

Inter-EURLs Working Group on NGS (NEXT GENERATION SEQUENCING)



European Union Reference Laboratory
Foodborne Viruses



EURL Lm
European Union Reference Laboratory for
Listeria monocytogenes
https://eur01.safelinks.europa.eu



Foreword:

The 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 the EU and ensure liaison with the work of the EURLs and the work of EFSA and ECDC on the NGS mandate sent by the Commission. The WG includes all the EURLs operating in the field of the microbiological contamination of food and feed.

Joint Training Course of the inter EURLs Working Group on NGS: Introduction to Bioinformatics for genomic data mining

Istituto Superiore di Sanità

Viale Regina Elena 299

00161 Rome, Italy

Organised by:

EURL VTEC

EURL *Listeria monocytogenes*

EURL *Salmonella*

EURL Coagulase Positive Staphylococci

EURL Parasites

EURL Foodborne viruses

EURL AMR

EURL *Campylobacter*

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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

DRAFT PROGRAM

June 14th 2022

9.30 **Registration**

9.45 Welcome and general overview on the joint training activities (S. Morabito)

10.00 Introduction to WGS

1. Sequencing platforms & output data (20') (EURL VTEC)
2. Bioinformatics analysis of NGS data: approaches and opportunities (command-line tools, commercial software, web servers) (20') (EURL Viruses)

10.40 **Coffee break**

11.10 Amplicon-based sequencing of viral genomes (20') (Luca De Sabato, ISS)

11.30 Introduction on quality check and trimming (EURL VTEC)

11.50 **Hands on exercises – Quality check and trimming**

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

FastQC and Positional and Quality Trimming on ARIES (EURL VTEC)

Quality check and trimming with Seqsphere (EURL Campylobacter)

12.50 **LUNCH BREAK**

14.30 Introduction on assembly and assembly statistics (EURL AMR)

14.45 **Hands on exercises – Assembly statistics**

Assembly statistics using different tools and platforms. Results interpretation.

Hands-on SPAdes and Quast from ARIES (EURL VTEC)

Demo: Seqsphere Assembly Quality Check (EURL Salmonella)

15.30 Introduction on the approaches for searching genetic features (alignments of reads or contigs) (TBA)

15.45 **Hands on exercises – Mapping approach**

Demonstration of mapping through different platforms.

Hands-on E. coli virulotyping using a mapping approach (EURL VTEC)

Demo: Mapping with Seqsphere (TBA)

16.30 End of the first day

19.00 Optionally, a group dinner will be organized (Supported by home institutions)

June 15th 2022

09.30 **Hands on exercises – Search of genetic features on contigs**

Identification of virulence and AMR genes using different tools and platforms. Results interpretation.

Demonstration of genes identification on contigs through different platforms

Hands-on VirulenceFinder on CGE webserver (TBA)

Hands-on ResFinder on CGE webserver (EURL AMR)

Demo: Salmonella virulotyping with Seqsphere (EURL Salmonella)

10.30 Introduction to genome comparisons: gene-by-gene VS SNPs
(Guidance document on cluster analysis) (EURL Campylobacter)

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- 11.00 Demonstration of gene-by-gene approach through different platforms:
ARIES (EURL VTEC)
Startflow (EURL *Listeria* and EURL CPS)
Seqsphere (EURL *Salmonella*)
Visualization tools (Phyloviz, iTol, Figtree ecc) (TBA)
- 11.45 Phylogenesis of parasites through NGS data (EURL Parasites)
- 12.00 Update on the collection and management of NGS data for molecular typing (EFSA)
- 12:30 **LUNCH**
- 13:30 Strategies and opportunities for NGS analysis applied to food-borne threats. Overview of documents released by the Inter EURLs WG:
Basic analytical tools (Document on bioinformatics tools for basic analysis) (EURL VTEC)
Reference Whole Genome Sequencing collection (EURL *Salmonella*)
Guidance document for NGS-Benchmarking (EURL *Listeria*)
Inventory of training supports (EURL CPS)
- 14:00 Wrap up
- 14.30 **Closure**