

Training programme in genomic epidemiology and public health bioinformatics –
“GenEpi-BioTrain”

Background of the training programme

Theresa Enkirch, ECDC (Microbiology and Bioinformatics Section, ECDC)
24 October 2025

EU investments triggered by the pandemic

- 'HERA Incubator' (February 2021), a new EU bio-defence preparedness plan against SARS-CoV-2 variants
 - Rapid detection of SARS-CoV-2 variants
- On 25 February 2021, President Ursula von der Leyen announced that the EU would provide EUR 200 M to strengthen detection and monitoring of SARS-CoV-2 variants:
 - Whole genome sequencing (WGS)
 - short-term support for access to high-capacity WGS services
 - longer-term support for national investments into WGS infrastructure for the public health laboratories
 - cross-border networking activities such as bioinformatics, standardisations, and training

Overview of European Commission/ECDC* activities to boost genomic epidemiology



Access to high-capacity, rapid turn-around time WGS services

National WGS and RT-PCR
infrastructure projects

National WGS and RT-PCR infrastructure projects (EU4Health)
Consolidation of national infrastructure (EU4Health)

Cross-border capacity-building support programme

2021

2022

2023

2024

Updated EU regulations, November 2022



The Centre should broaden its collection and analysis of data in terms of epidemiological surveillance and related special health issues, progression of epidemic situations, unusual epidemic phenomena or new diseases of unknown origin, including in third countries, **molecular pathogen data** and health systems data.

Updated ECDC mandate

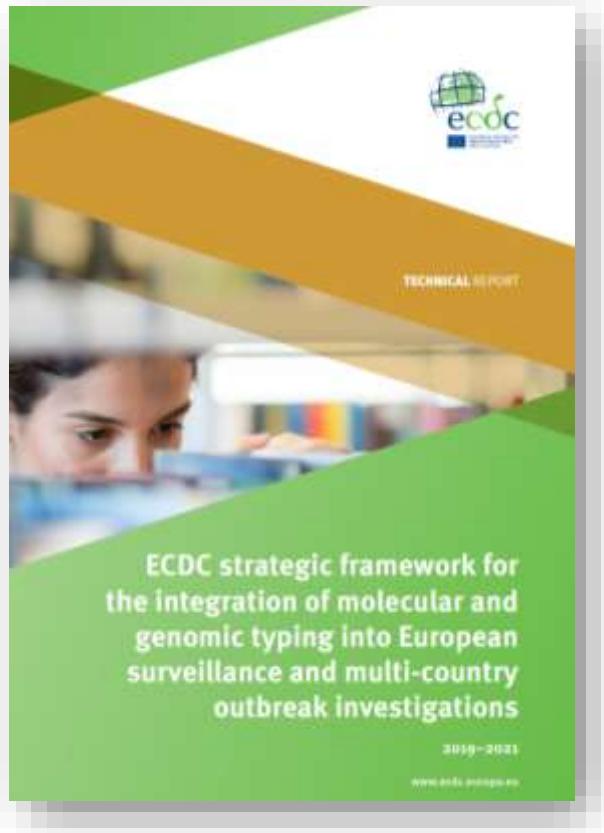


Regulation on serious cross-border threats to health and repealing Decision No 1082/2013/EU

The national competent authoritiesshall communicate the following information...to the participating authorities of the network for epidemiological surveillance:

...molecular pathogen data, if required for detecting or investigating serious cross-border threats to health

ECDC strategy for integrated genomic typing



Support to multi-country outbreak investigations through sequence-based typing:

Campylobacter spp., *Clostridium difficile*, hepatitis A virus, *Legionella* spp., *Listeria monocytogenes*, multidrug-resistant *Mycobacterium tuberculosis* (MDR TB), *Neisseria meningitidis*, *Salmonella enterica*, Shiga-toxin producing *E. coli*, West Nile virus and emerging multi- or extensively drug-resistant (MDR or XDR) bacteria, Methicillin-resistant *Staphylococcus aureus* (MRSA), new pathogens or new modes of transmission of healthcare-associated or community pathogens.

