In an overlap graph, a directed edge from A to B indicates that:

○ A does not equal B

○ A is longer than B

◉ A suffix of read A is similar to a prefix of read B

○ A is similar to a substring of B

✓ **Correct**

The greedy shortest common superstrings works by repeatedly:

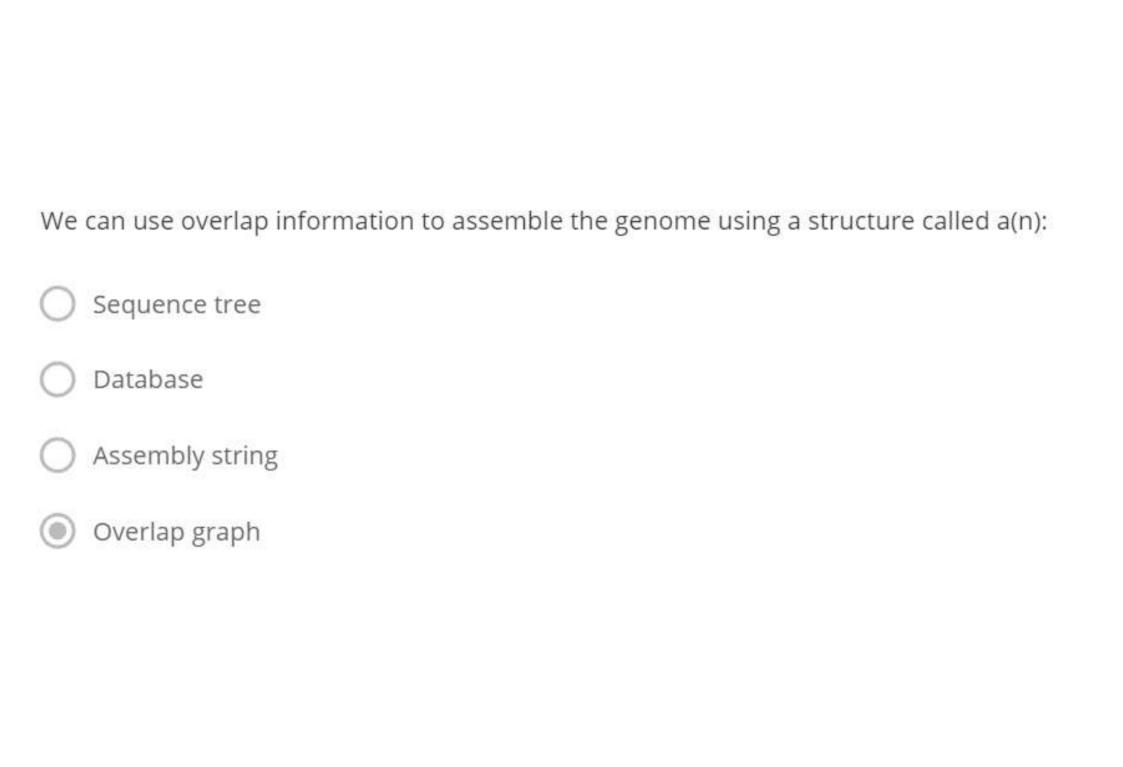○ finding the read that contains the most other reads as substrings

○ discarding reads that don't belong in the genome

○ concatenating random pairs of reads

◉ merging pairs of reads that overlap each other

✓ **Correct**

After filling the approximate matching matrix, we can find the minimal edit distance between P and a substring of T by:

○ Taking the value of the element in the lower right corder

○ Taking the minimum element in the first (top) row

● Taking the minimum element in the last (bottom) row

○ Taking the minimum element in the matrix

We can use overlap information to assemble the genome using a structure called a(n):

