Module 4

TOTAL POINTS 7

1. The slow (sometimes called "brute force") algorithm for finding the shortest common superstring of the strings in set S involves: 1 point

   - ○ Iteratively removing strings from S that don't belong in the superstring
   - ○ Concatenating the strings in of S
   - ◉ Trying all orderings of the strings in S
   - ○ Finding the longest common substring of the strings in S

2. Which of the following is **not** a true statement about the slow (brute force) shortest common superstring algorithm. 1 point

   - ○ It might collapse repetitive portions of the genome
   - ◉ The superstring returned might be longer than the shortest possible one
   - ○ The amount of time it takes grows with the factorial of the number of input strings

3. Which of the following is **not** a true statement about the greedy shortest common superstring formulation of the assembly problem? 1 point

   - ○ It might collapse repetitive portions of the genome
   - ◉ The amount of time it takes grows with the factorial of the number of input strings
   - ○ The superstring returned might be longer than the shortest possible one

4. True or false: an Eulerian walk is a way of moving through a graph such that each node is visited exactly once 1 point

   - ◉ False
   - ○ True

5. If the genome is repetitive and we try to use the De Bruijn Graph/Eulerian Path method for assembling it, we might find that: 1 point

   - ◉ There is more than one Eulerian path
   - ○ The De Bruijn graph breaks into pieces
   - ○ The genome "spelled out" along the Eulerian path is not a superstring of the reads

6. In a De Bruijn assembly graph for given k, there is one edge per 1 point

   - ◉ k-mer
   - ○ read
   - ○ k-1-mer
   - ○ genome

7. Which of the following does not help with the problem of assembling repetitive genomes: 1 point

   - ○ Longer reads
   - ◉ Increasing minimum required overlap length for the overlap graph
   - ○ Paired-end reads

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