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Marks	8.00/8.00
Grade	**10.00** out of 10.00 (**100**%)

Question 1

Correct

Mark 8.00 out of 8.00

Your work team has the mission of sequencing a collection of 30 bacterial strains that have caused an outbreak of nosocomial infections. The sequencing of these strains aims to taxonomically identify the strains, study their virulence profiles and antibiotic resistance mechanisms.

Based on the above, answer the following questions:

1. Indicate and justify the sequencing platform you would propose as the best option to sequence these strains.

- a- Illumina HiSeq, using a paired-end library and 1000bp read length
- b- Sanger sequencing using a 100bp read length library.
- c- Nanopore sequencing with an output of 20Gb, paired-end library and 300bp read length
- d- Illumina MiSeq using a paired-end library and 250bp read length ✔

2. If the genomes that need to be analyzed have an average genome lenght of 7.3Mb, what sequencing output do you need to sequence the 30 complete genomes with a depth of 100X? Indicate the result in Gb.

Numerical answer 21.9 ✔ Gb

3. What number of reads do you need to obtain if you sequence all the 30 genomes at 100X depth ? Consider a read size of 150bp and a genome size of 7.3Mb.

Numerical answer | 146000000 ✔ | reads.

4. What number of reads are needed to sequence a single complete genome at 100X? Consider a reads size of 125bp and a genome size of 7.3Mb.

Numerical Answer | 5840000 ✔ | reads.

5. a) If the sequencer can generate a maximum of 20Gb of information per sequencing run. What is the maximum number of 5Mb genomes that can be sequenced at 100X depth?

Numerical answer 41 ✔ genomes.

b) Considering a sequencing output of 20Gb, how many reads of 100 bp in paired-end format will be produced?

Numerical Answer 100000000 ✔ reads.

6. a) If the sequencer can generate a maximum of 20Gb of information per sequencing run. How many genomes could be sequenced if the depth is lowered to 10X? Consider a genome size of 7.5Mb and include one decimal.

Numerical answer 266.7 ✔ genomes.

6. b) What effects could a lower sequencing depth bring to the assembly of sequences?

- a-The quality will decrease due to the low number of sequences produced per genome, which will make it difficult to assemble contigs and scaffolds. ✔
- b- The quality of the assembly will improve since there will be less of data to analyze per genome and therefore a smaller number of contigs will be generated.
- c- The assembly will not be affected since it does not depend on the sequencing depth.
- d- Due to the low depth it will not be possible to obtain contigs