Foreword

The Working Group (WG) has been established by the European Commission with the aim to promote the use of NGS 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 NGS mandate sent by the Commission. The WG includes all the EURLs operating in the field of the microbiological contamination of food and feed and this document represent a deliverable of the WG and is meant to be diffused to all the respective networks of NRLs.

Inventory of training supports

Version 06 – 26/01/2026

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EURL for Coagulase Positive Staphylococci

Introduction

From the survey sent in 2018 by the EURLs to their respective NRLs network, an inventory of training supports used by different organisations was performed and presented to the working group in November 2018. As all NRLs expressed their need for training in each step of NGS analyses (wet-lab and dry-lab), it was decided by the working group to draft a guidance document on training possibilities, including links to the training supports available to the EURLs.

1 Training programs available within EURLs

EURLs organise regularly NGS training course to their respective network.

EURL – Antimicrobial Resistance (AMR) organised seven training courses:

- In **2024** (5, 11, 12, and 18 December, online and on-site): Four days of training on Oxford Nanopore Sequencing – the first day included a virtual session on Oxford Nanopore Technologies. The second and third day included a wet-lab session at DTU on how to extract HMW gDNA and sequencing using MinION. The last day was dedicated to bioinformatic analysis of long-read sequencing data.
- in **2022** (21 and 23 November, online): Whole genome sequencing prediction of AMR (MRSA).
- in **2021** (26-29 April, online): Whole genome sequencing prediction of AMR.
- in **2020** (19-23 October, on-site): Whole genome sequencing prediction of AMR.
- in **2019** (24-27 September, on-site): Enhancing WGS capacity of AMR surveillance in the EURL-AR network.
- in **2018** (25-28 September, on-site): Four days of training with wet-lab and dry-lab about NGS for surveillance of AMR.
- in **2017** (27-29 September, on-site): Three days of training with wet-lab and dry-lab on the use of Whole Genome Sequencing (WGS) in monitoring of Antimicrobial Resistance”.

EURL *Campylobacter* organized three training courses:

- in **2025** (13-14 November, on-site): Bioinformatic analysis of *Campylobacter* whole genome sequence data.
- in **2024** (25-26 January, on-site): Bioinformatic analysis of *Campylobacter* whole genome sequence data.
- in **2020** (9-10 December, online): Introductory course describing the process from generating whole genome sequences to quality control and sequence analysis. The training was accompanied with a tutorial for home practice, which can be accessed upon contact with the EURL *Campylobacter*.

EURL for Coagulase positive staphylococci (CPS) organized three training sessions on NGS bioinformatics analysis:

- in **2025**: a one-day training course, on October 22nd, 2025, held online.
- in **2024**: a two-day training course on October 15th-16th 2024 was held at the EVH Institute of Food safety, Feed and Environment (Ljubljana, Slovenia).
- in **2022**: a two days training course on October 5th -6th 2022 was organised at the National Food Chain Safety Office (Budapest, Hungary).

The trainings provided description of sequencing technologies, tools for analysis, concepts in NGS and data formats and analysis for short reads. The course included practical sessions on the Galaxy website carried out with the trainee with hands-on exercises on reads quality control, assembly, typing and BLAST search of genetic features specific to *Staphylococcus aureus*. The supports of the training can be accessed upon contact with the EURL for CPS.

EURL for *Escherichia coli*, including Shiga toxin-producing *E. coli* (VTEC) organised ten training sessions, based on bioinformatics analysis:

- in **2022** and **2024**, two days for Bioinformatics for tools for aiding STEC outbreak investigation (online).
- in **2021, 2023 and 2025**, two days for Bioinformatics for NGS data mining for typing pathogenic *E. coli* (online).
- in **2020**, two days for Bioinformatics (online);
- in **2019**, two days for Bioinformatics (on-site);
- in **2018**, two days for Bioinformatics analysis (on-site);
- in **2016**, two days for Bioinformatics analysis (on-site);
- in **2015**, two days for Bioinformatics analysis (on-site).

EURL for Foodborne viruses organised one training course:

- in **2024**: a two-days training course on norovirus capsid typing with amplicon based NGS was held in Uppsala (between the 3rd and 4th December). The course gave an introduction to norovirus capsid typing, an overview of NGS typing methods and strategies, an amplicon-based metagenomic protocol. Moreover, it included a hands-on experience of NGS wet lab and bioinformatic data treatment.

EURL *Listeria monocytogenes* (*Lm*) organised two training sessions:

- in **2025**: a three-days training course was held on 15-17 December 2025 at ANSES. Three NRLs attended this training. The course trained in genomic DNA extraction, library preparation and quality control, short-read sequencing, and data analysis and interpretation using StarFlow. This was the first training dedicated to library preparation, including the development of a standard operating procedure (SOP) for MiSeq library preparation.
- in **2019**: on-site three-days training course, on the 21st to 23rd May 2019 on WGS wet lab and dry lab: the first day included bacterial cell preparation and DNA extraction, the second day included quality control of DNA and the last day was dedicated to bioinformatic analysis of sequencing data.

