TASK 1

1. download raw reads

2. quality control to rawreads using fastqc

3. trimming using fastp

4. quality control to trimmed reads

5. genome assembly using spdes

6. insilico serotyping using seqsero2 🡪 TSV

7. plasmidtyping using abricate plasmidfinder 🡪 CSV

8. AMR gene detection using amrfinderplus 🡪 CSV

**Faizan**

INTIAL 20 RAW READS

**Ayo**

MID 15 RAW READS

**Mariam**

LAST 15 RAW READS

TASK2

50 RAW READS DOWNLOAD > FASTQC > FASTP > SNIPPY > SNIPPYCORE >RAXML-NG > TREEFILE

TASK3

Plotting the phylogenetic tree [plot function], heatmap [Heatmap function in ComplexHeatmap package] and the summary data “isolation country, isolation date, and sample source” [rowAnnotations functions in ComplexHeatmap Function] using Rstudio.