



✓ **Congratulations! You passed!**

TO PASS 70% or higher

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GRADE
100%

Module 1

LATEST SUBMISSION GRADE

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1. Which of the following is not a suffix of CATATTAC?

1 / 1 point

✓ Correct

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

1 / 1 point

✓ Correct

3. Which of the following is not a substring of GCTCAGCGGGCA?

1 / 1 point

✓ Correct

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

1 / 1 point

✓ Correct

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

1 / 1 point

✓ Correct

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

1 / 1 point

✓ Correct

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:

1 / 1 point

✓ Correct

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:

1 / 1 point

✓ Correct

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:

1 / 1 point

✓ Correct

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...

1 / 1 point

✓ Correct