2 Training courses organized by the Inter EURL working group on NGS

2.1 Overview of the Joint Training Courses

The Inter-EURLs Working Group on NGS organises annual joint training sessions on NGS data analysis for the respective NRL networks. Each year, approximately 30 participants are invited to attend the training courses, with up to three candidates funded by each EURL. These joint sessions aim to strengthen harmonisation, capacity building, and networking across the EURL/NRL system.

The main objectives of these joint training courses are as follows:

- Provide an overview of the different possible approaches to NGS data analysis;
- Ensure participants understand the terminology used in NGS data analysis;
- Illustrate the basic steps of data analysis (quality control, trimming, assembly, and identification of genomic features);
- Provide guidelines for cluster analysis and explain the concepts behind different clustering approaches;
- Support participants in evaluating and interpreting the results obtained;
- Present and discuss guidance documents on NGS analysis published by the Inter-EURLs Working Group;
- Facilitate the exchange of experiences among participants and strengthen networking.

2.2 Organization of the Joint Training Sessions

To date, five editions of the joint training sessions have been organized:

- **First edition (2019)**: Organised by EURL *Salmonella*, EURL *Listeria monocytogenes* (Lm), and EURL VTEC; held on 17–18 October 2019 at ANSES, Maisons-Alfort (France).

- **Second edition (2022)**: Organised by EURL VTEC, EURL Lm, EURL *Salmonella*, EURL CPS, EURL Parasites, EURL Foodborne Viruses, EURL AMR, and EURL *Campylobacter*; held on 14–15 June 2022 at the Istituto Superiore di Sanità (ISS), Rome (Italy).
- **Third edition (2023)**: Organised by the same group of EURLs as in 2022; held on 20–21 June 2023 at the National Institute for Public Health and the Environment (RIVM), Bilthoven (The Netherlands).
- **Fourth edition (2024)**: Organised by the same group of EURLs; held on 25–26 June 2024 at the Swedish Veterinary Agency (SVA) and the Swedish Food Agency (SFA), Uppsala (Sweden).
- **Fifth edition (2025)**: Organised by the same group of EURLs; held on 17–18 June 2025 at ANSES, Maisons-Alfort (France).

2.3 Efficacy of the Joint Training Courses on NGS

In September 2025, the Inter-EURLs Working Group on NGS administered an anonymous survey to participants from the first three editions of the Joint Training Courses organized by the eight EURLs comprising the Inter-EURLs WG (2022, 2023, and 2024). The aim was to evaluate the effectiveness of the courses and to support the fine-tuning of future training activities. Participants who attended the 2025 edition were excluded, as it was considered too soon to obtain meaningful feedback.

Each EURL was asked to distribute the survey to selected participants from previous editions, as outlined below:

- **EURL AMR**: 2024 (2 participants), 2023 (2 participants), 2022 (3 participants)
- **EURL *Campylobacter***: 2024 (4 participants), 2023 (3 participants), 2022 (3 participants)
- **EURL CPS**: 2024 (2 participants), 2023 (1 participant), 2022 (3 participants)
- **EURL *E. coli***: 2024 (5 participants), 2023 (3 participants), 2022 (3 participants)
- **EURL Foodborne Viruses**: 2024 (4 participants), 2023 (2 participants), 2022 (3 participants)
- **EURL *Listeria monocytogenes***: 2024 (3 participants), 2023 (3 participants), 2022 (3 participants)
- **EURL Parasites**: 2024 (3 participants), 2023 (2 participants), 2022 (3 participants)
- **EURL *Salmonella***: 2024 (3 participants), 2023 (3 participants), 2022 (3 participants)

The deadline for survey completion was 17 October 2025. The questionnaire included 26 questions and three open-ended questions (Annex 1). It aimed to gather information regarding the participants experiences, perceptions, and preferences regarding the training courses.
In total, 18 responses were received, representing a well-distributed sample across the EURL/NRL networks (Figure 1A). Participation was highest in the *Campylobacter* and *Listeria monocytogenes* networks, followed by Foodborne viruses and *Salmonella*.

Most respondents showed an even distribution across training activities between 2022 and 2024 (Figure 1B). Most respondents (14) were identified as researchers/scientists, while only two were laboratory technicians or reported as other professional roles; no respondents were identified primarily as bioinformaticians (Figure 1C). The majority of the respondents reported having applied the skills and knowledge acquired during the training either frequently (8) or occasionally (7) in their professional activities (Figure 1D).

Figure 1

Participants reported a broad range of positive work-related outcomes (Figure 2A). The most frequently cited benefit was improved interpretation of sequencing results (14 respondents), highlighting the training impact on analytical understanding and result assessment. Ten respondents also indicated an improved ability to review and validate NGS reports, underscoring gains in critical evaluation and quality assurance capacities. Many participants reported faster or more accurate data analysis (6) and more efficient troubleshooting (7), suggesting that the training contributed to more effective and timely handling of NGS workflows. Six respondents noted also improved communication with external NGS providers and bioinformatics partners, reflecting enhanced shared understanding of analytical processes and terminology.

