
DTU

Simulated exercise on multispecies CPE outbreak

1st Meeting – Introduction to the exercise

EURGen-RefLabCap
Virtual multidisciplinary training workshop
November 2024

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Simulated exercises - background

- Series of multidisciplinary training workshops
  - Sept/Oct 2022: introduction to SNP analysis and cgMLST for cluster analysis (WS1)
  - May 2023 : Simulated exercise on outbreak analysis (*Klebsiella pneumoniae*, WS1)
  - Sept 2023: Simulated exercise on outbreak analysis (*Pseudomonas aeruginosa*, WS2)
  - Jan 2024: Simulated exercises on outbreak analysis (*Acinetobacter baumannii, WS2*)
  - Nov 2024: Simulated exercises on outbreak analysis (*WS2 Pathogens*)

WS1: CCRE/ *E. coli* and *Klebsiella* spp.
WS2: CPO/ *Pseudomonas aeruginosa* and *Acinetobacter baumannii*

Purpose of the workshop

- To build capacity to work with outbreak investigations
  - background information about bacterial subtyping and cluster analysis
  - Web-based bioinformatics tools to get started on bacterial phylogenetics and outbreak detection
  - To use WGS analyses and epidemiological data to elucidate the role of plasmids in dissemination of AMR during outbreaks

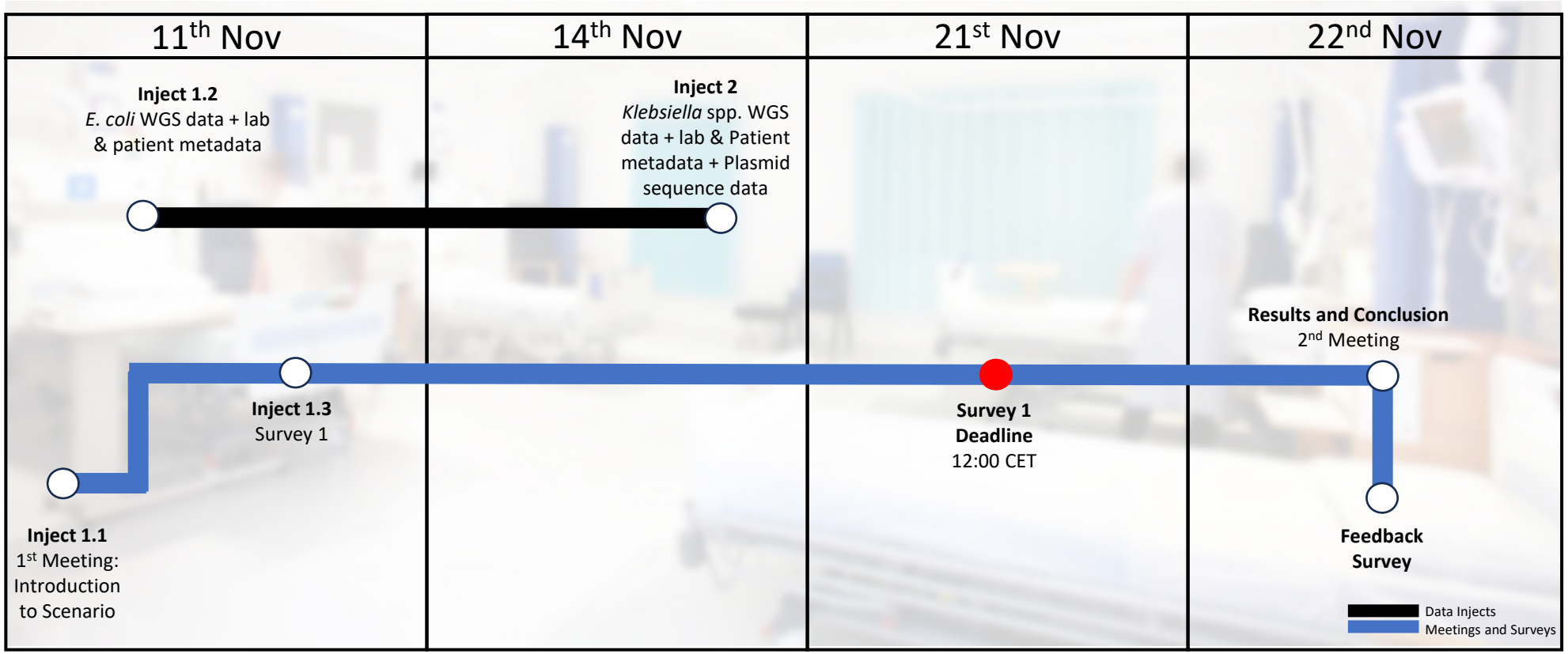
The workshops build on the previous workshops

– video recordings of previous workshops are available

Learning objectives

- To be able to perform a **cluster analysis of bacteria** to look into possible genetic relatedness in a dataset
- To be able to perform plasmid characterisation using WGS data and understand the pros and cons of using different types of data
  - Illumina vs ONT
  - Hybrid assembly
- To learn about other relevant **tools for sequence analysis** and work with a **real outbreak data set**
- Hands-on work on using the results from the cluster analysis, bacterial typing, and simulated patient metadata to elucidate a possible nosocomial outbreak

Exercise overview



Outbreak scenario background

Location: Hospital X, Europe

- Increased detection of carbapenem resistant *P. aeruginosa* (CRPa) in the ICU was observed.
- The infection prevention and control team (IPCT) has been alerted and initiated the screening of ICU for the multidrug resistant organisms (MDRO) upon admission, discharge, and twice weekly for patients in the ICU.
- There was an endemic problem with *Stenotrophomonas maltophilia* in the ICU detected in 2021 with a water reservoir as suspected source.
- Since *P. aeruginosa* and *S. maltophilia* are closely related environmental species and commonly associated with nosocomial infections, screening of environmental surfaces is being carried out in the ICU.

