exercise you will perform a manual computation of the likelihood for column 2 in the alignment (the column labeled by the asterisk):

```
1:  A A G C T
2:  A A G C T
3:  A C G C T
4:  A G G C T
      *
```

The computation should be done using the following tree (the labels "1" and "2" indicate ancestral nucleotides, see below for details):



We will assume that all branches in the tree have the same length and that this branch length corresponds to the transition probability matrix shown below:

P = from

	A	^{to} C	G	T
A	0.793	0.078	0.104	0.026
C	0.052	0.819	0.104	0.026
G	0.052	0.078	0.844	0.026
T	0.052	0.078	0.104	0.767

Finally, the four nucleotides are assumed to have the following frequencies:

$$\pi_A = 0.2 \quad \pi_C = 0.3 \quad \pi_G = 0.4 \quad \pi_T = 0.1$$

Using the recipe from the lecture, you should now compute the likelihood of the indicated column in the alignment (which corresponds to the nucleotides listed at the leaves of the tree above), for the two ancestral nucleotides listed below (there are 16 possible pairs of ancestral nucleotides, and each time you run this quiz you will get one randomly selected pair).

Question 1

What is the likelihood of the indicated column in the alignment, given the information above, for the following ancestral nucleotides (numbers correspond to labels on the tree figure above):

- 1: A
- 2: T

Please use at least two significant digits in your response.

You entered:

0.0000265263600576

Your Answer		Score	Explanation
0.0000265263600576	✓	1.00	
Total		1.00 / 1.00	