**Exercise 1.**

Download the 3 fasta files that are in the EVA space.

1. Can you tell me which is the species we are analyzing?
2. To which ST and cgMLST they belong?
3. Which AMR genes are present? Which tool have you used?
4. Can you predict the AMR phenotype?
5. Are these phenotypes in line with the current epidemiology?

**Exercise 2.**

Download the 5 fasta files that are in the EVA space.

1. Which AMR genes are present? Which tool have you used?
2. Can you predict the AMR phenotype?
3. Are these phenotypes in line with the current epidemiology?