Fictitious

Scenario-Roles

Outbreak Management Team (OMT)

- Inter-department communication
- Patient health records
- Environmental assessment (e.g. identification of contaminated food or food handling equipment, infection control breaches, cleaning, environmental sampling)
- epidemiological data (e.g. movements and contacts of cases)
- Laboratory data (e.g. whole genome sequencing)

Participant's Role

The role of exercise participants is to support OMT in the analyses of epidemiology and laboratory data (including WGS data) to generate a hypothesis of the most likely exposure that has caused the outbreak.

Inject 1

Nov 11, 2024

-Introduction to the exercise outbreak scenario

-Tools for plasmid replicon typing

Inject 1.1 (Introduction)

09 carbapenem resistant *E. coli* isolates from different patients from Hospital X

- Epidemiological and laboratory data
- MLST, cluster analysis, AMR, Plasmid replicon analysis

Inject 1.2

Survey 1

Submit answers by Nov 21, 12:00 CET

Inject 1.3

Inject 2

Nov 14, 2024

Further 17 CPE from Hospital X will be available for cluster analysis, MLST and plasmid analysis

Inject 2

Results/discussion

Remember to respond to survey 1 by Nov 21, 12:00 CET

Nov 22, 2024

-Results and conclusion of the exercise

-Questions

A total of 26 CPE isolates

Tasks - analyses

Analyses

- Characterisation:
  - Carbapenem resistance mechanism?
  - Plasmid replicons
- Subtyping:
  - MLST
- Cluster analysis

Bioinformatics Tools

- ResFinder/CARD/AmrFinderPlus
- MOB-Suite (Galaxy server)
- MyDbFinder with custom replicon database
- MLST at CGE (or Pasteur)
- CSIPhylogeny

No need characterize all isolates! Analyse isolates that are relevant to answer the survey questions.

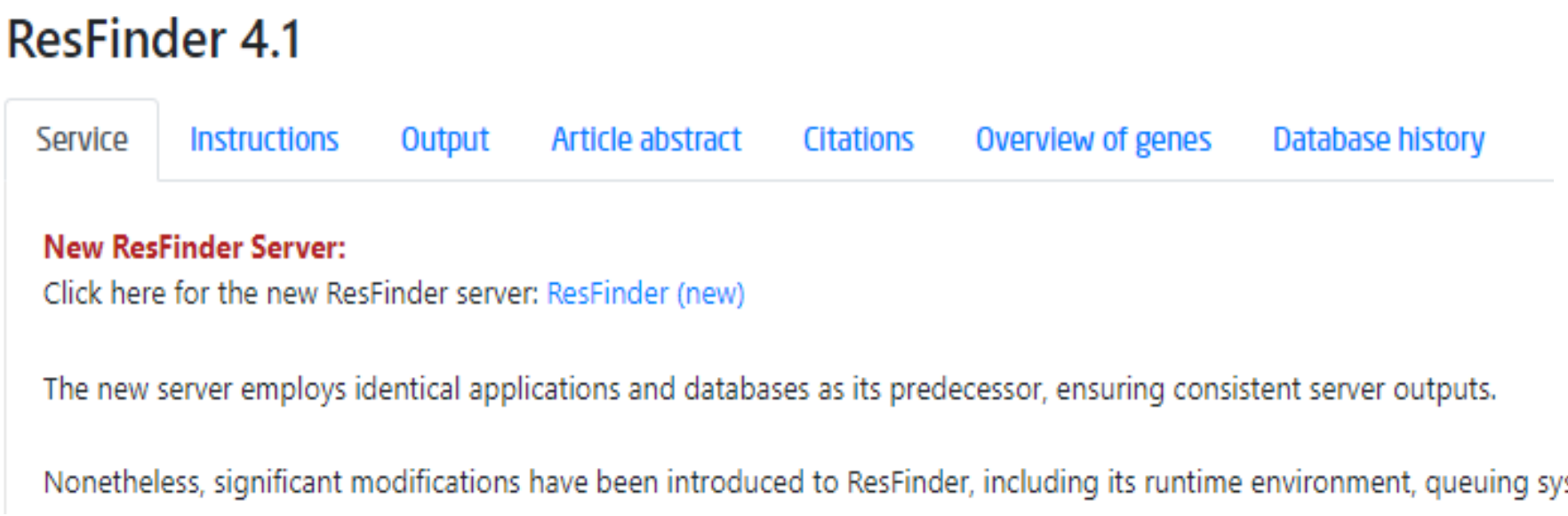
(Disclaimer: In the real outbreak, you need to characterize all the suspected case isolates)

