

## Inter EURLs Working Group on NGS (Next Generation Sequencing)



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### PROGRAM

## Joint Training Course of the inter EURLs Working Group on NGS

### Introduction to Bioinformatics for genomic data mining

17 and 18 June 2025

#### Location:

ANSES - French agency for food, environmental and occupational health & safety  
14 rue Pierre et Marie Curie 94701  
Maisons-Alfort

#### Organised by:

EURL-*Listeria monocytogenes*  
EURL-Coagulase Positive Staphylococci (CPS)  
EURL-AMR  
EURL-*Campylobacter*  
EURL-Foodborne viruses  
EURL-Parasites  
EURL-*Salmonella*  
EURL-VTEC

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## Foreword

The inter EURLs Working Group (WG) has been established by the European Commission with the aim to promote the use of NGS across the EURLs' networks, build NGS capacity within EU and ensure liaison with the work of EURLs and the work of EFSA and ECDC on NGS mandate sent by the European Commission. The WG includes all EURLs operating in the field of the microbiological contamination of food and feed.

## Training course objectives:

- Providing an overview of different possible approaches for NGS data analysis.
- Illustrating the basic steps for data analysis (quality check, trimming, assembly, search of genetic features of interest).
- Providing guidelines for cluster analysis.
- Illustrating guidance documents on NGS analysis published by the Inter EURLs Working Group.
- Exchanging experiences among participants and reinforcing networking.

## After the course, the participants will be able to:

- Choose a solution for NGS data analysis.
- Understand the vocabulary connected to NGS data analysis.
- Perform basic analysis on NGS data (quality check, trimming, assembly, search of genetic features of interest).
- Evaluate and interpret the results obtained.
- Understand the concepts behind different cluster analysis approaches.

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European Union Reference Laboratory  
Foodborne Viruses



EURL Lm  
European Union Reference Laboratory for  
*Listeria monocytogenes*  
https://eur1-listeria.ecdc.europa.eu



## TUESDAY 17 JUNE 2025

### 08.45 Registration (for entering the premises of ANSES)

09.00 Welcome and general overview of the joint training activities (Adrien Asséré, EURL-*Listeria monocytogenes*)

09.15 Introduction of the inter EURLs Working Group on NGS and the guidance documents released (Valeria Michelacci, EURL-VTEC)

09.30 Introduction to WGS

1. Sequencing platforms & output data (Maroua Sayeb, EURL-*Listeria monocytogenes*)
2. Verification of the integrity of the raw data files (like md5sum) (Angela van Hoek, EURL-*Salmonella*)
3. Bioinformatics analysis of NGS data: approaches and opportunities (command-line tools, commercial software, webserver) (Joakim Skarin, EURL-Foodborne viruses)

### 10.20 Coffee break

10.50 Introduction to quality check and trimming (Valeria Michelacci, EURL-VTEC)

### 11.05 Hands-on exercises – Quality check and trimming

Quality check and trimming using different tools and platforms. Results interpretation.

*FastQC and Positional and Quality Trimming on ARIES* (Valeria Michelacci, EURL-VTEC)

*Demo: Quality check and trimming with alternative tools* (Bo Segerman, EURL-*Campylobacter*)

### 12.45 Lunch break

14.00 Introduction to assembly and assembly statistics (Joana Mourão, EURL-AMR)

### 14.15 Hands-on exercises – Assembly statistics

Assembly statistics using different tools and platforms. Results interpretation.

*Hands-on SPAdes and Quast from ARIES* (Luca De Sabato, EURL-VTEC)

15.15 Introduction to gene detection using mapping approach: tools and data formats data (Paolo Vatta, EURL-Parasites)

### 15.25 Hands-on exercises – Mapping approach

Demonstration of mapping through different platforms.

*Hands-on E. coli virulotyping using a mapping approach* (Rosangela Tozzoli, EURL-VTEC)

*Demo: Mapping with SeqSphere* (Maroua Sayeb, EURL-*Listeria monocytogenes*)

16.40 Amplicon-based sequencing of viral genomes (Luca De Sabato, EURL-VTEC)

### 17.00 End of the first day

19.00 Optionally, a group dinner will be organised (for participants own costs)

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## WEDNESDAY 18 JUNE 2025

- 09.00 Introduction to gene detection using BLAST approach (Marina Cavaiuolo, EURL-CPS)
- 09.15 **Hands-on exercises – Search of genetic features on contigs**  
Identification of virulence and AMR genes using different tools and platforms. Results and interpretation.  
Demonstration of genes identification on contigs through different platforms.  
*Hands-on ResFinder on CGE webserver* (Joana Mourão, EURL-AMR)  
*Demo: Salmonella virulotyping with Seqsphere* (Angela van Hoek, EURL-Salmonella)
- 10.30 Introduction to genome comparisons: gene-by-gene vs SNP approach (Bo Segerman, EURL-Campylobacter)
- 10.50 **Coffee break**
- 11.20 Demonstration of gene-by-gene approach through different platforms:  
ARIES (Rosangela Tozzoli, EURL-VTEC)  
Starflow (Maroua Sayeb, EURL-*Listeria monocytogenes* and Marina Cavaiuolo, EURL-CPS)  
Seqsphere (Angela van Hoek, EURL-Salmonella)
- 12.30 **Lunch break**
- 13.45 **Hands-on exercises – Visualisation of clustering data**  
Demonstration via Grapetree (Maroua Sayeb, EURL-*Listeria monocytogenes*)
- 14.00 Parasites WGS: opportunities and challenges (Simone Cacciò, EURL-Parasites)
- 14.30 EFSA One Health WGS database and demo (Mirko Rossi, EFSA)
- 15.30 Wrap up (Adrien Asséré, EURL-*Listeria monocytogenes*)
- 16.00 **Closure**