Although reported less frequently, four participants indicated that the training enabled them to contribute more effectively to outbreak investigations, demonstrating the practical application of acquired skills in public health contexts. Additional open responses emphasized better comprehension of NGS concepts, which facilitated communication with competent authorities and supported the implementation of EU legislation. The training was perceived to have increased the confidence in handling and interpreting NGS data (Figure 2B).

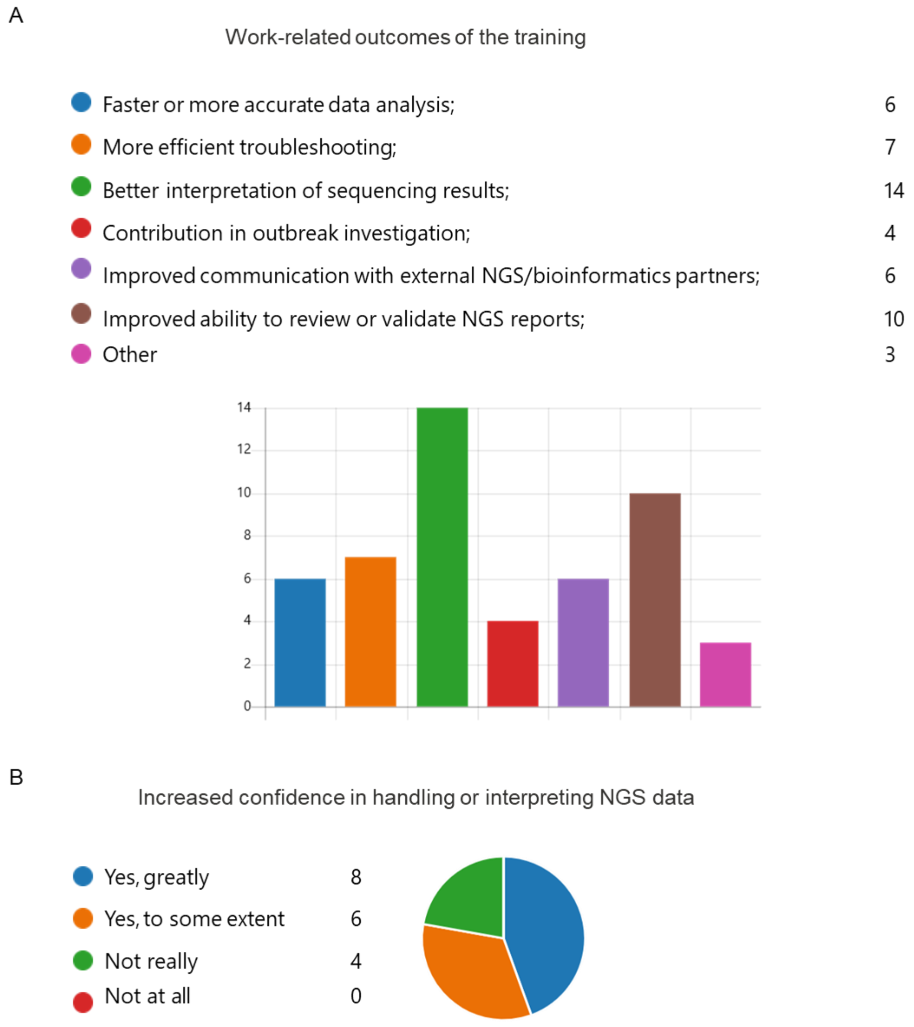

Figure 2

In response to an open-ended question about how the training helped in real work situations, eleven participants provided concrete examples. They reported increased confidence in cgMLST interpretation and a better overall understanding of the approach, and described applying this knowledge to tasks such as characterising enterotoxin genes in *S. aureus* from food. Others reported improved understanding of complex sequencing analysis (e.g., norovirus) while supervising method development projects, helping them avoid common pitfalls such as chimeras and QC issues.

Others highlighted improved troubleshooting through discussions with bioinformatics colleagues and the practical use of Galaxy ARIES and cgMLST workflows (e.g., chewBBACA) for the analysis of *Campylobacter* strains. Participants also reported applying the training knowledge to perform genome assembly, use Galaxy platform tools for analyzing multiple foodborne pathogens, analyze proficiency test data, and support the implementation of WGS in their laboratories. Finally, some participants noted that the course improved communication with external NGS service providers.

Knowledge transfer beyond individual participants was evident: 17 respondents reported sharing the training content with colleagues (Figure 3A) and five reported using what they learned to support the development or revision of SOPs and internal guidelines (Figure 3B). Regarding the adoption or improvement of tools and workflows at institutional level (Figure 3C), five respondents reported full adoption or improvement of specific tools or workflows at their institution based on the training content, and eight indicated partial adoption, reflecting ongoing implementation processes or institutional constraints. Five respondents reported no direct adoption, citing organizational limitations rather than a lack of relevance of the training.