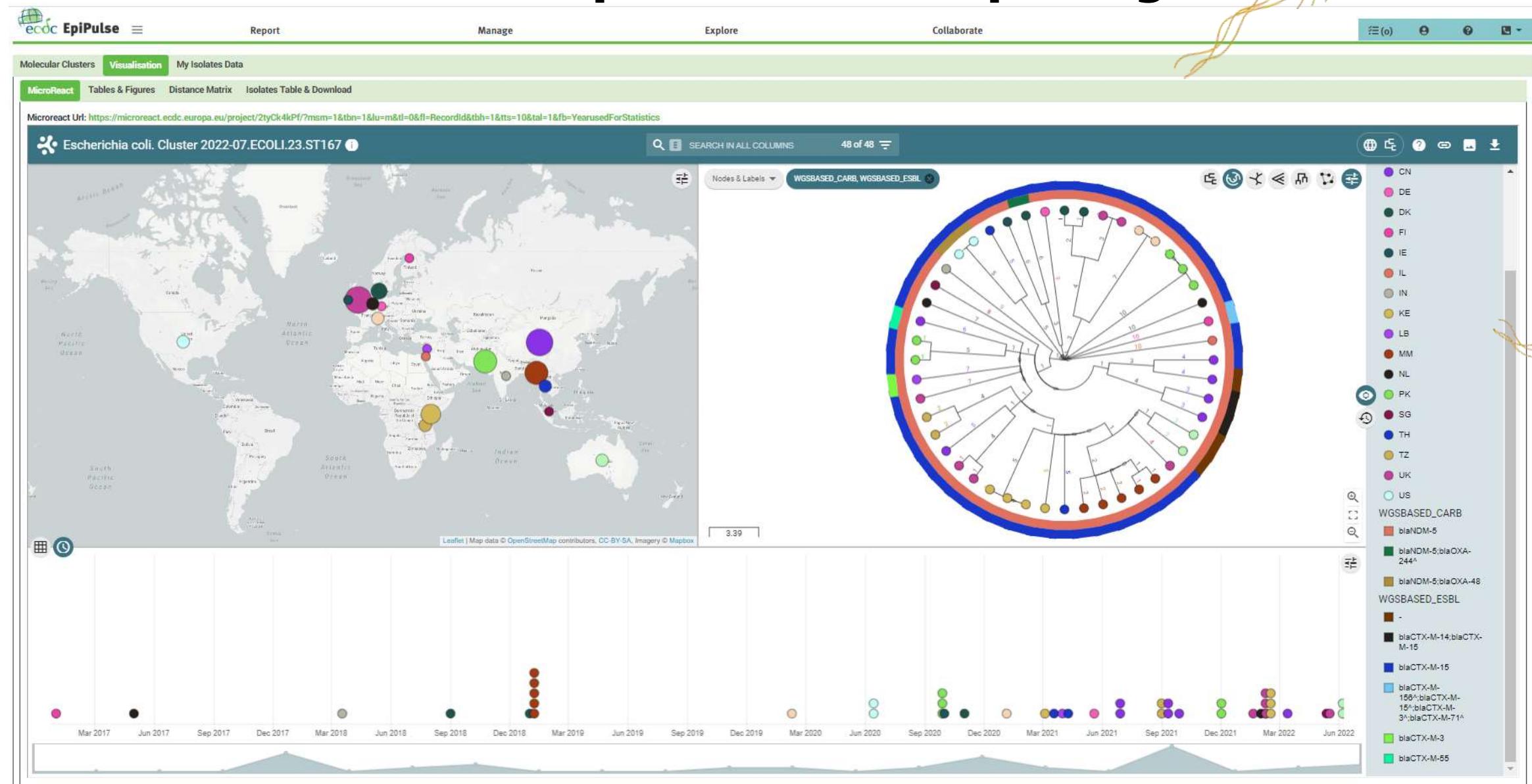
EU-wide sequence-based continuous surveillance:

Influenza virus, *Listeria monocytogenes*, MDR TB, *Neisseria meningitidis*, *Salmonella enterica* and Shiga-toxin producing *E. coli*.

Sentinel surveillance or surveys:

Antibiotic-resistant *Neisseria gonorrhoeae*, *Bordetella pertussis*, carbapenem- or colistin-resistant Enterobacteriaceae, carbapenem-resistant *Acinetobacter baumannii*, HIV-transmitted drug resistance, and *Streptococcus pneumoniae*.

Whole Genome Sequencing in EpiPulse WGS surveillance expanded to new pathogens



ECDC Bioinformatic training needs assessment, November 2021



- Survey was sent to the NMFPs of all EU/EEA and Western Balkan countries
- Objectives
 - Identify training needs for bioinformatics, microbiology and epidemiology in order to build and deliver a genomic epidemiology training programme
- Key findings
 - Two main groups: 40% low or no knowledge in bioinformatics, 40% need advanced training
 - 89% interested in evolutionary biology; 93% in metagenomics for surveillance
 - >60% of microbiologists want training in phylogenetic analysis
 - All countries stress need for standardised data collection/sharing
 - 93% of microbiologists and 89% of epidemiologists value multidisciplinary exercises

Cross-border capacity-building support programme in genomic epidemiology



Framework contract:

“Training programme in genomic epidemiology and public health bioinformatics”

- GenEpi-BioTrain

Aim:

Increase capacity to respond to Covid-19 pandemic

Increase capacity for genomic epidemiology for other diseases

- Value of the contract: ~5.2 Mio EUR for up to 48 months
- The kick off meeting was held in January 2023



Training programme in genomic epidemiology and public health bioinformatics “GenEpi-BioTrain”

Information meeting – 24 October 2025

Anders Rhod Larsen

Statens Serum Institut (SSI), Denmark

What's in the next 10 minutes



1. Overview of the training programme
2. Pathogen waves
3. Training activities and timeline
4. Why applying for GenEpi-BioTrain activities

GenEpi-BioTrain at a glance

WHY?

Support countries in building capacity for the routine use of genomic information for surveillance, preparedness and outbreak response

WHO?

