2nd joint training – June 20th-21st 2023

Introduction to Bioinformatics for genomic data mining

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, webservers) (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)*

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**

Participants – geographic distribution
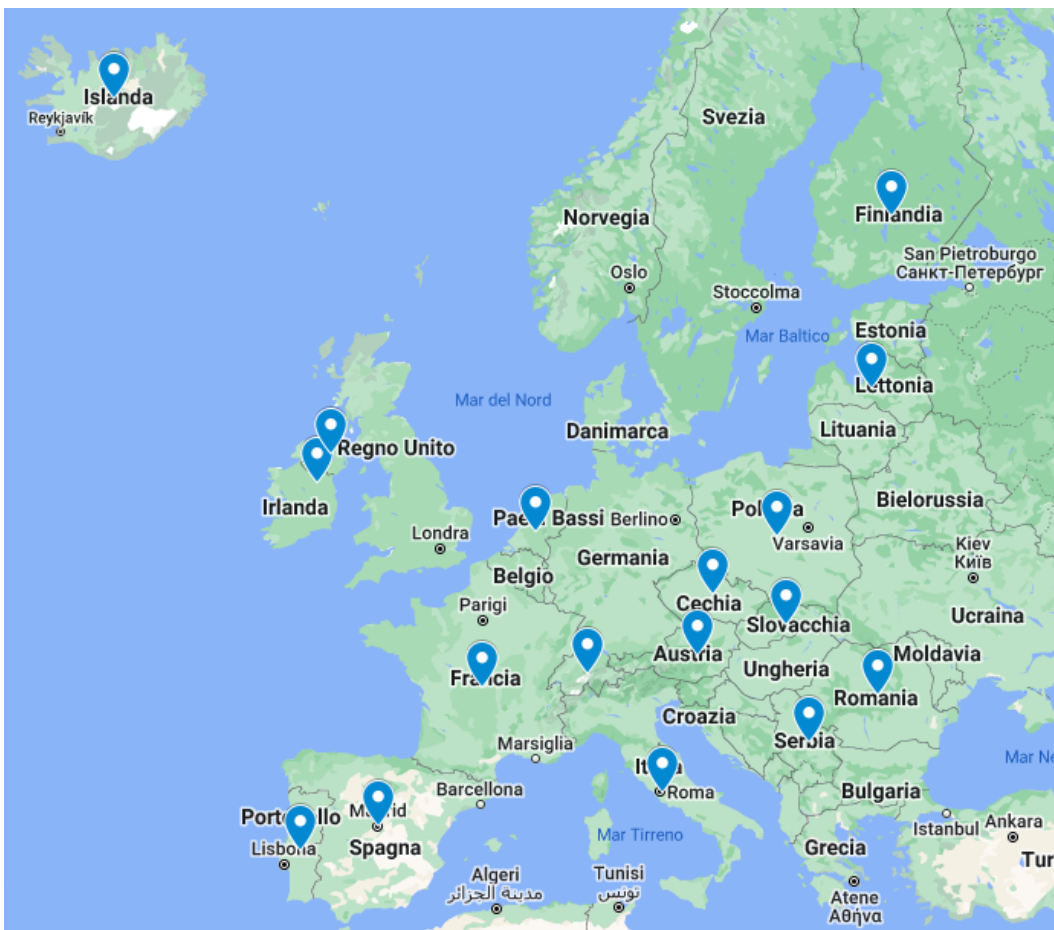
24 participants from different NRLs
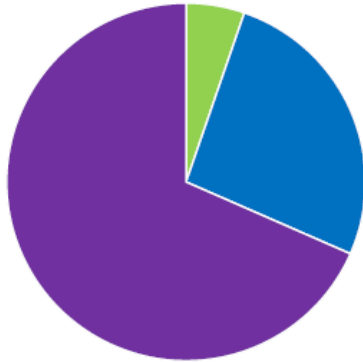4 at own costs
2 supported by EURL VTEC

17 different countries
(13 Member States + 2 EFTA/EEA + Northern Ireland + 1 Candidate Country)

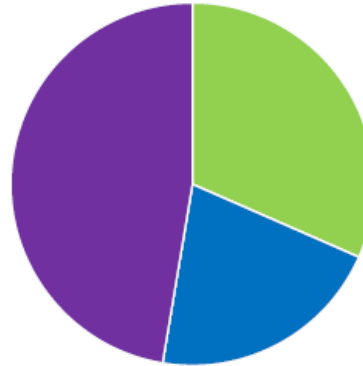**Many participants came from labs appointed as NRLs for multiple pathogens**

2023 - Training satisfaction survey

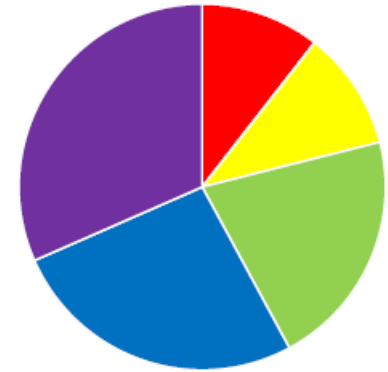Legend: ■ Poor ■ Fair ■ Good ■ Very good ■ Excellent

Relevance topics
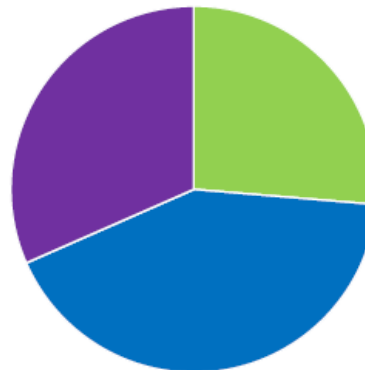
Completeness presentations

ratio theory - 'Hands-on exercises'

Possibilities and time for raising questions

Complying with expectations

Applicability