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:

○ $x + y$

◉ $x(y - x + 1)$

○ $y - x + 1$

○ xy

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...

◉ minimum possible

○ maximum possible

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

   ◉ TAC

   ○ TATTAC

   ○ CAT

   ○ C

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

   ◉ CACAC

   ○ C

   ○ CAC

   ○ CACACTG

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

- GCG

- ● GCC

- GCT

- GCA

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

- DNA microarrays

- ● Second-generation sequencing

- Double sequencing

- Sanger sequencing

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

○ The sequence of bases that make up the read

◉ Which chromosome the read originated from

○ The sequence of base qualities corresponding to the bases

○ A "name" for the read

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

○ Sequencing read

◉ Reference genome

○ Sequencer

○ Gene database

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:

○ ● de novo shutgun assembly problem

○ prime factorization problem

○ read alignment problem

○ gene finding problem

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:

○ x(y - x + 1)

○ ● y - x + 1

○ xy

○ x + y