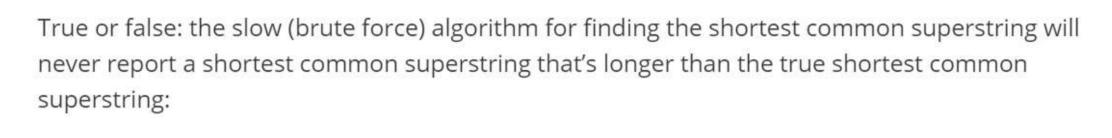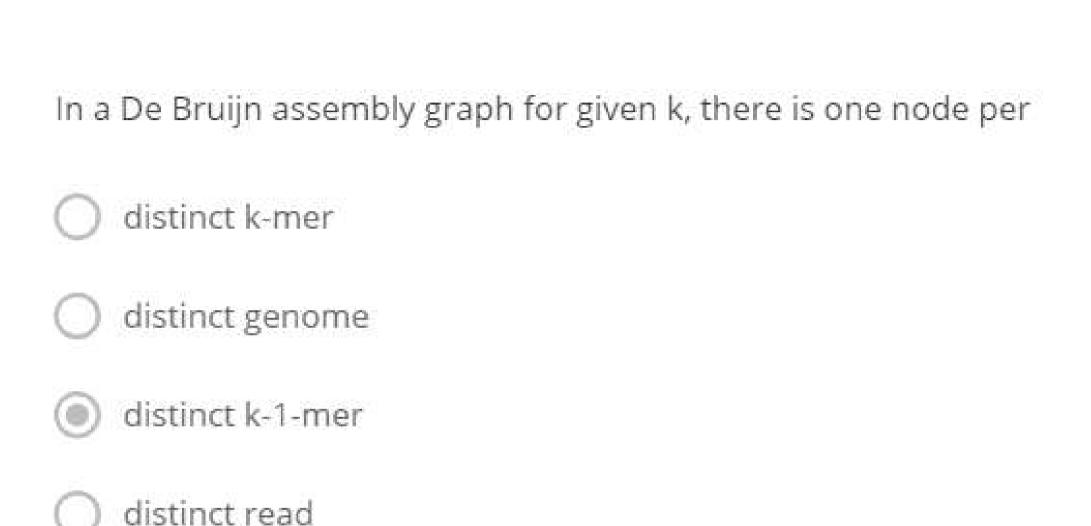In practice, assemblers deal with repetitive genomes by:

● splitting the assembly into unambiguous pieces

○ refusing to assemble them

○ reporting many possible reconstructions of the genome

Repetitive genomes pose a problem to De Bruijn graph assembly because:

O there is no Eulerian path

O the De Bruijn graph can have an infinite number of nodes

● the De Bruijn graph can have multiple Eulerian walks

True or false: the slow (brute force) algorithm for finding the shortest common superstring will never report a shortest common superstring that's longer than the true shortest common superstring:

⦿ True

◯ False

In a De Bruijn assembly graph for given k, there is one node per

○ distinct k-mer

○ distinct genome

◉ distinct k-1-mer

○ distinct read

A De Bruijn assembly graph is a multigraph, meaning it can:

○ represent multiple genomes

◉ have multiple edges between a given pair of nodes

○ have multiple nodes with the same label