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

○ Concatenating the strings in of S

◉ Trying all orderings of the strings in S

○ Finding the longest common substring of the strings in S

○ Iteratively removing strings from S that don't belong in the superstring

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

- ⦿ The superstring returned might be longer than the shortest possible one

- ◯ It might collapse repetitive portions of the genome

- ◯ 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?

○ 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

- ● 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:

○ The genome "spelled out" along the Eulerian path is not a superstring of the reads

⦿ There is more than one Eulerian path

○ The De Bruijn graph breaks into pieces

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

- ⦿ k-mer
- ◯ genome
- ◯ read
- ◯ k-1-mer

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

○ Paired-end reads

○ Longer reads

● Increasing minimum required overlap length for the overlap graph