Public health professionals:

- w. background in computational biology/bioinformatics
 - w/o. specific background in bioinformatics (e.g. microbiologists and epidemiologists)

**WHERE?
HOW?
WHEN?**

- SSI & DTU, Denmark; IP, France; RCB, Germany; THL, Finland; KUH, Sweden;
- In person & Online
- 2023 - 2026

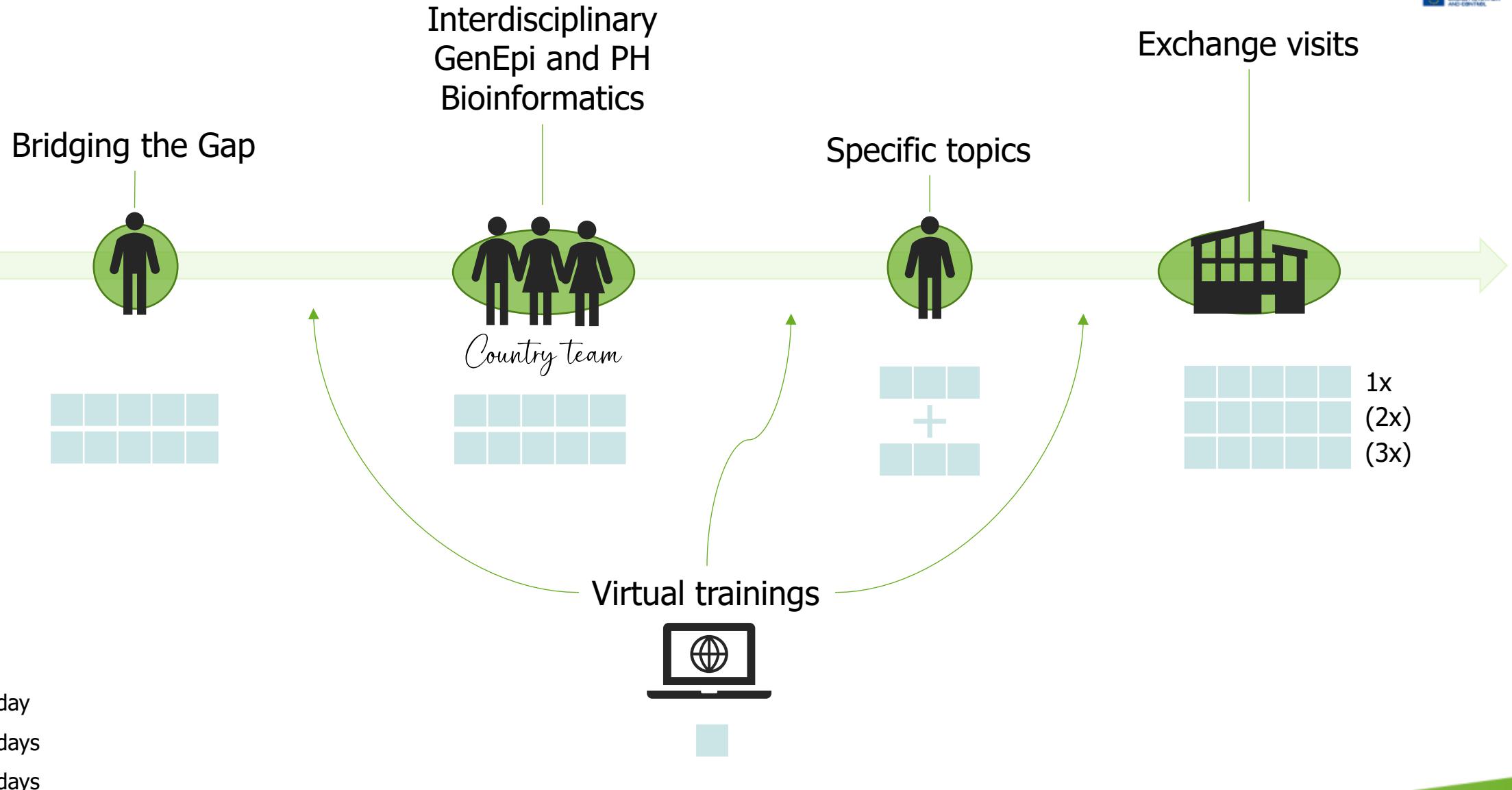
WHAT?

Pathogen waves

Pathogen waves

Year		Site
1	Respiratory viruses (SARS-CoV-2, influenza)	AMR (CCRE, MRSA and <i>C. difficile</i>)
2	FWD (<i>Listeria</i> , <i>Salmonella</i> , STEC)	VPI (<i>N. meningitidis</i> , <i>B. pertussis</i>)
3	Tuberculosis	AMR
4	One Health (bacteria)	To be announced in 2026

Training activities per wave



Bridging the gaps in bioinformatics (BTG)



In-person

2 weeks

10 trainees/course

- The aims are to **strengthen programming knowledge and skills** for use and development of bioinformatics tools in the public health context
- Trainees have basic bioinformatics skills (beginners)
- Dates: **23 February - 6 March 2026**

Interdisciplinary genomic epidemiology and public health bioinformatics (InterD)



In-person

2 weeks

30 trainees/course
(10 country teams)

- The aim is to **improve the knowledge of and capacity for applied genomic epidemiology** and bioinformatics for public health action
- Trainees will be **“country teams”**. It is up to each country to decide if the country team should be composed by:
 - three nominees from public health OR
 - two nominees from public health and one from the food/veterinary sectorIn any case, the country team should be composed by a bioinformatician, a microbiologist and an epidemiologist.
If support to nominate colleagues from the food/veterinary sector is needed, please contact the ECDC Microbiology team
- Dates: **27 April – 8 May 2026**

Exchange visits for bioinformaticians

In-person

40 trainees x 1 week
15 trainees x 2 weeks

3-5 trainees/visit

- The aims are to **learn best practices** for public health bioinformatics and to **build a network** for support
- Host institutions for 1-week visits for Block 1 trainees in 2026:
 - IP – time to be decided, but no earlier than May 2026
 - THL - time to be decided, sometime in autumn 2026
- Trainee should express their training needs and possibly bring their own data to analyse during the visit
- 2-week visits are announced separately