○ Sequence tree

○ Database

○ Assembly string

◉ Overlap graph

Which problem corresponds to a situation where we are analyzing sequencing data from a species that has never been sequenced before:
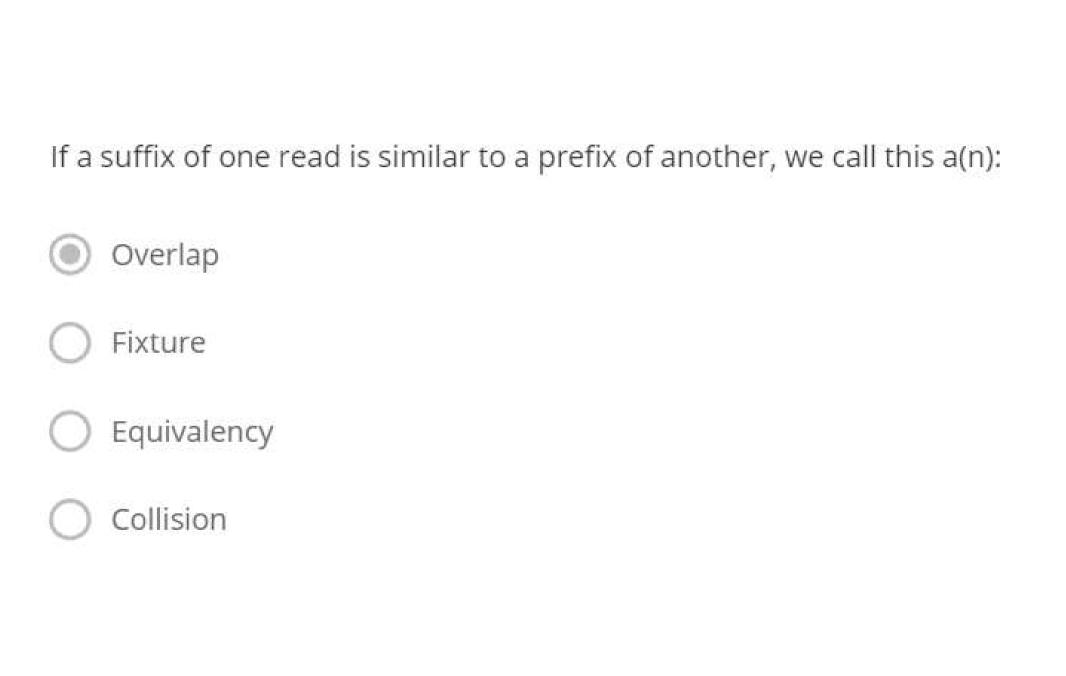
◉ Assembly

◯ Read alignment

✓ **Correct**

True or false: the greedy shortest common superstring algorithm will never report a shortest common superstring that's longer than the true shortest common superstring:

○ True

◉ False

✓ **Correct**

If a suffix of one read is similar to a prefix of another, we call this a(n):

○ Overlap

○ Fixture

○ Equivalency

○ Collision

Global alignment is concerned with the overall similarity between two strings X and Y, whereas local alignment is concerned with

○ the longest common prefix of X and Y

○ similarities between several strings, including but not limited to X and Y

○ the places where X occurs approximately within Y

◉ similarities between substrings of X and Y

✓ **Correct**

A vertical move in the traceback corresponds to:

○ An match in P with respect to T

○ An deletion in P with respect to T

○ A substitution between P and T

● A insertion between P and T

✓ **Correct**

The shortest common superstring problem is: given a set S of strings, we would like to find a string that:

○ Is shorter than any of the strings in S

◉ Contains all the strings in S as substrings

○ Is a permutation of all the strings in S

○ Is different from all the strings in S

The main difference between edit distance and global alignment is that

○ edit distance weighs all differences equally, where as global alignment can give different weights to different mutations

○ edit distance deals with two strings, whereas global alignment can deal with any number of strings

○ edit distance is substantially more work than global alignment

○ edit distance is only defined between two strings of the same length, where as global alignment score is defined for two strings regardless of length

✓ **Correct**