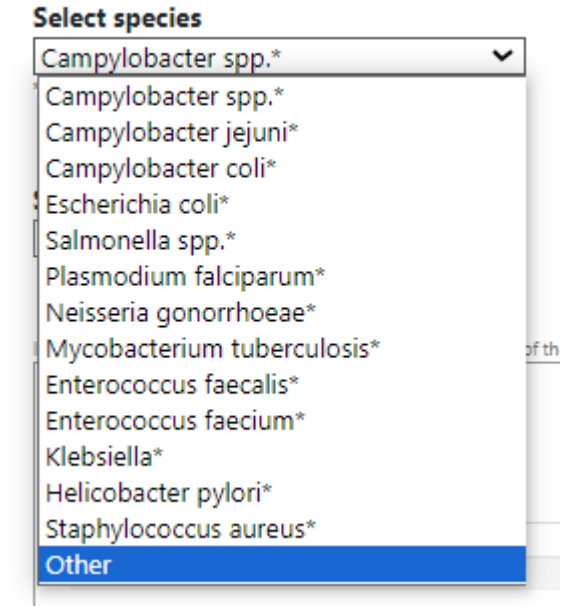
Survey questions

- AMR genes (carbapenemase gene and gene variant?)
- MLST's?
- How many clusters?
- Part of a cluster?
  - How many SNPs difference within core-cluster?
- Plasmid carrying carbapenemase gene?
- Possible source of the outbreak?
  - Environmental vs clinical isolates

PDFs of the survey questions (Inject 1.3 + 3.3) available

New ResFinder server & entry





Old:

https://cge.food.dtu.dk/services/ResFinder/

New:

http://genepi.food.dtu.dk/resfinder

Both are working and run-time should be faster!

Be aware – ResFinder does not have a point mutation scheme for Pseudomonas

– you can only search for acquired genes

Carbapenem resistance in *P. aeruginosa*

- Several mechanisms of resistance in action
  - Acquired carbapenemase genes
  - Point mutations
  - Porin modification/deletion
  - Efflux pumps

- Acquired genes are often on plasmids
  - Plasmid content is continuously evolving
  - High volume of small mobile genetic elements (MGE) on plasmids
  - Other MGEs can also carry resistance genes

Detection of plasmids from WGS data

- Several bioinformatics tools and databases are available for plasmid identification

- Usually, only the plasmid replicon is detected
- Numerous variants of some replicons

- Limited analysis possible using Illumina short reads!
  - Plasmid DNA can be assembled into several contigs
  - Hybrid plasmids are hard to detect

  - ONT MinION or other long read sequence data typically used for confirmation and full assembly/characterisation of plasmids

Co-localisation of plasmid replicons and resistance genes on same contig

- For *E. coli, Klebsiella* and other *Entrobacterales* there are several suitable tools
  - We have available CGE tools
    - **Limited** to Gram Positive & *Enterobacterales* plasmids

- It is more challenging to analyse other pathogens like:
  - *Pseudomonas aeruginosa*
  - *Acinetobacter baumannii*

https://cge.food.dtu.dk/services/MobileElementFinder/

https://cge.food.dtu.dk/services/PlasmidFinder/

MobileElementFinder: *E. coli* vs. *P. aeruginosa*

MobileElementFinder Results

Sample name: *E. coli*
Date:
MGEfinder version: 1.0.3
MGEdb version: 1.0.2

Displaying: **21** of **166** mobile elements

Contig	Plasmid	#MGEs	Resistance
NODE_57_length_12689_cov_1.779...		1	sul2
NODE_83_length_3482_cov_1.5576...		0	dfrA17, aadA5
NODE_45_length_31502_cov_5.278...	IncX4	0	mcr-1.26
NODE_79_length_3955_cov_2.1724...		0	tet(A)
NODE_41_length_41695_cov_5.106...	IncX1	1	blaTEM-32, blaTEM-40
NODE_35_length_44591_cov_1.855...		1	blaCTX-M-1
NODE_6_length_182344_cov_3.375...		2	
NODE_22_length_84699_cov_3.299...		2	
NODE_70_length_7174_cov_2.9338...		0	
NODE_31_length_49762_cov_2.263...	IncFII(pSE11)	0	
NODE_60_length_10308_cov_3.487...		0	
NODE_16_length_115775_cov_3.17...		0	
NODE_61_length_10163_cov_2.768...		0	
NODE_12_length_137967_cov_3.19...		0	

MobileElementFinder Results

Sample name: *P. aeruginosa*
Date:
MGEfinder version: 1.0.3
MGEdb version: 1.0.2

Displaying: **4** of **38** mobile elements

Contig	Plasmid	#MGEs	Resistance
contig00005 len=433304 cov=38....		0	fosA
contig00029 len=5266 cov=40.7 ...		0	tet(G)
contig00001 len=743927 cov=38....		0	blaPAO, aph(3')-IIb
contig00028 len=5992 cov=37.8 ...		0	rmtB
contig00022 len=84655 cov=38.1...		2	qacE, qnrVC1, ...
contig00010 len=272534 cov=39....		1	blaOXA-395
contig00051 len=930 cov=78.0 c...		0	sul1
contig00023 len=83036 cov=39.1...		0	catB7
contig00039 len=1569 cov=39.4 ...		0	blaNDM-1
contig00003 len=517527 cov=38....		0	crpP
contig00004 len=472663 cov=38....		1	

