**Technical synopsis of the project (Antimicrobial resistance)**

Publically available dataset was downloaded from ENA database. The search was based on WGS of *E.coli* which were paired end data. The link to the project is given below:

* [PRJNA557416](https://www.ebi.ac.uk/ena/browser/view/PRJNA557416)
* [PRJNA595034](https://www.ebi.ac.uk/ena/browser/view/PRJNA595034)
* [PRJNA720242](https://www.ebi.ac.uk/ena/browser/view/PRJNA720242)
* [PRJNA799078](https://www.ebi.ac.uk/ena/browser/view/PRJNA799078)

Analysis of the dataset was done using command line and scripted in bash code. Different tools were used for analysis which are listed below in sequential manner:

* FastQC
* MultiQC
* Fastp
* Spades
* ResFinder

For computing I used Google cloudshell and entering the server address provided by the hackbio team but due to lot of storage problem, server crash problem, I couldnot continue the analysis. Thus I shifted to cloudshell itself without entering the hackbio server address. I also used gitpod for some analysis. Overall finding a proper space for computing was difficult however I used multiple spaces for that and some of them are listed below:

* Google cloud shell
* Google cloud shell (Hackbio address port)
* Windows powershell (in Ubuntu)
* Gitpod (using github)