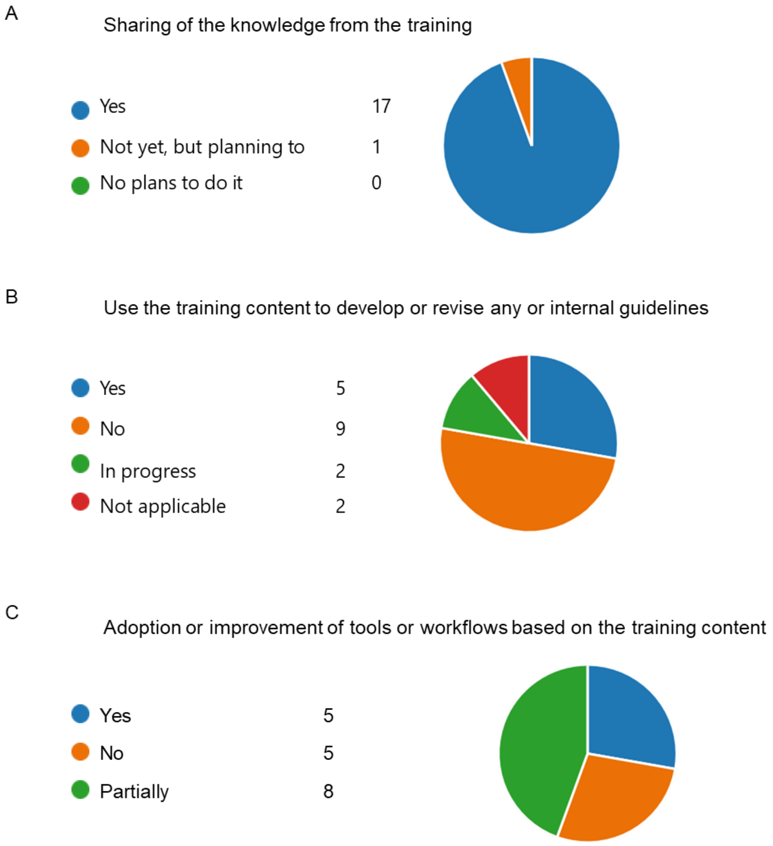

Figure 3

When asked which topics covered during the course were most useful for their work (Figure 4), respondents consistently highlighted the theoretical background, including guidance documents released by the Inter-EURLs Working Group on NGS, and the hands-on data analysis sessions (13 respondents each). The overview of available analytical platforms (e.g. ARIES, SeqSphere, CGE tools) was also frequently cited as useful (12 respondents). No respondents selected “Other”, indicating that the core content of the training adequately addressed participants needs and expectations.

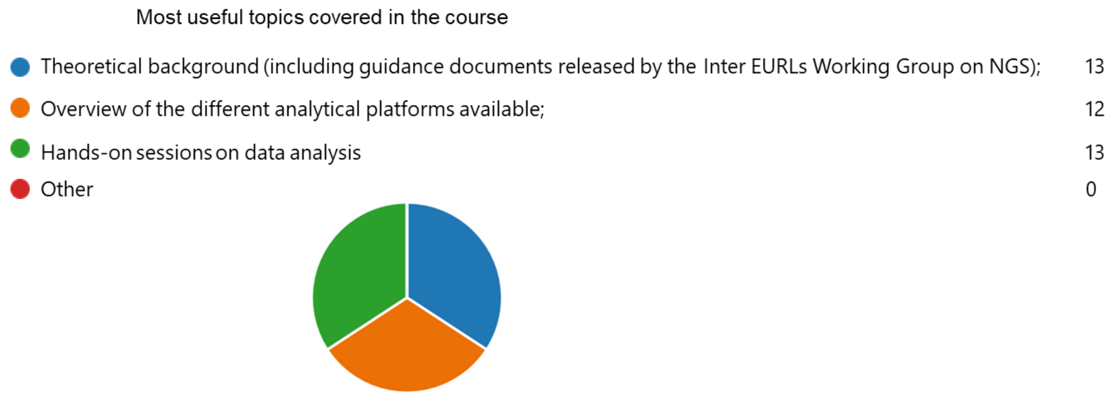

Figure 4

Responses on the analysis environments and tools currently available at participants institutions (Figure 5) indicate a heterogeneous but generally well-developed analytical capacity for NGS data analysis. The most commonly available tools were CGE web tools (9 respondents) and Ridom SeqSphere+ (9 respondents), followed by Linux command-line–based custom or in-house pipelines (8 respondents). ARIES and other Galaxy-based instances (e.g. usegalaxy.eu) were each reported by 7 respondents.

