

[9E] Using online tools for analysis of WGS data

Here you are asked to submit your answers to questions connected to the exercise using online tools. For this exercise you will perform analysis on four (4) separate genome assemblies of bacterial genomes using the online tools presented to you.

You have been provided with assembled sequencing data files generated from Illumina sequencing of genomic DNA extracted from pure cultures of bacteria. Using the online tools that have been demonstrated to you, please identify and characterize the isolates with respect to their genus, species (serotype (if applicable) and MLST (if applicable)). Also investigate and report on any presence of AMR determinants (acquired AMR genes or mutations in existing genes).

- Download the assembled genomes (fasta files) to your computer via [Jottacloud](#):
 - <https://www.jottacloud.com/s/25954b1afc443c140a78ff2707cf231ba2a>
 - There are four separate genome assemblies called Isolate 1-4.
- Run each of the four genomes through the appropriate online tools. I.e.
 1. Tool(s) to identify the bacterial species (genus, species, serotype if applicable)
 2. MLST (if applicable)
 3. Determine the presence of AMR determinants (acquired AMR genes or mutations in existing genes)
- Study the output results and answer the questions in the following survey:
<https://www.surveymonkey.com/r/9Eonlinetools>