

1. If you only had two reads, how would you assemble them into one sequence?

Example 1:

```
GTTTAACCGACTCCCTCAACTAAAGCACCCGGTA  
AATCCGAGGTGGATCTGTTTAACCGACTCCCTC
```

Example 2:

```
TAACTGTTTCGCATCATCATCAT  
CATCATCATCATCATCATCATGCATGCT
```

2. What is the N50 of the following contig lengths?

100
300
400
800
1000

3. Build a de Bruijn graph for the following two examples:

read 1: TGCCA
read 2: GCCAA

read 1: ATATAT
read 2: TATGCA