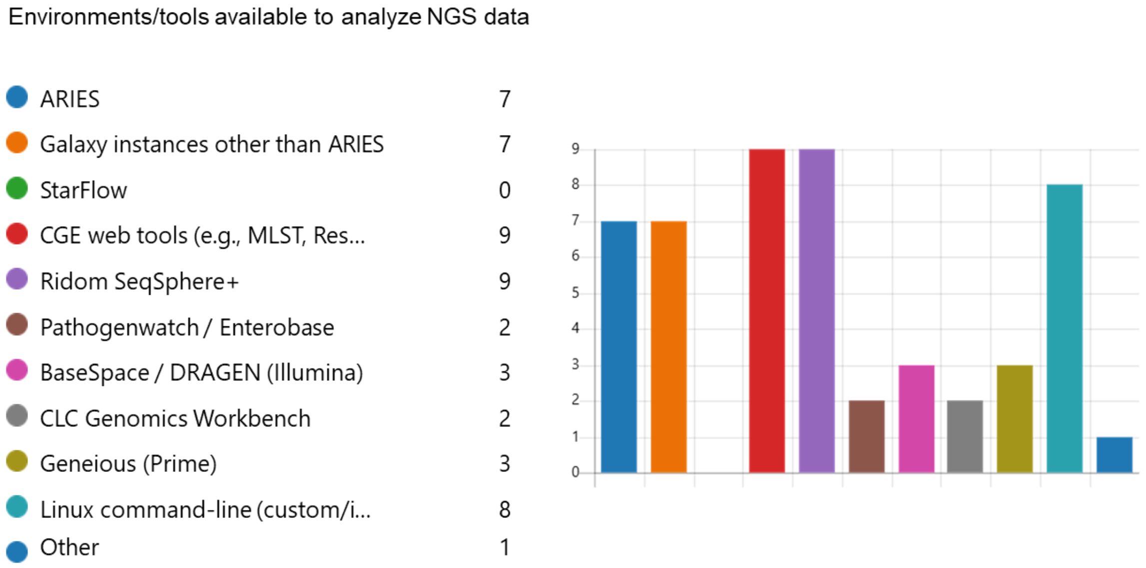

Figure 5

The overall usefulness of the courses was rated highly, with most respondents assigning scores of 4 or 5 on a 5-point scale (Figure 6A). Consistent with this positive assessment, 15 out of 18 respondents indicated that the training content did not require further elaboration, while three suggested that some topics could have been covered in greater detail (Figure 6B). Suggestions from the open-ended question included NGS applications for viruses, clarification of clustering concepts (e.g. cluster definition, thresholds, and criteria for identifying potential outbreak-related clusters), and *Campylobacter*-specific considerations in cluster analysis. The perceived value of the training was further supported by a strong willingness to recommend it to colleagues: 13 respondents gave the highest recommendation score (5), and most of the remaining respondents scored 4 (Figure 6C). Finally, 16 participants indicated that the training met their expectations and one reported that it went beyond their expectations, confirming the overall relevance and quality of the training activities (Figure 6D).

