



Module 1

TOTAL POINTS 10

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

1 point

- ☐ C
- ☒ CAT
- ☐ TAC
- ☐ TATTAC

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

1 point

- ☒ CACAC
- ☐ C
- ☐ CACACTG
- ☐ CAC

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

1 point

- ☐ GCG
- ☒ GCC
- ☐ GCA
- ☐ GCT

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

1 point

- ☐ Double sequencing
- ☐ Sanger sequencing
- ☒ Second-generation sequencing
- ☐ DNA microarrays

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

1 point

- ☐ The sequence of base qualities corresponding to the bases
- ☒ Which chromosome the read originated from
- ☐ A "name" for the read
- ☐ The sequence of bases that make up the read

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

1 point

- ☒ Reference genome
- ☐ Gene database
- ☐ Sequencer
- ☐ Sequencing read

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 point

- ☐ gene finding problem
- ☒ de novo shotgun assembly problem
- ☐ prime factorization problem
- ☐ read alignment 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:

1 point

- ☐ $x(y - x + 1)$
- ☐ xy

☒ $y - x + 1$

☐ $x + y$

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 point

☐ $x + y$

☐ xy

☒ $x(y - x + 1)$

☐ $y - x + 1$

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 point

☐ maximum possible

☒ minimum possible

☒ I, **THOMAS JOHN JAMES**, understand that submitting another's work as my own can result in zero credit for this assignment. Repeated violations of the Coursera Honor Code may result in removal from this course or deactivation of my Coursera account.



[Learn more about Coursera's Honor Code](#)

Save

Submit