Plasmid replicon typing: alternative tools

- MOB-Typer is a tool from MOB-suite
  - Command-line tool and has no official web-based application

- Two ways we can still use MOB-suite without command-line interface
  - CGE tools: MyDBFinder (https://cge.food.dtu.dk/services/MyDbFinder/)
    - Simple tool for BLASTing your query sequence (.fa) against your specified database
      - Use the MOB Suite database to search for plasmid replicons
      - one isolate at a time!

  - European Galaxy server (https://usegalaxy.eu/)
    - MOB-Suite incorporated
      - Can handle batch-upload

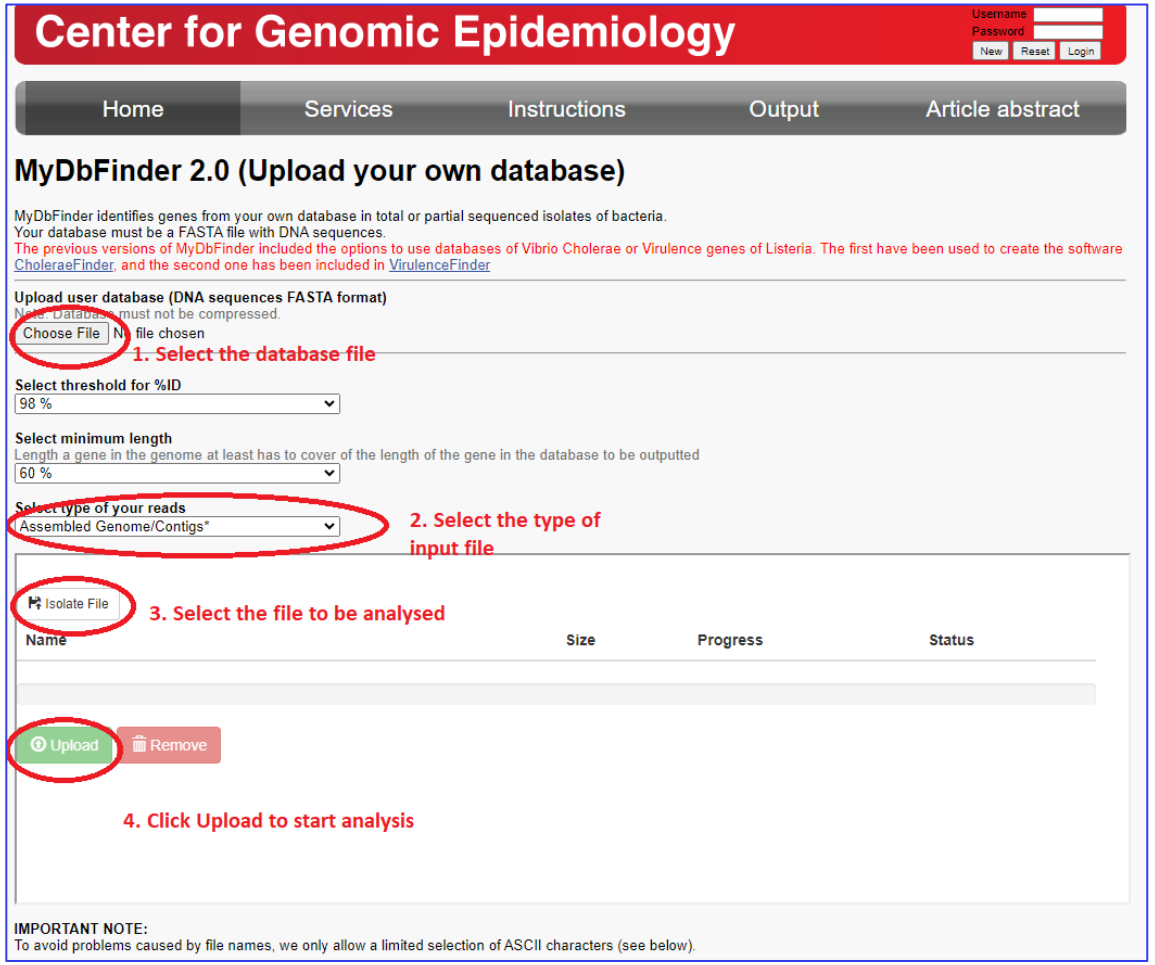
MOB-suite: Software tools for clustering, reconstruction and typing of plasmids from draft assemblies

https://github.com/phac-nml/mob-suite

Finding plasmids using MyDBFinder

- Choose the MOB Suite database (text file) as user data base (located in Inject 1.1 folder on ScienceData)
- Adjust threshold for ID if you like
- Analyse one strain per upload