Specific topics in genomic epidemiology and/or public health bioinformatics



In-person

3 days

10 trainees/course

- Topics to be defined based on trainees' skills. Different trainings can cover different proficiency levels
- Dates for 2026:
 - Course on SQL (or similar topic based on needs of Block 1 trainees): @SSI, late May/early June 2026
 - Course on plasmids: @SSI, 1-3 September 2026
 - Course on *Legionella*: IP (with contributions from EUR-LPH-LEGI are currently explored)

Virtual trainings on genomic epidemiology and public health bioinformatics



Virtual

1 day

Open to many trainees

- Wide range of topics
 - Countries are welcome to express needs for specific topics
- It does not need to follow the pathogen waves strictly
- Approximately once per month
- Announced via the ECDC Learning Portal

Information sharing activities



- Yearly virtual meeting with ECDC national contact points (24 October 2025)
- Yearly virtual information sessions with the appointed trainees (January 2026)
- Quarterly newsletter
- ECDC Learning Portal – open to everyone!
<https://learning.ecdc.europa.eu/>

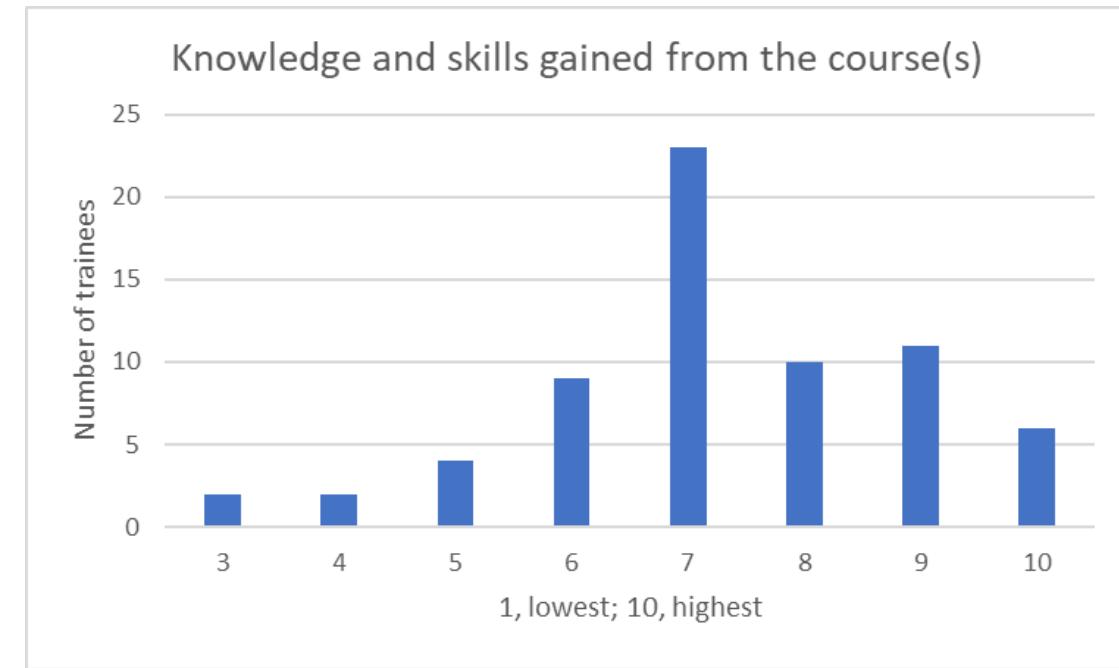
What are the benefits of attending GenEpi-BioTrain activities?



Improve individual and institutional bioinformatic skills for routine use of WGS in public health

From basic bioinformatics to tailored trainings through mixed training activities

Network creation, national and international



Trainees' survey: long-term impact of GenEpi-BioTrain

67 respondents (45% response rate), one or two years after the training

Details on Block 1 activities

Kirsten Ellegaard, PhD

Department of Bioinformatics
Statens Serum Institut
Denmark

Block 1 content

- “Bridging the gaps in bioinformatics” (face-to-face)
 - “Crash-course” in bioinformatics
 - 23 February – 6 March 2026 (2 weeks, face-to-face)
 - At SSI (Copenhagen, Denmark)

Block 1 content

- “Bridging the gaps in bioinformatics” (face-to-face)
 - “Crash-course” in bioinformatics
 - 23 February – 6 March 2026 (2 weeks, face-to-face)
 - At SSI (Copenhagen, Denmark)
- 3-day specialized course (face-to-face)
 - Introduction to SQL (or similar topic, based on training needs of participants)
 - Late May/early June 2026
 - At SSI (Copenhagen, Denmark)

Block 1 content

- “Bridging the gaps in bioinformatics” (face-to-face)
 - “Crash-course” in bioinformatics
 - 23 February – 6 March 2026 (2 weeks, face-to-face)
 - At SSI (Copenhagen, Denmark)
- 3-day specialized course (face-to-face)
 - Introduction to SQL (or similar topic, based on training needs of participants)
 - Late May/early June 2026
 - At SSI (Copenhagen, Denmark)
- 1-week exchange visit
 - Topic adjusted to individual participants needs
 - Possibilities for trainees to bring their own data for analysis
 - Location (participants on each):
 - Finnish institute for Health and Welfare (THL): Helsinki or Kuopio, Finland
 - Time to be decided, no earlier than May 2026

