

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

20 and 21 June 2023

Location:

National Institute for Public Health and the Environment (RIVM)
Antonie van Leeuwenhoeklaan 9
3721 MA Bilthoven
The Netherlands
Meeting room V1.34

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Organised by:

EURL-AMR
EURL-*Campylobacter*
EURL-Coagulase Positive Staphylococci (CPS)
EURL-Foodborne viruses
EURL-*Listeria monocytogenes*
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 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.

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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TUESDAY 20 JUNE 2023

- 9.15 **Registration (for entering the premises of RIVM)**
- 9.45 Welcome and general overview on the joint training activities (Wilma Jacobs, EURL-*Salmonella*)
- 10.00 Introduction to WGS
1. Sequencing platforms & output data (20') (Adrien Asséré, EURL-*Listeria monocytogenes*)
 2. Verification of the integrity of the raw data files (like md5sum) (20') (Angela van Hoek, EURL-*Salmonella*)
 3. Bioinformatics analysis of NGS data: approaches and opportunities (command-line tools, commercial software, web servers) (20') (Joakim Skarin, EURL-Viruses)
- 11.00 **Coffee break**
- 11.20 Introduction on quality check and trimming (Valeria Michelacci, EURL-VTEC)
- 11.40 **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)
Quality check and trimming with Seqsphere (Bo Segerman, EURL-Campylobacter)
- 12.45 **Lunch break**
- 13.45 Introduction on assembly and assembly statistics (Lauge Holm Sørensen, EURL-AMR)
- 14.00 **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)
- 15.00 From BAM to BCF and beyond, making sense of aligned data (Paolo Vatta, EURL-Parasites)
- 15.30 **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 (Déborah Merda, EURL-Listeria monocytogenes)
- 16.30 Amplicon-based sequencing of viral genomes (Luca De Sabato, ISS)
- 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 21 JUNE 2023

- 8.45 **Registration (for entering the premises of RIVM)**
- 9.15 Introduction to gene detection using BLAST approach (Marina Cavaiuolo, EURL-CPS)
- 9.30 **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 ResFinder on CGE webserver (Lauge Holm Sørensen, EURL-AMR)
Demo: Salmonella virulotyping with Seqsphere (Angela van Hoek, EURL-Salmonella)
- 10.15 Parasites WGS: opportunities and challenges (Simone Cacciò, EURL-Parasites)
- 10.45 **Coffee break**
- 11.00 Introduction to genome comparisons: gene-by-gene VS SNPs ([Guidance document for cluster analysis](#)) (Bo Segerman, EURL-Campylobacter)
- 11.30 Demonstration of gene-by-gene approach through different platforms:
ARIES (EURL-VTEC)
Seqsphere (Angela van Hoek, EURL-Salmonella)
Starflow (Déborah Merda, EURL-Listeria monocytogenes and Marina Cavaiuolo, EURL-CPS)
- 12.15 **Hands-on exercises – Visualisation of clustering data**
Demonstration via Grapetree (Déborah Merda, EURL-Listeria monocytogenes)
- 12:45 **Lunch break**
- 13.45 Update on the EFSA OneHealth WGS database (Mirko Rossi, EFSA)
- 14:15 Information on activities of inter EURLs Working Group on NGS and guidance documents released (Valeria Michelacci, EURL-VTEC)
- 14:45 Wrap up (Wilma Jacobs-Reitsma, EURL-Salmonella)
- 15.00 **Closure**