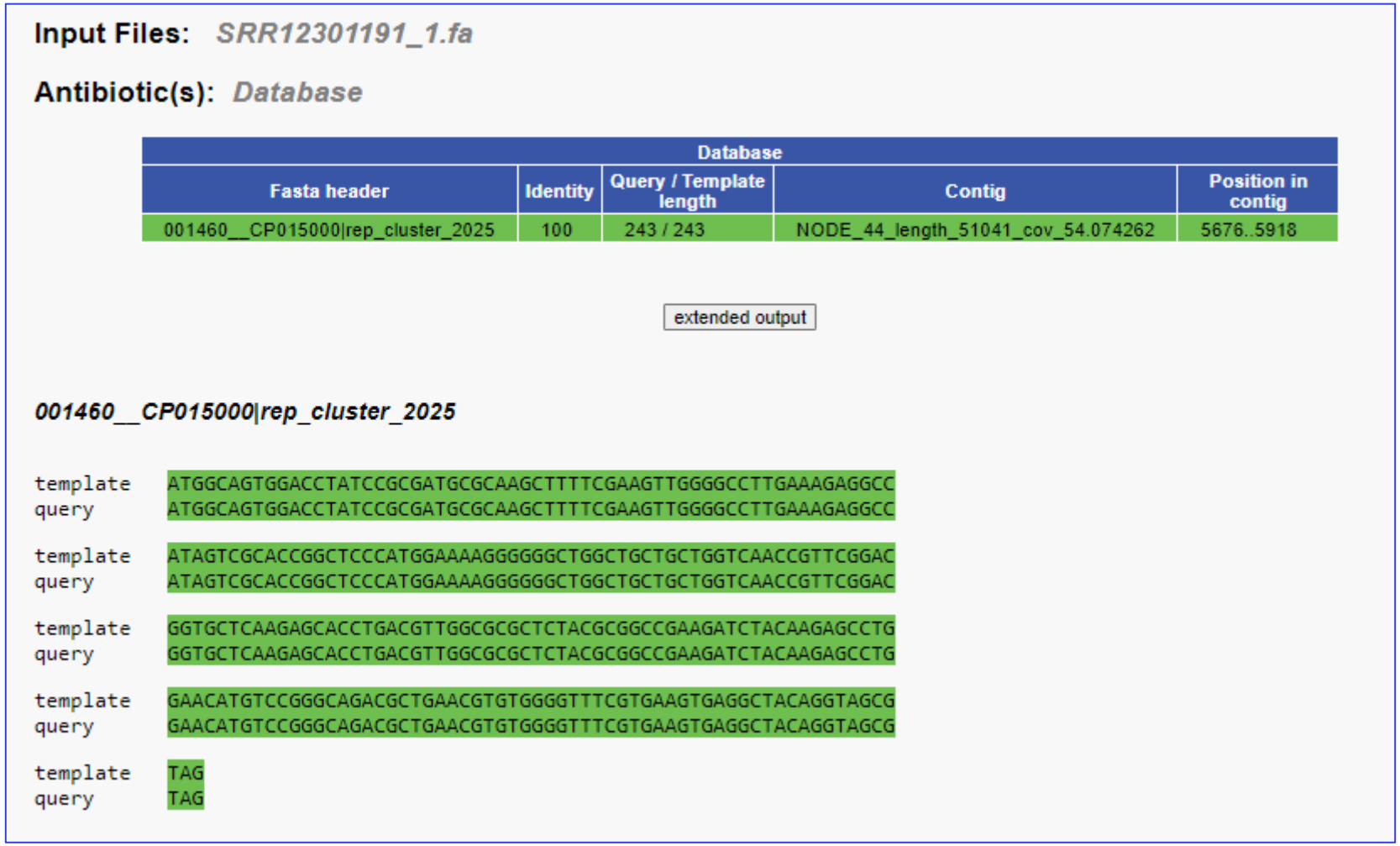
Database file: *rep.dna.fas*



Latest database can also be downloaded from MOB-Suite github page. See Annex. 3 in Inject 1.1

Output from MyDBFinder

- MOB Suite DB fasta header
  - Accession number: CP15000
  - Rep_cluster_#: 2025
  - Identity %
  - Length of replicon
  - Which contig (NODE_44)
  - Length of contig (51,041 bp)
  - Position in contig
- Extended output
  - Variations in bases



