

Feedback — Module 1

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Thank you. Your submission for this quiz was received.

You submitted this quiz on **Sat 12 Sep 2015 10:04 PM CDT**. You got a score of **10.00** out of **10.00**.

Question 1

Which of the following is not a suffix of CATATTAC?

Your Answer	Score	Explanation
<input type="radio"/> TAC		
<input checked="" type="radio"/> CAT	1.00	
<input type="radio"/> C		
<input type="radio"/> TATTAC		
Total	1.00 / 1.00	

Question 2

What's the longest prefix of CACACTGCACAC that is also a suffix?

Your Answer	Score	Explanation
<input type="radio"/> CAC		
<input type="radio"/> C		
<input checked="" type="radio"/> CACAC	1.00	
<input type="radio"/> CACACTG		

Total

1.00 / 1.00

Question 3

Which of the following is not a substring of GCTCAGCGGGGCA?

Your Answer	Score	Explanation
<input type="radio"/> GCA		
<input type="radio"/> GCT		
<input type="radio"/> GCG		
<input checked="" type="radio"/> GCC	✓ 1.00	
Total	1.00 / 1.00	

Question 4

Starting around 2007, the cost of DNA sequencing started to decrease rapidly because more laboratories started to use:

Your Answer	Score	Explanation
<input type="radio"/> DNA microarrays		
<input checked="" type="radio"/> Second-generation sequencing	✓ 1.00	
<input type="radio"/> Double sequencing		
<input type="radio"/> Sanger sequencing		
Total	1.00 / 1.00	

Question 5

Which of the following pieces of information is not included in a sequencing read in the FASTQ format:

Your Answer	Score	Explanation
<input type="radio"/> A "name" for the read		
<input type="radio"/> The sequence of bases that make up the read		
<input checked="" type="radio"/> Which chromosome the read originated from	✓ 1.00	
<input type="radio"/> The sequence of base qualities corresponding to the bases		
Total	1.00 / 1.00	

Question 6

If read alignment is like "looking for a needle in a haystack," then the "haystack" is the:

Your Answer	Score	Explanation
<input checked="" type="radio"/> Reference genome	✓ 1.00	
<input type="radio"/> Sequencer		
<input type="radio"/> Sequencing read		
<input type="radio"/> Gene database		
Total	1.00 / 1.00	

Question 7

The Human Genome Project built the initial "draft" sequence of the human genome, starting from sequencing reads. The computational problem they had to solve was the:

Your Answer	Score	Explanation
<input type="radio"/> prime factorization problem		
<input type="radio"/> gene finding problem		
<input type="radio"/> read alignment problem		
<input checked="" type="radio"/> de novo shotgun assembly problem	✓ 1.00	
Total	1.00 / 1.00	

Question 8

If the length of the pattern is x and the length of the text is y , the minimum possible number of character comparisons performed by the naive exact matching algorithm is:

Your Answer	Score	Explanation
<input checked="" type="radio"/> $y - x + 1$	✓ 1.00	
<input type="radio"/> $x(y - x + 1)$		
<input type="radio"/> $x + y$		
<input type="radio"/> xy		
Total	1.00 / 1.00	

Question 9

If the length of the pattern is x and the length of the text is y , the maximum possible number of character comparisons performed by the naive exact matching algorithm is:

Your Answer	Score	Explanation
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<input type="radio"/> xy		
<input type="radio"/> $x + y$		
<input type="radio"/> $y - x + 1$		
<input checked="" type="radio"/> $x(y - x + 1)$	✓	1.00
Total		1.00 / 1.00

Question 10

Say we have a function that generates a random DNA string, i.e. the kind of string we would get by rolling a 4-sided die (A/C/G/T) over and over. We use the function to generate a random pattern P of length 20 and a random text T of length 100. Now we run the naive exact matching algorithm to find matches of P within T. We expect the total number of character comparisons we perform to be closer to the...

Your Answer	Score	Explanation
<input checked="" type="radio"/> minimum possible	✓ 1.00	
<input type="radio"/> maximum possible		
Total		1.00 / 1.00