Update from the Inter EURL working group on NGS





INTER EURLS WORKING GROUP ON NGS

















AIM

to promote the use of WGS across the EURLs' networks, build WGS capacity within the EU and ensure liaison with the work of the EURLs and the work of EFSA and ECDC on the WGS mandate sent by the Commission

from November 2017

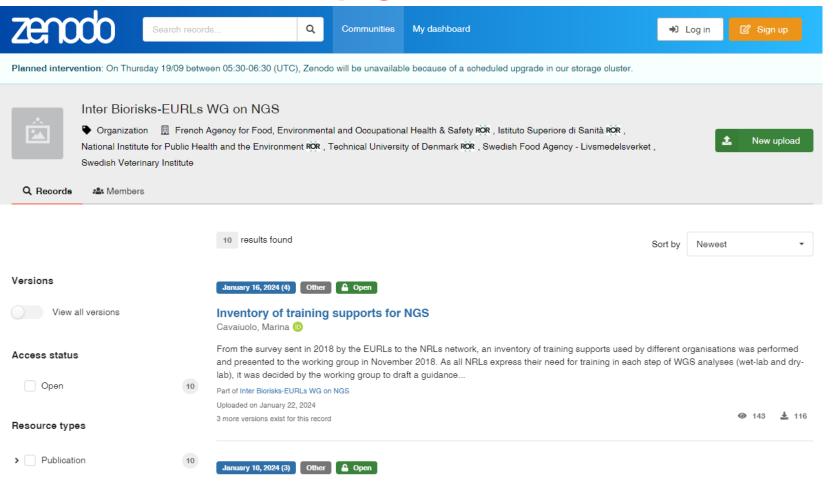
Meeting twice a year (14 meetings done)





Inter EURLs WG webpage

The webpages of each EURL contain the direct link to the new webpage dedicated to the Inter EURLs WG on NGS





Direct link!

https://zenodo.org/communities/eurls-biorisks_wg_on_ngs

All the versions of all the documents are always available on Zenodo

The new versions always appear as first choices

Supporting documents available

Overview of conducted and planned PTs – curated by EURL Antimicrobial Resistance

Reference Whole Genome Sequencing collection – curated by EURL Salmonella

Guidance document for WGS-laboratory procedures – curated by EURL Parasites

★ Bioinformatics tools for basic analysis of Next Generation Sequencing data — curated by EURL VTEC

Guidance document for Whole Genome Sequencing - cluster analysis – curated by EURL Campylobacter

Guidance document for NGS-Benchmarking – curated by EURL Listeria

★ Inventory of training supports — curated by EURL Coagulase Positive Staphylococci

Survey on the use of NGS across the NRLs networks – curated by EURL VTEC

Supporting document for preparing high quality DNA for Whole Genome Sequencing – curated by EURL VTEC

in continuous update

Webinar dedicated to NGS PTs

Proficiency Tests on Next Generation Sequencing: approaches in use at the European Union Reference Laboratories

Friday September 29th 2023, 10 am - 12 am

Online through Microsoft Teams

Organised by the Inter EURLs WG on NGS, involving:

EURL-AMR

EURL-Campylobacter

EURL-Coagulase Positive Staphylococci (CPS)

EURL-Foodborne viruses

EURL-Listeria monocytogenes

EURL-Parasites

EURL-Salmonella

EURL-VTEC

178 participants29 Countries

22 EU Member States

3 EEA + EFTA

2 EU Candidates

2 Extra EU

1 EC

https://www.iss.it/en//proficiency-tests-on-nextgeneration-sequencingapproaches-in-use-at-theeuropean-union-referencelaboratories-webinar-29-

september-2023-

Presentations have been published on EURL *E. coli* website and mirrored in all the websites of the other EURLs





3rd joint training – June 25th-26th 2024, Uppsala (Sweden)

Introduction to Bioinformatics for genomic data mining

TUESDAY 25 JUNE 2024		WEDNESDAY 26 JUNE 2024	
8.45	Registration (for entering the premises of SVA)	8.45	Registration (for entering the premises of SFA)
09.00	Welcome and general overview of the joint training activities (Hanna Skarin, EURL- Campylobacter)	9.00	Introduction to gene detection using BLAST approach (Marina Cavaiuolo, EURI CPS)
09.15	Introduction of the inter EURLs Working Group on NGS and the guidance documents released (Valeria Michelacci, EURL-VTEC) Introduction to WGS 1. Sequencing platforms & output data (20') (Maroua Sayeb, EURL-Listeria monocytogenes) 2. Verification of the integrity of the raw data files (like md5sum) (10') (Angela van Hoek, EURL-Salmonella) 3. Bioinformatics analysis of NGS data: approaches and opportunities (command-line tools, commercial software, webservers) (20') (Joakim Skarin, EURL-Foodborne viruses)	9.15	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) Introduction to genome comparisons: gene-by-gene vs SNP approach (Bo Segerman, EURL-Campylobacter)
10.20	Coffee break	10.30	Coffee break
10.50 11.10	Introduction to quality check and trimming (Valeria Michelacci, EURL-VTEC) 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)	11.00 11.45 12.15	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) Parasites WGS: opportunities and challenges (Simone Cacciò, EURL-Parasites Lunch break
12.30	Lunch break		
13.40	Introduction to assembly and assembly statistics (Lauge Holm Sørensen, EURL-AMR)	13.15	Hands-on exercises – Visualisation of clustering data Demonstration via Grapetree (Maroua Sayeb, EURL-Listeria monocytogenes)
14.00	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)	13.45 14.45	The EFSA One Health WGS database and demo (Mirko Rossi, EFSA) Wrap up (Magnus Simonsson, EURL-Foodborne viruses)
15.00	Introduction to data alignment (Paolo Vatta, EURL-Parasites)	15.00	Closure
15.20	Hands-on exercises – Mapping approach Hands-on E. coli virulotyping using a mapping approach (Rosangela Tozzoli, EURL VTEC) Demo: Mapping with Seqsphere (Maroua Sayeb, EURL-Listeria monocytogenes)		
16.20	Amplicon-based sequencing of viral genomes (Luca De Sabato, EURL-VTEC)		
17.00	End of the first day		