OR

- Institut Pasteur (IP): Paris, France
- Autumn 2026

Bridging the gaps in Bioinformatics - 4th edition

- ❖ We (the trainers) are also learning
- ❖ Course continues to evolve, but overall schedule is settled

Intended learning outcomes

- ❖ Process sequencing data (from raw data to genomes)
- ❖ Perform basic analysis supporting epidemiological investigations, including interaction with public databases
- ❖ Critically evaluate data quality at all steps of the process
- ❖ Write basic python/bash scripts, to extract relevant information from processed data
- ❖ Write a basic processing pipeline

Intended learning outcomes

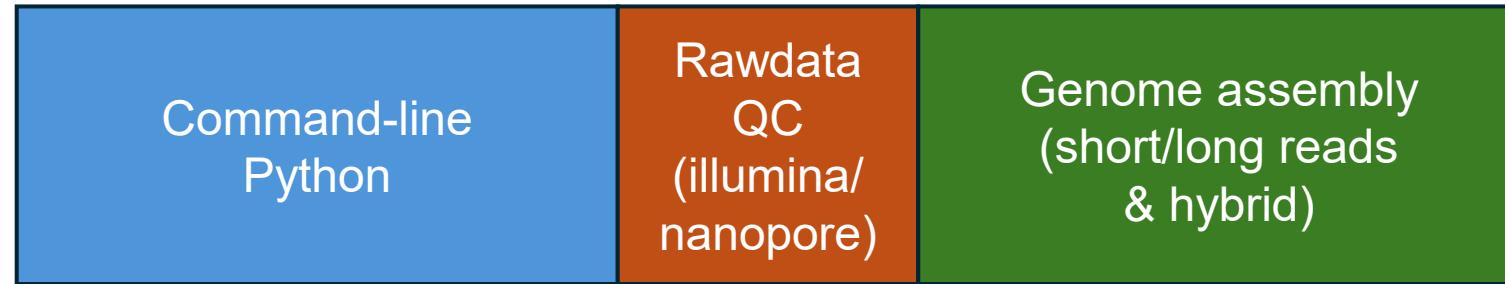
- ❖ Process sequencing data (from raw data to genomes)
- ❖ Perform basic analysis supporting epidemiological investigations, including interaction with public databases
- ❖ **Critically evaluate data quality at all steps of the process**
- ❖ Write basic python/bash scripts, to extract relevant information from processed data
- ❖ Write a basic processing pipeline

Intended learning outcomes

- ❖ Process sequencing data (from raw data to genomes)
- ❖ Perform basic analysis supporting epidemiological investigations, including interaction with public databases
- ❖ Critically evaluate data quality at all steps of the process
- ❖ Write basic python/bash scripts, to extract relevant information from processed data
- ❖ Write a basic processing pipeline

The programme at a glance

Week 1



Week 2



* Programme changes each year. Focused on methods.

How the training is done

Hands-on



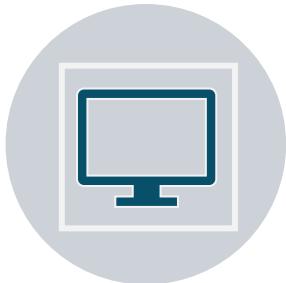
- Practicals with real data
- Minimal theory/lectures

Team-work

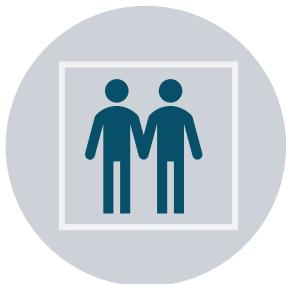


- Peer-to-peer learning

The trainers



We are
bioinformaticians



We work in teams of
two (minimum)



Each trainer team is
responsible for 1-2
days of the programme



Experts in their fields

Who should apply

- ❖ It's a two-week course, aimed at beginners
- ❖ Motivation is key

- It takes years to become proficient
- We aim to get the participants started on the journey



GenEpi-BioTrain - Pathogen Wave 7, One Health (bacteria)

Details on Block 2 and Block 3 activities at SSI

Information meeting – 24 October 2025

Interdisciplinary genomic epidemiology and public health bioinformatics (Block 2) 27 April – 8 May 2026



Main topics:

- Training will focus mainly on FW pathogens
 - such as *Campylobacter*, *Salmonella*, *Listeria* and AMR-related issues
- Plasmid-related topics in One Health (cross-species analyses, outbreak tracking)
- Host-factor analysis to trace spill-over events Issues at the interface of food, animals, and human health
- Other (details to be defined)

Interdisciplinary genomic epidemiology and public health bioinformatics (Block 2)



What participants will gain from this course:

- Hands on experience for outbreak investigations under a One Health approach
Enhanced knowledge and skills in the use of open source tools for integrated analysis and visualisation of WGS and epidemiological data

Practical experience on how interdisciplinary integration of microbiology, epidemiology and bioinformatics can inform public health action

