**Project 2**

**Comparative Genome Analysis of Antibiotic Resistance Genes in *Escherichia coli* and *Staphylococcus aureus***

**Objective:** Identify and compare resistance genes between *E. coli* and *S. aureus*.

**Data Source:**

* NCBI Genome (download 2–3 complete genomes each of *E. coli* and *S. aureus*).
* CARD database (for resistance gene annotation).

**Steps:**

1. Download genome FASTA files from NCBI.
2. Use **RAST server (online genome annotation)** or **Prokka** to annotate genes.
3. Extract antibiotic resistance genes by BLASTing predicted proteins against **CARD** database.
4. Compare ARG types between *E. coli* and *S. aureus*.
5. Visualize results in a heatmap or table (R/Python/Excel).

**Deliverables:**

* Table/heatmap of resistance genes
* Report comparing resistance mechanisms in Gram-negative vs Gram-positive bacteria