Input Files: *SRR12301191_1.fa*

Antibiotic(s): *Database*

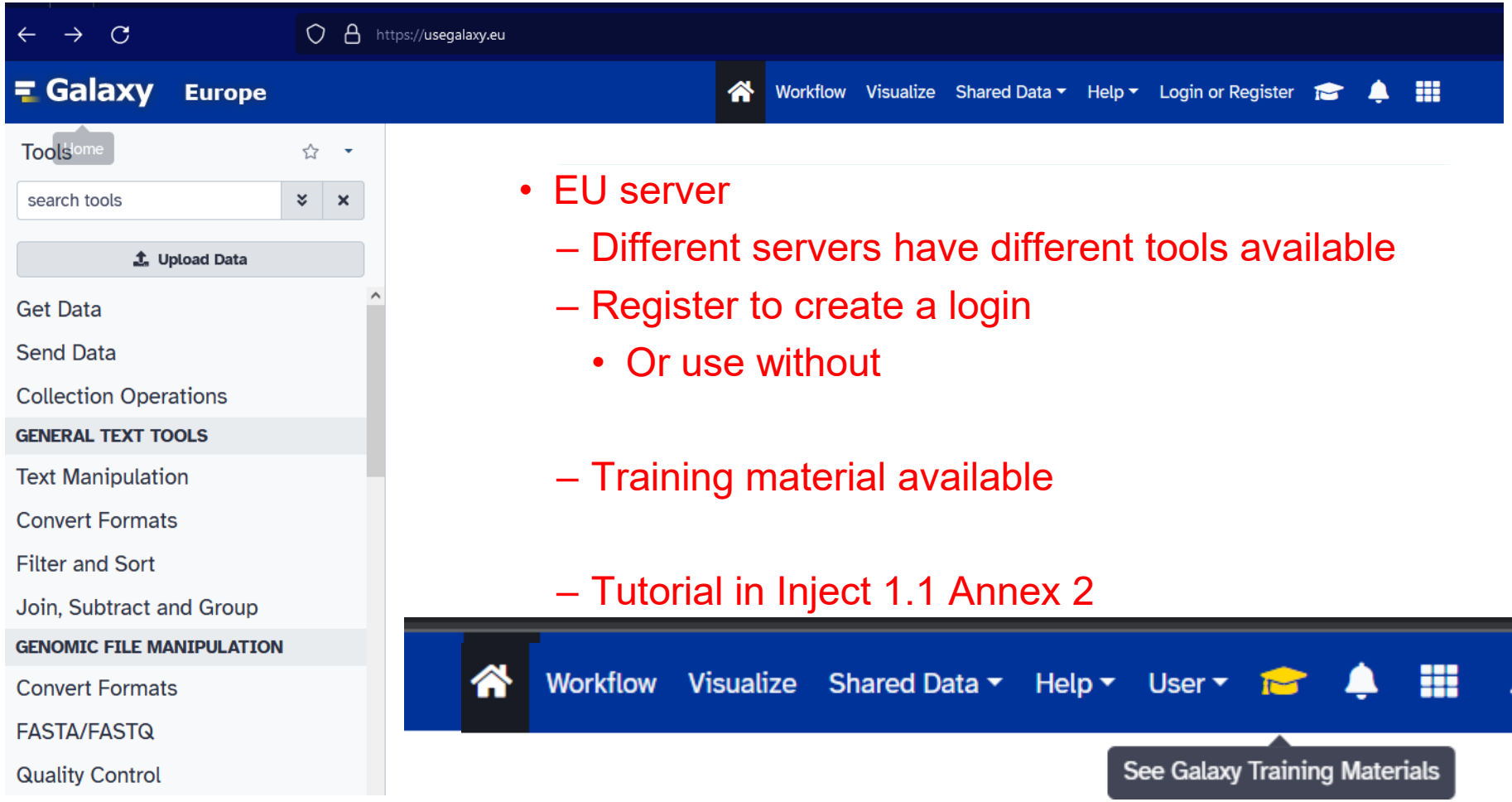
Database				
Fasta header	Identity	Query / Template length	Contig	Position in contig
001460__CP015000|rep_cluster_2025	100	243 / 243	NODE_44_length_51041_cov_54.074262	5676..5918

extended output

001460__CP015000|rep_cluster_2025

```
template  ATGGCAGTGGACCTATCCGCGATGCGCAAGCTTTTCGAAGTTGGGGCCTTGAAAGAGGCC
query     ATGGCAGTGGACCTATCCGCGATGCGCAAGCTTTTCGAAGTTGGGGCCTTGAAAGAGGCC

template  ATAGTCGCACCGGCTCCCATGGAAAAGGGGGGCTGGCTGCTGCTGGTCAACCGTTCGGAC
query     ATAGTCGCACCGGCTCCCATGGAAAAGGGGGGCTGGCTGCTGCTGGTCAACCGTTCGGAC

template  GGTGCTCAAGAGCACCTGACGTTGGCGCGCTCTACGCGGCCGAAGATCTACAAGAGCCTG
query     GGTGCTCAAGAGCACCTGACGTTGGCGCGCTCTACGCGGCCGAAGATCTACAAGAGCCTG

template  GAACATGTCCGGGCAGACGCTGAACGTGTGGGGTTTCGTGAAGTGAGGCTACAGGTAGCG
query     GAACATGTCCGGGCAGACGCTGAACGTGTGGGGTTTCGTGAAGTGAGGCTACAGGTAGCG

template  TAG
query     TAG
```

