

## AMR Gene Annotation of *de novo* Assembled Genomes using [Abricate](#)

(1) Run the Abricate pipeline using CARD and Resfinder as reference databases on the 2 *E. coli* and 2 *S. typhi* genomes you've assembled using Shovill. Save the output to a .csv file as below.

```
abricate --csv --db resfinder [sample_name.fa] > [sample_name]_resf.csv
```

```
abricate --csv --db card [sample_name.fa] > [sample_name]_card.csv
```

(2) Combine reports aligned with CARD and Resfinder and save each set to a .csv file.

```
abricate --csv --summary [sample-1_name.fa] [sample-2_name.fa] > summary_CARD.csv
```

```
abricate --csv --summary [sample-1_name.fa] [sample-2_name.fa] > summary_RESF.csv
```

(3) Plot the number of AMR genes of the genomes you characterised. Only include results with 95-100% identity match with those in the two databases.