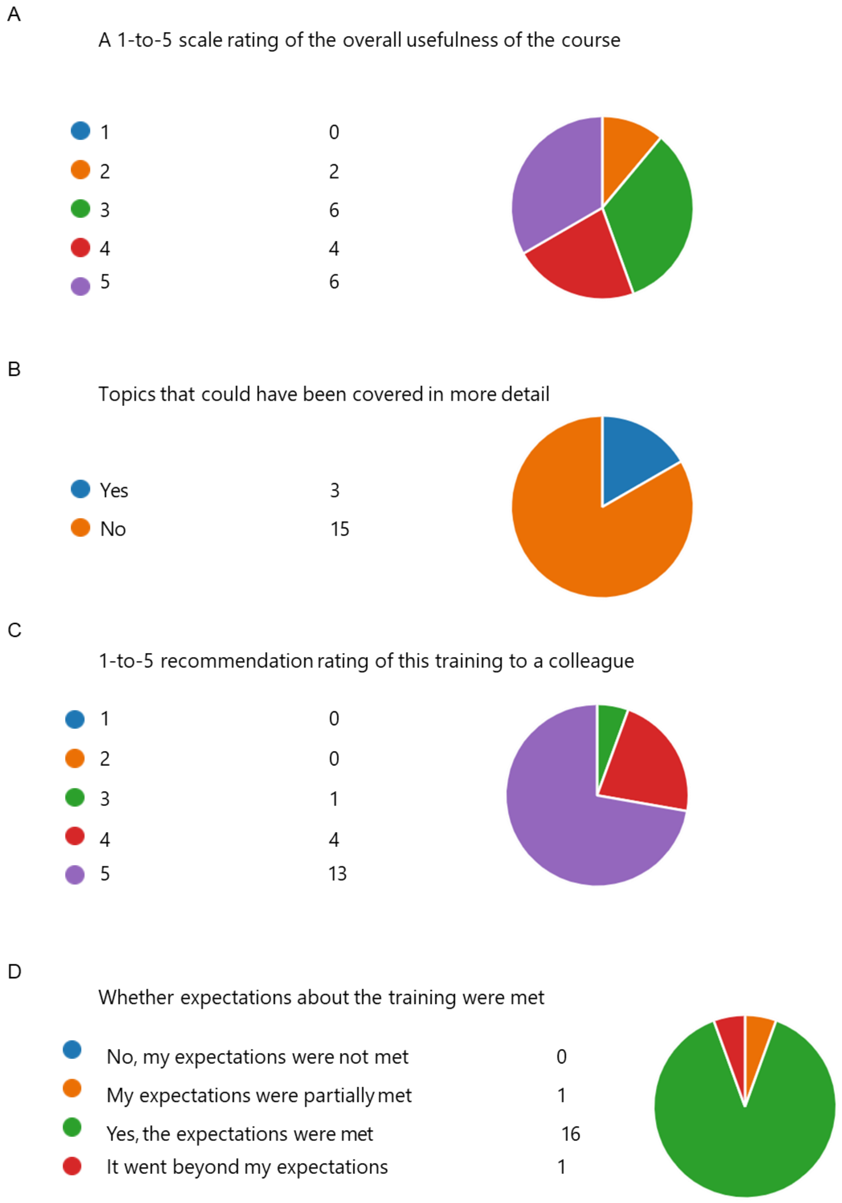

Figure 6

Regarding future training needs, responses to the open-ended question on topics for future editions highlighted a demand for more advanced and specialized content. Participants requested deeper coverage of pathogen-specific analyses, particularly for viruses and parasites, more detailed SNP-based analysis and interpretation, clearer guidance on outbreak cluster definition and threshold setting, and further discussion of quality standards and accreditation requirements for WGS analyses. Concerning improvement of future training editions, a couple of respondents emphasized the need to address practical challenges related to specific food matrices, include a session on viruses, and reduce the number of participants per training course.

In conclusion, the overall feedback confirms the effectiveness and relevance of the joint NGS training programs. The training had a tangible practical impact, directly supporting the implementation of NGS in laboratories and enhancing analytical confidence in real operational contexts. While immediate full implementation may not always be feasible, the training has contributed to the gradual integration of NGS-related tools and workflows across laboratories.

3 Supports for training courses

Several training courses supports are available for both wet-lab and dry-lab procedures related to NGS. Hyperlinked supports are listed in the following subsections and were created either by EURLs, by the inter EURL WG on NGS or by companies providing sequencing technologies and programs for bioinformatic analyses.

3.1 Wet-lab

Learning resources from **YouSeq** offers educational materials on NGS, it includes introductory guides and videos on NGS basics—such as workflows, adapters and indexes, bioinformatics, and different sequencing approaches. There are also FAQs that explain practical aspects of NGS workflows and library preparation/quantification.

3.1.1 DNA extraction

EURL-AMR (available upon request):

- DNA extraction – kits and procedures
- From Isolate to Whole Genome Sequencing (Part 1)

Promega:

- DNA Purification guide

Roche Diagnostics:

- Video of MagnaPure 24 and 96 systems

3.1.2 DNA quality control

Support from **Promega**:

- How do I determine the concentration, yield and purity of a DNA sample?

Support from **Illumina**:

- DNA/RNA Isolation Considerations for illumina library preparation

3.1.3 Sequencing technologies

EURL-AMR (available upon request):

- Sequencing Platforms

EURL CPS (available upon request)**:**

- Introduction to WGS

EURL VTEC:

- Next Generation Sequencers: from the bacterial culture to raw data

Illumina

- Video on sequencing by synthesis technology

PacBio

- Video on Single Molecule Real Time Sequencing technology

Ion Torrent

- Ion Torrent Next-Generation Sequencing Technology

Oxford Nanopore

- How nanopore sequencing works

3.1.4 Library preparation: short reads and long reads

EURL-AMR for Illumina library preparation with the Nextera kit (available upon request):

- Whole genome sequencing (WGS) - there’s a new tool in town
- From isolate to whole genome sequence (Part 2)

Illumina:

- Illumina Training Opportunities
- Library Preparation Tutorials for NGS
- Best Practices for Nextera Library Prep Expert Video Tip
- Illumina DNA Prep (formerly Nextera DNA Flex): Introduction

Ion Torrent

- Courses proposed by Thermofisher
- Video of IonTorrent sequencing: The Workflow | Ion S5 Next Generation Sequencing System