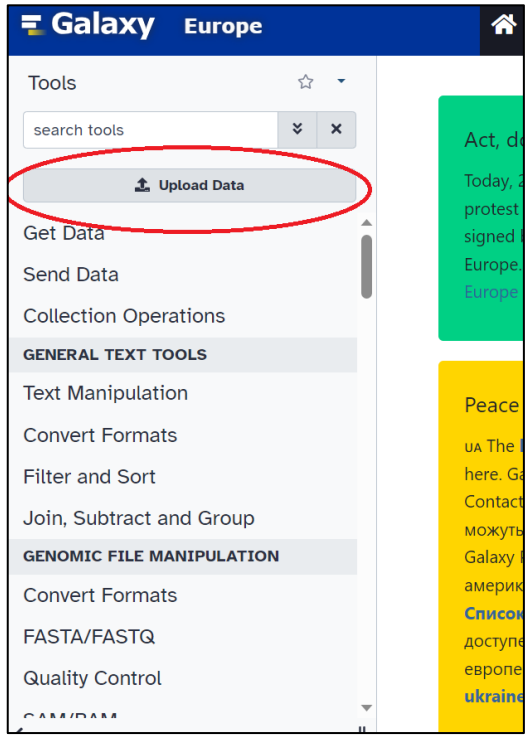
Use Galaxy – https://usegalaxy.eu/

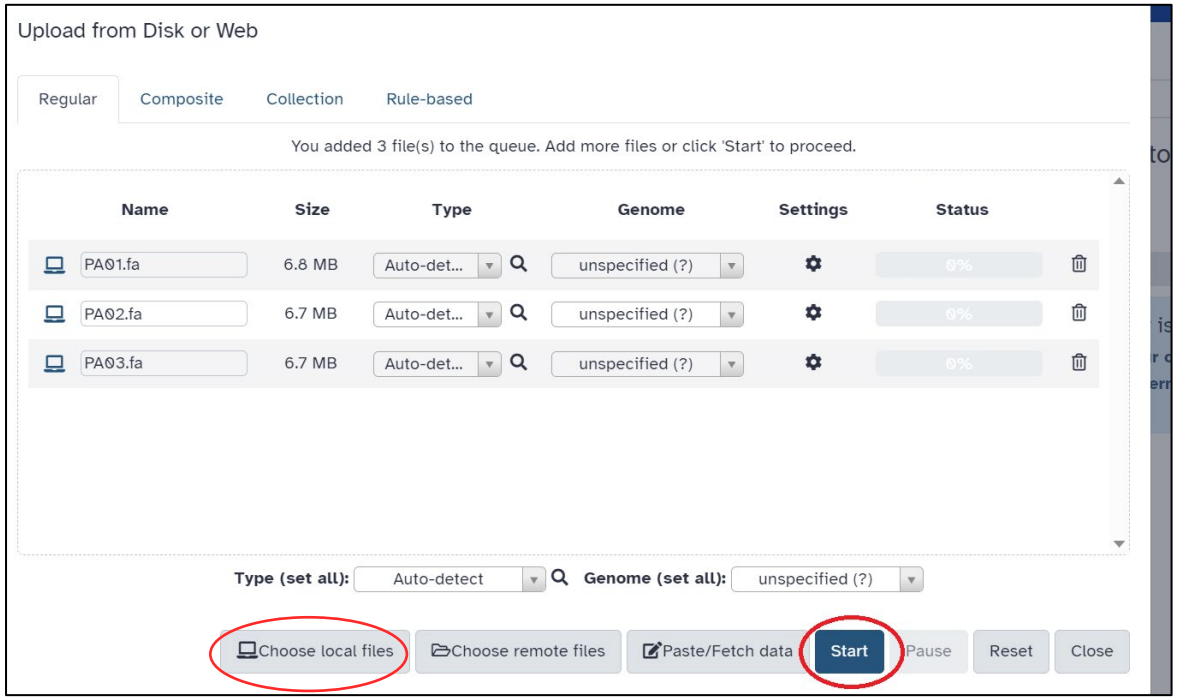


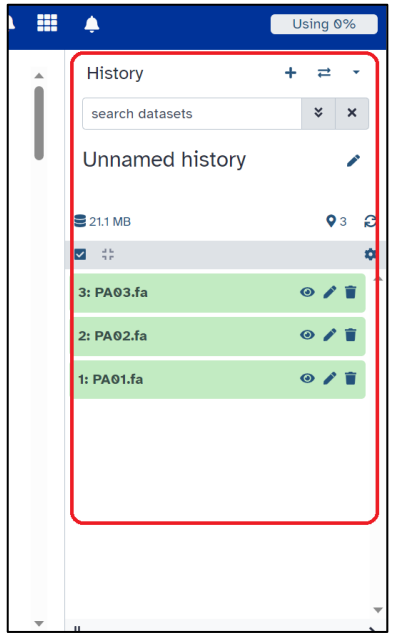
- EU server
  - Different servers have different tools available
  - Register to create a login
    - Or use without
  - Training material available
  - Tutorial in Inject 1.1 Annex 2

Galaxy: MOB typer

- Upload the genomes (fasta files) that you want to analyse with MOB-typer.

