Score:

All aids including classmates

1. Explain what reads, contig and scaffold means. Draw the relationship between the 3
2. De Bruijn graphs are used for *de novo* assembly. What are the main advantages compared to overlap-layout consensus (OLC) assembly?
3. What is the optimal k-mer size for de Bruijn graph assembly of metagenomes?
4. What kind of sequence causes problems for de Bruijn graph assembly?
5. Why is *de novo* assembly harder with metagenomic samples than isolate DNA?
6. Why would we do metagenomic binning?
7. Why would we not do metagenomic binning?
8. What kind of information does Metabat use for binning?
9. CheckM is used for assesing the quality of metagenomic bins. It looks for single-copy genes, but this list of genes is not universal but based on?
10. Why is bin dereplication used?