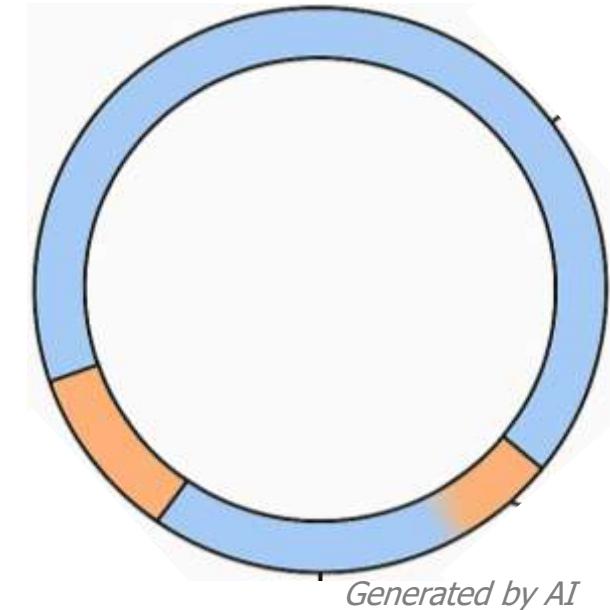
Who should apply to InterD 2026

- Bioinformaticians, epidemiologists/food specialists and microbiologists working with FWD and AMR surveillance
- Bioinformaticians should have at least basic skills in using the command-line and working in Linux. Beginners in bioinformatics are still encouraged to apply but will be asked to follow some E-learnings before the course

3-day course on plasmids (Block 3) 1-3 September 2026

What participants will learn in this course:

- Biology of plasmids in Enterobacteriales, focusing on AMR plasmids
- Plasmid sequencing – short-reads, long-reads - and bioinformatics analyses
- Epidemiology of plasmids carrying carbapenemase-encoding genes



3-day course on plasmids (Block 3) – **Who should apply**



Prerequisites:

- Ability to use the command-line and work in Linux
- Capacity for WGS by long-read data (ONT, Pacbio,..) at the home institute
- Willingness to contribute to a field not fully established



- GenEpi-BioTrain

On-site course in Institut Pasteur — Wave 7 (2026)

October 24th, 2025

INSTITUT
Pasteur

1-week exchange visits

Wave 7: One Health approach

- June 2026 (dates to be confirmed)
- We encourage participants to bring their own genomic datasets
- The focus will be on *Listeria* and *Salmonella*, but we could also involve experts on *E. coli* and *Yersinia*.
- The content will be tailored to participants' needs; however, based on our expertise, we could cover the following topics:
 - Tools and approaches for genomic taxonomy of bacterial strains
 - Genomic surveillance using NGS data
- Pr Sylvain Brisse will be the course director.

3-days face to face training

Wave 7: One Health approach

- May 2026 (dates to be confirmed)
- The focus will be on *Legionella*.
- Target groups: advanced bioinformaticians who works with *Legionella* typing/*Legionella* genomic surveillance
- The following topics could be covered:
 - Quality control methods and challenges
 - Data submission and analysis in national and in EU levels
 - Species ID
 - ST determination and cgMLST
 - SNPs detection and phylogenetics in outbreak investigation
 - AMR detection

Thank you for your attention!

Acknowledgements

The creation of this training material was commissioned by ECDC to Institut Pasteur with the direct involvement of Dr Solène Cottis, Pr Sylvain Brisse and Dr Thierry Lang.

Contact at Institut Pasteur: gebt@pasteur.fr

Research Group for Global Capacity Building

National Food Institute

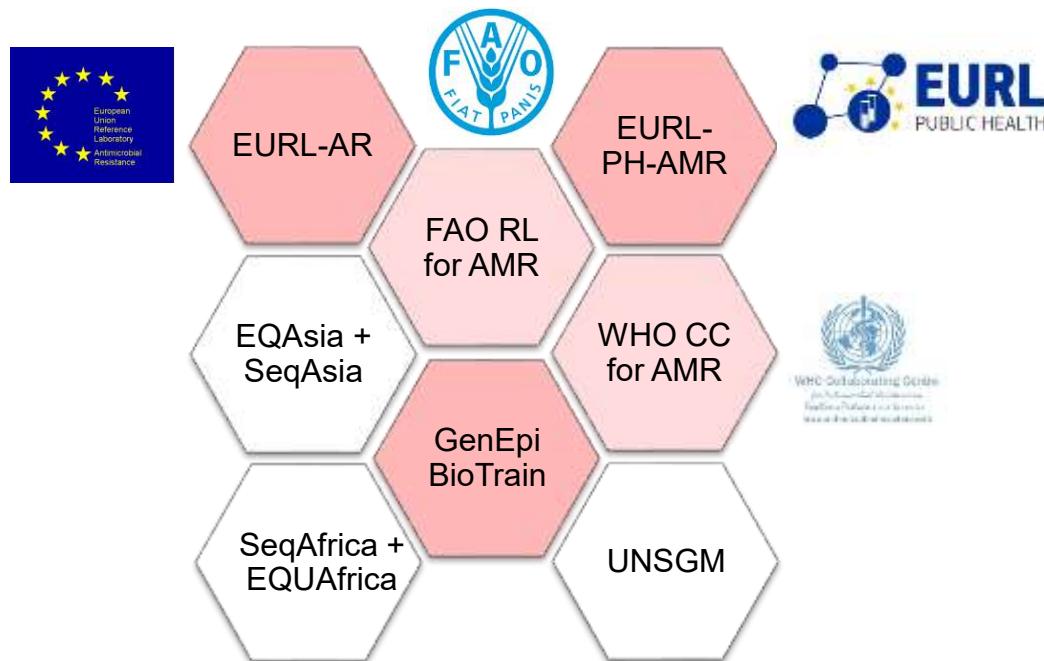
Technical University of Denmark

Prof. René S. Hendriksen
National Food Institute,
Technical University of Denmark (DTU FOOD)



Who we are

~ 30 employees; projects in Europe, Asia, Africa, ...