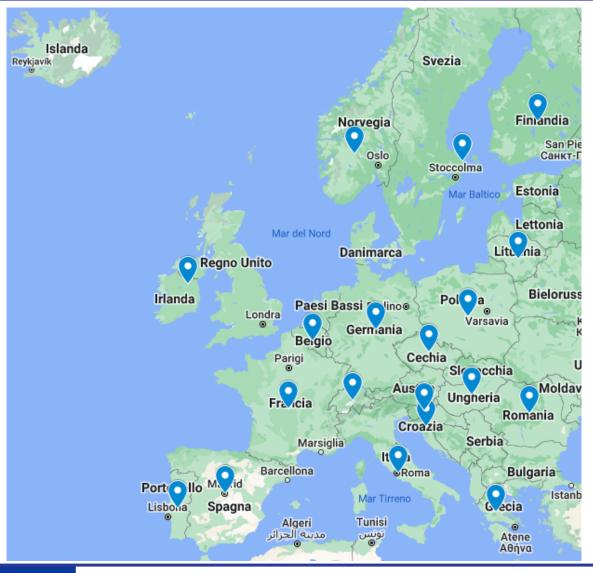
Optionally, a group dinner will be organised (at own costs)







Participants – geographic distribution



28 participants from different NRLs

7 at own costs
3 supported by EURL VTEC

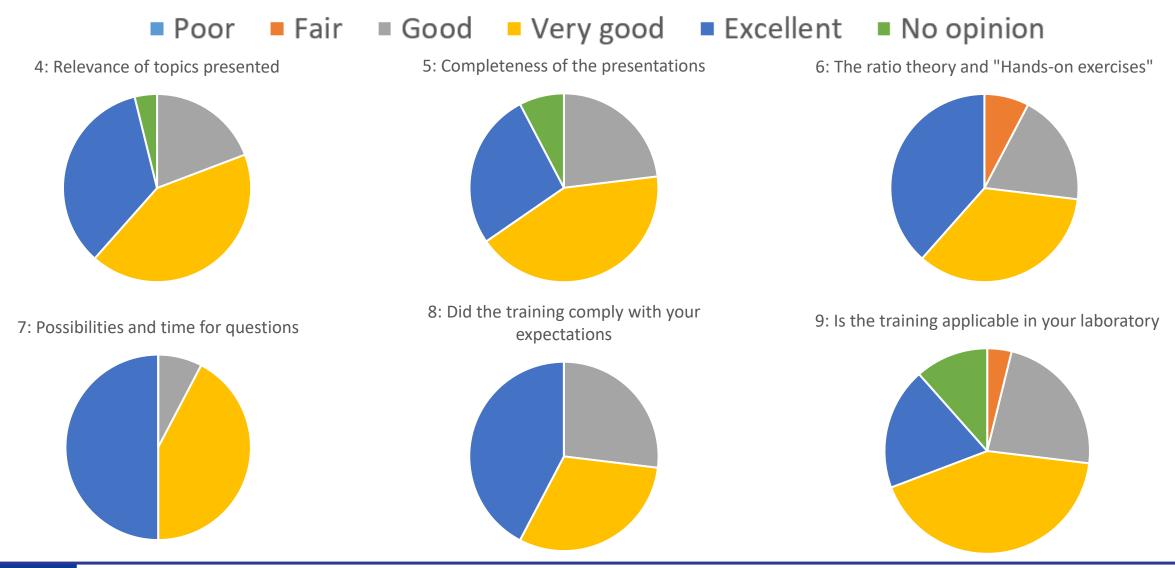
19 different countries (17 Member States + 2 EFTA/EEA)

Many participants came from labs appointed as NRLs for multiple pathogens





Training satisfaction survey







Work in progress

Supporting document for Quality Check of NGS data (EURL Listeria lead)

The topic will be discussed in a specific meeting of the WG in October to start drafting the document

Supporting document for Wet-lab part of sequencing viral genomes (EURL Foodborne Viruses lead)

In preparation

• Webinar dedicated to reference whole genome sequences

In discussion for 2025







Questions?

Suggestions?