PacBio

- Training on library preparation proposed by **PacBio**

Oxford Nanopore

- Nanopore training: Essentials to advanced

3.2 Dry-lab

3.2.1 Inter-EURLs WG for NGS Joint-training materials (by year)

- The presentations from the **2022** edition of the joint course in Rome (IT) available at this link;
- The presentations from the **2023** edition of the joint course in Bilthoven (NL) available at this link;
- The presentations from the **2024** edition of the joint course in Uppsala (SE) available at the Inter Biorisks-EURLs WG on NGS page on Zenodo:
    1. Introduction of the inter EURLs Working Group on NGS and the guidance documents released (EURL-VTEC)
    2. Sequencing platforms & output data (EURL-Listeria monocytogenes)
    3. Verification of the integrity of the raw data files (like md5sum) (EURL-Salmonella)
    4. Bioinformatics analysis of NGS data: approaches and opportunities (command-line tools, commercial software, webservers) (EURL-Viruses)
    5. Introduction on quality check and trimming (EURL-VTEC)
    6. Intro ARIES and FastQC and Positional and Quality Trimming on ARIES (EURL-VTEC)
    7. Demo: Quality check and trimming with alternative tools (EURL-Campylobacter)
    8. Introduction on assembly and assembly statistics (EURL-AMR)
    9. Hands-on SPAdes and Quast from ARIES (EURL-VTEC)
    10. Data alignment (EURL-Parasites)
    11. Hands-on E. coli virulotyping using a mapping approach (EURL-VTEC)
    12. Demo: Mapping with Seqsphere (EURL-Listeria monocytogenes)
    13. Amplicon-based sequencing of viral genomes (ISS and EURL-Foodborne Viruses)
    14. Introduction to gene detection using BLAST approach (EURL-CPS)
    15. Hands-on ResFinder on CGE webserver (EURL-AMR)

16. Introduction to genome comparisons: gene-by-gene vs SNP approach (EURL-Campylobacter)
17. Demonstration of gene-by-gene approach through different platforms:
    - ARIES (EURL-VTEC)
    - Starflow (EURL-Listeria monocytogenes and EURL-CPS)
    - Seqsphere (EURL-Salmonella)
18. Parasites WGS: opportunities and challenges (EURL-Parasites)
19. Demonstration via Grapetree (EURL-Listeria monocytogenes)
20. EFSA One Health WGS database and demo (EFSA)

- The presentations from the **2025** edition of the joined course in Maisons-Alfort (FR) available at the Inter Biorisks-EURLs WG on NGS page on Zenodo:

1. Introduction of the inter EURLs Working Group on NGS and the guidance documents released (EURL-VTEC)
2. Sequencing platforms & output data (EURL-Listeria monocytogenes)
3. Verification of the integrity of the raw data files (like md5sum) (EURL-Salmonella)
4. Bioinformatics analysis of NGS data: approaches and opportunities (command-line tools, commercial software, webservers) (EURL-Viruses)
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14. Introduction to gene detection using BLAST approach (EURL-CPS)
15. Hands-on ResFinder on CGE webserver (EURL-AMR)
16. Introduction to genome comparisons: gene-by-gene vs SNP approach (EURL-Campylobacter)
17. Demonstration of gene-by-gene approach through different platforms: ARIES (EURL-VTEC), Starflow (EURL-CPS and EURL-Lm) & Seqsphere (EURL-Salmonella)
18. Demonstration via Grapetree (EURL-Listeria monocytogenes)

19. Parasites WGS: opportunities and challenges (EURL-Parasites)
20. EFSA One Health WGS database and demo (EFSA)

3.2.2 EURLs training materials (by topic covered)

3.2.2a: General aspects for data analysis and quality control of raw data

EURL-AMR (available upon request):

- WGS data sharing for improved public health
- Quality control (QC) metrics for WGS data

EURL CPS (available upon request):

- Reads quality check

EURL VTEC

- Introduction to: Basic Course on bioinformatics tools for next generation sequencing data mining
- VTEC strains typing: from traditional methods to NGS
- Introduction to NGS data formats, basic tools and servers for analysis
- Systems and servers for NGS data analysis
- Introduction to NGS data formats, quality check and analytical tools

Galaxy training

- Tutorials on quality control of NGS raw data
- Quality Control
- Quality control: contamination

3.2.2b: Assembly, annotation and typing

EURL-AMR (available upon request):

- Tools - ENGAGE benchmarking for AMR gene detection
- AMR prediction based on WGS data
- Finding the appropriate method, with a special focus on: Mapping and alignment

EURL CPS (available upon request):

- Assembly and quality
- CPS characterisation
- Detection of staphylococcal enterotoxin coding genes in assembled genomes

EURL VTEC:

- From Reads To Contigs
- Assembly, assembly stats, virulotyping, serotyping
- Decode NGS data: search for genetic features
- Basic characterization: Serotyping, 7-genes Multi Locus Sequence Typing (MLST) and Virulotyping

Galaxy training:

- Assembly
- Genome annotation: plasmids, integrons, IS
- Genome annotation with Prokka
- Detection AMR genes

Geneious:

- De novo assembly

Ridom SeqSphere:

- Tutorial for SeqSphere+ Assembly and cgMLST Analysis Pipeline

3.2.2c: Cluster analysis

EURL-AMR (available upon request):

- Typing (SNP, cgMLST)

EURL CPS (available upon request):

- WGS clustering (SNP, cgMLST)

EURL VTEC:

- Introduction to core genome MLST (cgMLST)
- Whole genome SNPs comparison

Galaxy Training:

- Microbial Variant Calling

Ridom SeqSphere:

