AMR Bioinformatics Practical:

1. Load the NGS AMR 2022 virtual environment using Oracle VM VirtualBox.
2. Make sure the shortcut to the folder ”manager” is on the desktop
3. Open the terminal
4. Rename the “**Genome Assembly**” folder to “**Genome_Assembly**”

Practical 1 – FastQC

1. Do quality check on all Ecoli and Styphi raw fastq data

   (hint: the Ecoli and Styhi data files are inside the **Genome_Assembly/Raw_fastq** folder)

Questions:

A) How many reads are in Ecoil-A forward read file?

B) Is there any adaptor sequence in Styphi-C reverse read file?

Practical 2 - MultiQC

1. Generate MultiQC report from Styphi raw .fastq fastQC results
2. Generate MultiQC report from Ecoli raw .fastq fastQC results

Questions

a) Which Ecoli sample has the most reads?

b) What is the GC content of the Styphi samples?

Practical 3 – Trim galore

1. Generate MultiQC report from Ecoli raw fastq fastQC results
2. Generate MultiQC report from Styhi raw fastq fastQC results

Questions:

A) How many reads are in Ecoil-A forward read file?

B) Is there any adaptor sequence in Styphi-C reverse read file?

Practical 4 - BactInspector

1. Run bactinspector check_species on Ecoli-A trimmed data
2. Run bactinspector closest_match on Ecoli-A

Questions:

A) From the check_species result, what is the speice ID and the top hit distance?

B) From the closest_match result, what is the closet ReSeq match? (hint refseq_organism_name?)