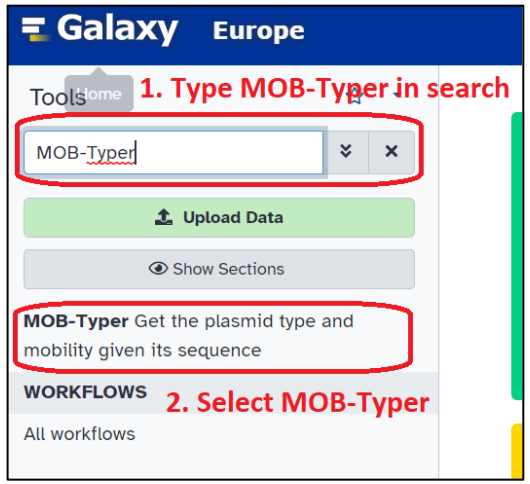




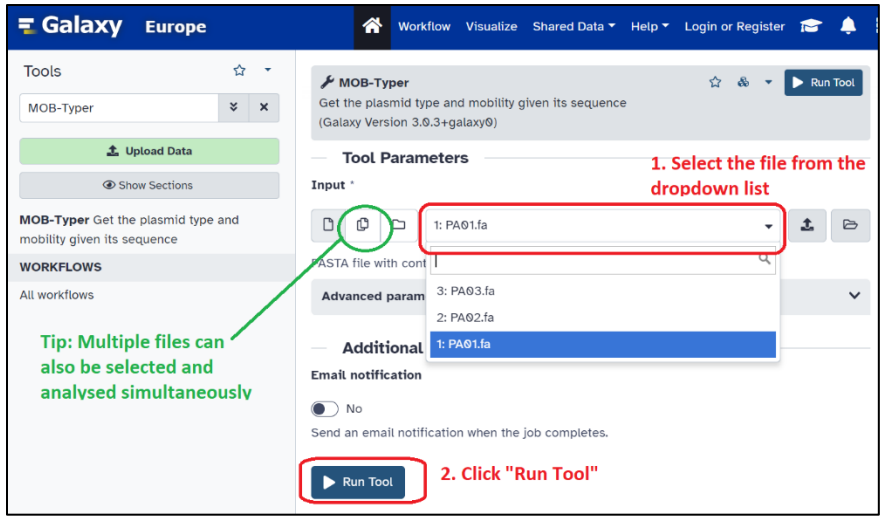


Galaxy: MOB typer

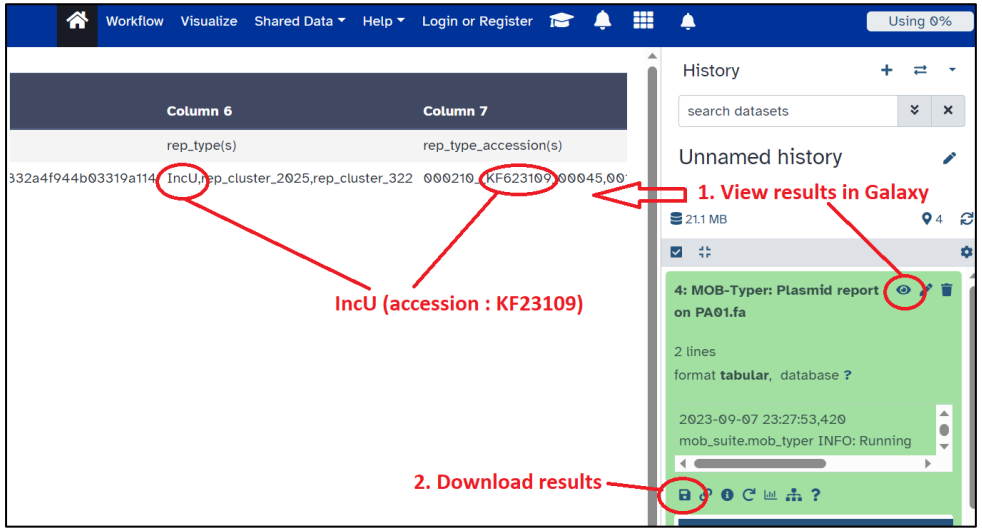
- Run **MOB-typer** from Galaxy Toolshed



Search MOB-Typer



Run the analysis



Interpret the results

Co-localisation of plasmid replicons and resistance genes on same contig?

- Use the Contig outputs from fasta file analysis
  - ResFinder or other AMR detection tool
  - MyDbFinder on plasmid database

  - Keep in mind that lack of consensus does not necessarily mean that the gene is not on a plasmid

Beta-lactam					
Resistance gene	Identity	Alignment Length/Gene Length	Position in reference	Contig or Depth	Position in contig
blaNDM-1	100.0	813/813	1..813	contig00039 len=1569 cov=39.4 corr=0 origname=NODE_39_length_1569_cov_39.422869 sw=shovill-spades/1.1.0 date=20230316	208..1020

Database				
Fasta header	Identity	Query / Template length	Contig	Position in contig
001460__CP015000|rep_cluster_2025	100	243 / 243	NODE_44_length_51041_cov_54.074262	5676..5918

Resources

- Slack
  - Injects (except sequence data)
  - Video recordings
  - Link to the surveys

- ScienceData folder: https://sciencedata.dk/shared/dd60004f4cccc3452d49f24cfb938af3
  - Sequence data
  - MOB-suite database (text file)
  - Inject text
  - Link to the surveys and PDF file of survey questions

- Data Injects: both fasta and fastq files for each isolate (Illumina)
  - No suitable MinION data available

Next Session (Friday, 22nd September 13:00-14:30 CET)

- Walkthrough of results and survey questions
- Discussion about cluster analysis
  - Input from participants
- Discussion about replicon typing tools
  - Input from participants
- MOB-Recon tool
- Feedback about the exercise

Questions/Comments?