- cgMLST Typing with Illumina Data
- Tutorial for stable cgMLST scheme
- MLST typing

3.2.2d: Introduction to web-based platforms for analysis of sequencing data

EURL-AMR (available upon request):

- EURL-AR hub

EURL CPS (available upon request):

- Galaxy Workflow for the analysis of CPS sequencing data

EURL CPS and EURL Lm:

- Starflow

EURL-VTEC:

Concept of galaxy servers

- NGS solutions in Microbiology
- The Galaxy architecture and ARIES cluster
- Introduction to the ARIES webserver user-interface

Annex 1

Efficacy of the Joint Training Courses on NGS organised by the Inter EURLs WG on NGS

This questionnaire is designed to collect information on the efficacy of the Joint Training Courses “Introduction to Bioinformatics for genomic data mining” organized by the inter EURLs Working Group on NGS in the period 2022-2024

* Obbligatoria

Basic Information

1. EURL network *

Select all that apply. Please include only the hazards for which your laboratory is officially appointed as National Reference Laboratory

☐ Antimicrobial Resistance

☐ Campylobacter

☐ Coagulase Positive Staphylococci

☐ Escherichia coli, including STEC

☐ Foodborne viruses

☐ Listeria monocytogenes

☐ Parasites

☐ Salmonella

Training Participation and Role

2. Year of participation in the training course *

○ 2022

○ 2023

○ 2024

3. What is your professional role? *

○ Laboratory technician

○ Researcher/Scientist

○ Bioinformatician

○ Other

4. If you selected “Other” in the previous question, please describe your role *

Application of Knowledge and Impact

5. Have you applied any of the skills or knowledge acquired during the training in your professional work? *

○ Yes, frequently

○ Yes, occasionally

○ Not yet, but I plan to

○ No

6. If you selected “Not yet” or “No” in the previous question, please explain why *

7. Has the training contributed to any of the following outcomes in your work? *

Select all that apply

☐ Faster or more accurate data analysis

☐ More efficient troubleshooting

☐ Better interpretation of sequencing results

☐ Contribution in outbreak investigation

☐ Improved communication with external NGS/bioinformatics partners

☐ Improved ability to review or validate NGS reports

☐ Other

8. If you selected “Other” in the previous question, please specify how the training contributed to your current work:

9. Did the course increase your confidence in handling or interpreting NGS data? *

   ○ Yes, greatly

   ○ Yes, to some extent

   ○ Not really

   ○ Not at all

10. Please describe one example where the training helped you in a real work situation *

Institutional Outcomes

11. Have you shared the knowledge from the training with your colleagues? *

○ Yes

○ Not yet, but planning to

○ No plans to do it

12. If you selected “No plans to do it” in the previous question, please explain why *

13. Did you use the training content to develop or revise any SOPs (Standard Operating Procedures) or internal guidelines? *

○ Yes

○ No

○ In progress

○ Not applicable

14. Were you able to adopt or improve specific tools or workflows at your institution based on the training content? *

○ Yes

○ No

○ Partially

Content evaluation

15. Which specific topics covered in the course have been the most useful for your work? *

Select all that apply

☐ Theoretical background (including guidance documents released by the Inter EURLs Working Group on NGS)

☐ Overview of the different analytical platforms available (e.g., ARIES, SeqSphere, StarFlow, CGE)

☐ Hands-on sessions on data analysis

☐ Other

16. If you selected "Other" in the previous question, please describe the topics

17. On a scale of 1 to 5, how would you rate the overall usefulness of the course for your job? *

(1 = Not useful at all, 5 = Extremely useful)

○ 1

○ 2

○ 3

○ 4

○ 5

18. Was there any topic that was included in the course but could have been covered in more detail? *

○ Yes

○ No

19. If yes, please specify which topic(s) and what you would have liked to explore further *

Tools Used and Future Topics

20. Which analysis environments/tools do you currently have available to analyze NGS data? *

Select all that apply

☐ ARIES

☐ Galaxy instances other than ARIES (e.g. usegalaxy.eu)

☐ StarFlow

☐ CGE web tools (e.g., MLST, ResFinder)

☐ Ridom SeqSphere+

☐ Pathogenwatch / Enterobase

☐ BaseSpace / DRAGEN (Illumina)

☐ CLC Genomics Workbench

☐ Geneious (Prime)

☐ Linux command-line (custom/in-house pipelines)

☐ Other

21. If you selected "Other" in the previous question, please specify

22. Are there any new topics or areas you would like to see covered in future training sessions that were not part of the course?

Overall Satisfaction and Feedback

23. How likely would you recommend this training to a colleague? *

(1 = Not at all, 5 = Extremely likely)

○ 1

○ 2

○ 3

○ 4

○ 5

24. Were your expectations about the training met? *

○ No, my expectations were not met

○ My expectations were partially met

○ Yes, the expectations were met

○ It went beyond my expectations

25. If you selected “No” or “Partially” in the previous question, please explain why *

26. Do you have any suggestions to improve future training courses?