**ASSIGNMENT**

**Module topic: Introduction to NGS technologies and NGS data formats**

**Group:** *<write your group name here>*

**Participant:** <*write first name of all group members here>*

**Date:** <*write today’s date here*>

1. **NGS technologies and workflow**
2. You have a collection of ESBL-*Enterobacterales* isolates from patients with renal failure, dialyze water and healthcare workers. Which sequencing platform do you plan to use for sequencing of the isolates? Justify your point.

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1. You have a 10-year collection of multidrug-resistant *Mycobacterium tuberculosis* isolates. You would like to assess the mutation encoding resistance to isoniazid, rifampicin, and ethambutol. Which sequencing platform do you plan to use for sequencing of the isolates? Justify your point.

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1. You want to assess the microbiome of poultry and pigs at abattoirs and farms during your PhD project. Which sequencing platform do you plan to use for sequencing of the isolates? Justify your point.

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1. **NGS Data formats**
2. You have two files named RIA7\_S51\_R1\_001.fastq.gz and PR31S20.fasta. Open them with your text editor. Note the particularity of each file.
   1. What is the difference between fastq and fasta file?
   2. What does the R1.fastq mean?
3. Match the bioinformatics steps on the left with the NGS file on the right.

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| --- | --- | --- | --- |
| **No** | **Bioinformatics steps** | **NGS file** | **No** |
| 1 | Quality check sequencing | .gbk | A |
| 2 | De novo assembly | .vcf | B |
| 3 | Reference mapping | .fastqc | C |
| 4 | Variant calling | .sam | D |
| 5 | Annotation | .fasta | E |