Subject matter experts in

- Classical microbiology
- Molecular microbiology
- Whole-genome sequencing
- Bioinformatics
- External quality assessments
- Capacity building
- Among others...

What we work on – on a global scale building capacity for AMR

- WHO Collaborating Centre for Antimicrobial Resistance and Foodborne Pathogens and Genomics
- FAO reference laboratory for Antimicrobial Resistance (joint IAEA program)
- European Union Reference Laboratory for Antimicrobial Resistance (EURL-AR) in Feed, Food, Animal Health
- Partner in the European Union Reference Laboratory for Antimicrobial Resistance (EURL-PH AMR) in Public Health
- Program contractors for European CDC
 - GenEpi-BioTrain
- UK Aid Fleming Fund regional project grantee
 - SeqAfrica
 - EQAsia and SeqAsia
- UNSGM grantee (bio-terrorism preparedness)

What we do

- Improve global surveillance of antimicrobial resistance (AMR) through capacity building, implementing and operational research
- Develop and implement methods and guidelines to support building the capacity of AMR and whole genome sequencing (WGS) surveillance
 - in collaboration with the EU, EFSA, ECDC, WHO, FAO/ IAEA, UK AID/ Fleming Fund (DHSC), UNEP, US CDC, US FDA among others
- Give scientific and technical assistance to supranational organizations, national reference laboratories, health organizations and foundations, globally
- Perform External Quality Assessment (EQA's) trials and training activities in detection of infectious diseases and AMR by phenotypic and genomic methodologies

Thank you for your attention



24 OCTOBER 2025

Pasteur team

Prof Sylvain Brisse & coll.



Institut Pasteur

- **A non-profit foundation with recognized charitable status**, founded by Louis Pasteur, in 1885
- **Staff** ~2700
- **4 missions:**
 1. Research
 2. Public Health
 3. Training
 4. Research applications
- 146 research units
- 16 National Reference Centers; WHO-CCs
- 35 Core facilities (Omics, ...)



IP teams involved in GenEpi-BioTrain

Biodiversity and Epidemiology of Bacterial Pathogens Unit

National Reference Center for diphtheria

National Reference Center for Whooping cough and other *Bordetella* infections

Genomic taxonomies of bacterial strains (BIGSdb-Pasteur)

Klebsiella genomics

Sylvain BRISSE, Head of Unit (coordinator for IP)

Solène COTTIS and Anvita BHARGAVA, Project Manager

Education Department

Monica SALA, Director of Education Department

Thierry LANG, International teaching, Education Department

Other research Units, NRCs and core facilities:

E. coli-*Shigella*-*Salmonella*, *Vibrio* (FX WEILL)

Meningococci / *Haemophilus influenza* (MK TAHIA)

