

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



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
AULA ROSSI
Via Giano della Bella, 34
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*

Funded by the European Commission – DG SANTE

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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

PROGRAM

June 14th 2022

- 9.30 **Registration**
- 9.45 Welcome and general overview on the joint training activities
(Stefano Morabito, EURL VTEC)
- 10.00 Introduction to WGS
1. Sequencing platforms & output data (20') (Maroua Sayeb, EURL *Listeria*)
 2. Bioinformatics analysis of NGS data: approaches and opportunities (command-line tools, commercial software, web servers) (20') (Joakim Skarin, EURL Viruses)
- 10.40 **Coffee break**
- 11.10 Amplicon-based sequencing of viral genomes (20') (Luca De Sabato, ISS)

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European Union Reference Laboratory
Foodborne Viruses



EURL Lm
European Union Reference Laboratory for
Listeria monocytogenes
http://eur-lex.europa.eu



- 11.30 Introduction on quality check and trimming (Valeria Michelacci, EURL VTEC)
- 11.50 **Hands on exercises – Quality check and trimming**
Quality check and trimming using different tools and platforms. Results interpretation.
Hands-on: FastQC and Positional and Quality Trimming on ARIES (Valeria Michelacci, EURL VTEC)
Demo: Quality check and trimming with SeqSphere (Ásgeir Ástvaldsson, EURL Campylobacter)
- 12.50 **LUNCH BREAK**
(a list of suggested snack bars and restaurants will be provided)
- 14.30 Introduction on assembly and assembly statistics (Lauge Holm Sørensen, 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 (Federica Gigliucci, EURL VTEC)
Demo: SeqSphere Assembly Quality Check (Angela van Hoek, EURL Salmonella)
- 15.30 From BAM to BCF and beyond, making sense of aligned data (Paolo Vatta, EURL Parasites)
- 16.00 **Hands on exercises – Mapping approach**
Demonstration of mapping through different platforms.
Hands-on: E. coli virulotyping using a mapping approach (Federica Gigliucci, EURL VTEC)
Demo: Mapping with SeqSphere (Maroua Sayeb, EURL Listeria)
- 16.45 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.

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Demonstration of genes identification on contigs through different platforms

Hands-on ResFinder on CGE webserver (Lauge Holm Sørensen, EURL AMR)

Demo: Salmonella virulotyping with SeqSphere (Angela van Hoek, EURL Salmonella)

- 10.10 Introduction to genome comparisons: gene-by-gene VS SNPs
(Guidance document on cluster analysis) (Ásgeir Ástvaldsson, EURL *Campylobacter*)
- 10.40 Demonstration of gene-by-gene approach through different platforms:
ARIES (Federica Gigliucci, EURL VTEC)
Startflow (Maroua Sayeb, EURL *Listeria* and Marina Cavaiuolo, EURL CPS)
SeqSphere (Angela van Hoek, EURL *Salmonella*)
- 11.15 Parasites WGS: opportunities and challenges (Simone M. Cacciò, EURL Parasites)
- 12.00 Update on the collection and management of NGS data for molecular typing (Mirko Rossi, EFSA)
- 12:30 **LUNCH**
(a list of suggested snack bars and restaurants will be provided)
- 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) (Valeria Michelacci, EURL VTEC)
 - Reference Whole Genome Sequencing collection (Angela van Hoek, EURL *Salmonella*)
 - Guidance document for NGS-Benchmarking (Maroua Sayeb, EURL *Listeria*)
 - Inventory of training supports (Marina Cavaiuolo, EURL CPS)
- 14:00 Wrap up
- 14.30 **Closure**