

Feedback — How Do We Find Disease-Causing Mutations? (Week 1)

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You submitted this quiz on **Fri 5 Feb 2016 10:51 PM PST**. You got a score of **10.00** out of **10.00**.

Question 1

True or False: The most efficient way to map reads to a reference genome is by assembling the reads into a genome, then comparing this genome with the reference.

Your Answer	Score	Explanation
<input type="radio"/> True		
<input checked="" type="radio"/> False	✓ 2.00	
Total	2.00 / 2.00	

Question 2

What is the runtime of BruteForcePatternMatching?

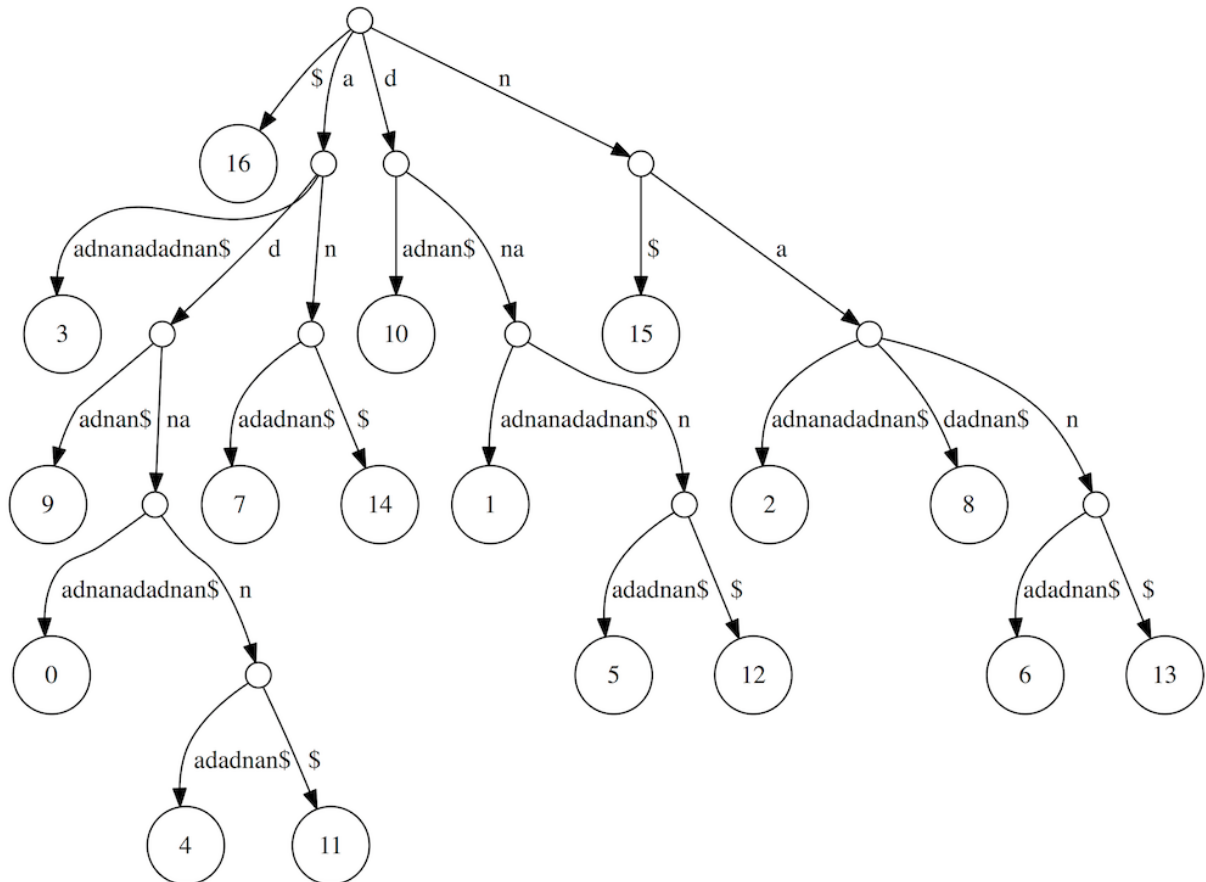
Your Answer	Score	Explanation
<input type="radio"/> $O(LongestPattern)$		
<input type="radio"/> $O(Text)$		
<input type="radio"/> $O(Patterns)$		
<input checked="" type="radio"/> $O(Text * Patterns)$	✓ 2.00	
Total	2.00 / 2.00	

Total

2.00 / 2.00

Question 4

Given the following suffix trie/suffix tree of an unknown text, identify all starting positions in the underlying text of Pattern = "adnan". Use 0-based indexing and enter the starting positions as space-separated integers **in increasing order**.



You entered:

4 11

Your Answer

Score

Explanation

4



1.00

11



1.00

Total

2.00 / 2.00

Question 5

How many leaves will *SuffixTree*("TCTGAGCCCTACTGTCTGAGAAATATGTATCTCGCCCCCGCAGCTT\$") have?

You entered:

46

Your Answer		Score	Explanation
46	✓	2.00	
Total		2.00 / 2.00	