Hub for Bioinformatics and Biostatistics

Listeria, *Legionella*, *Leptospira*, *Polio*, *Rabies*, ... experts/labs



Merci





GenEpi-BioTrain: Introduction of the Host Institute



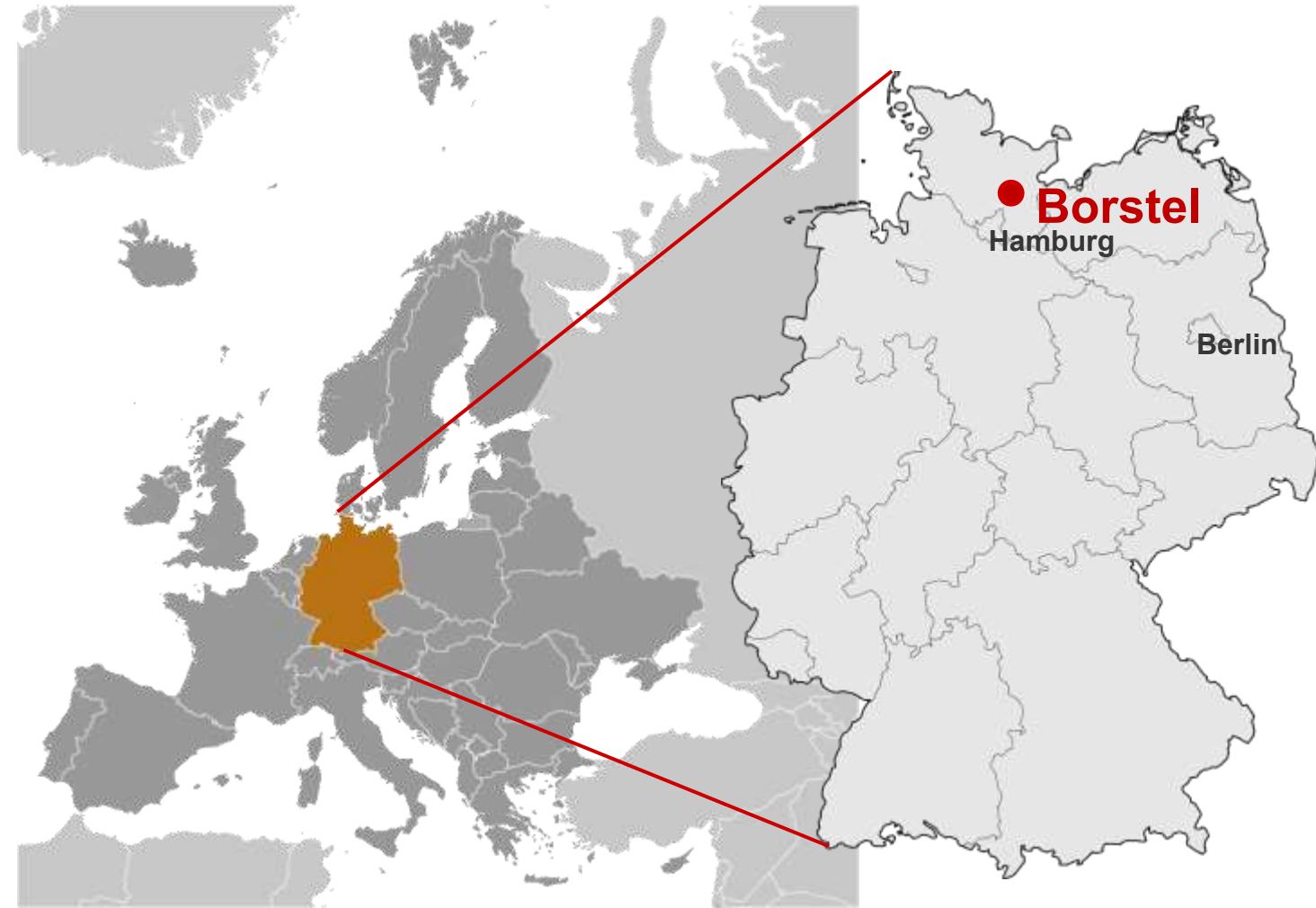
Founded in 1947



Annual budget (Federal, State, Third Party) - ca. 36 Mio. Euro

Member of the Leibniz Association - *theoria cum praxi*

Nationally and internationally linked within networks





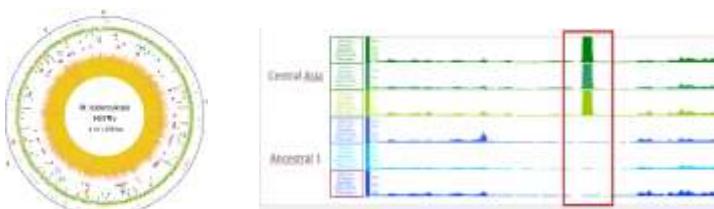
Elucidation of the causes and mechanisms of chronic inflammatory lung diseases

Development of new innovative concepts for their monitoring, diagnostics, prevention and therapy

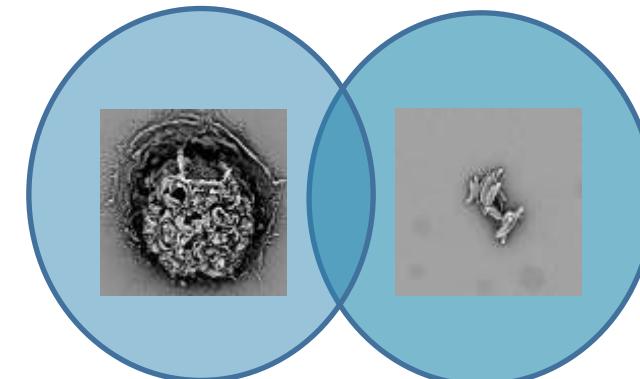
CURE tuberculosis

PREVENT asthma, COPD

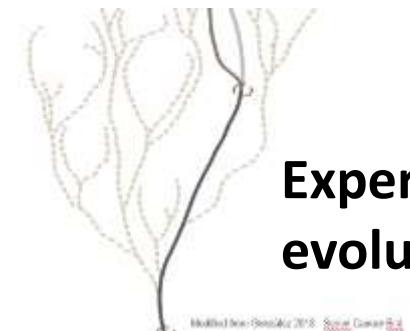
Genomics/Bioinformatics



Experimental Mycobacteriology



Host –Pathogen
Interaction



REM-Pictures: S. Homolka, T. Gutsmann

Implementation team



field studies

RCB: Team

Viola Dreyer



Stefan Niemann



Christian Utpatel



Ivan Barilar



Christiane Gerlach

Matthias Merker



Margo Diricks



THANK YOU



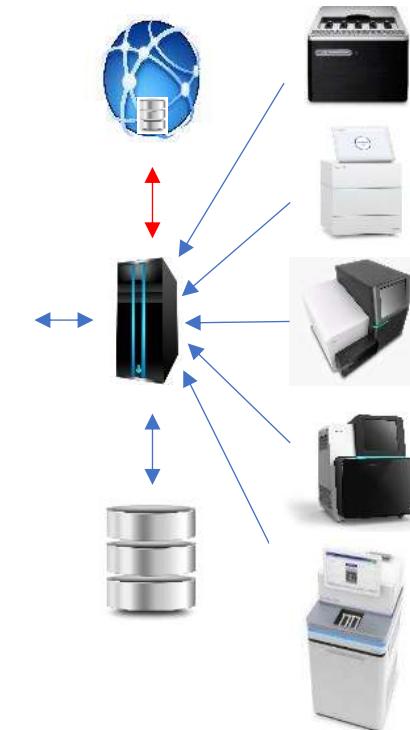
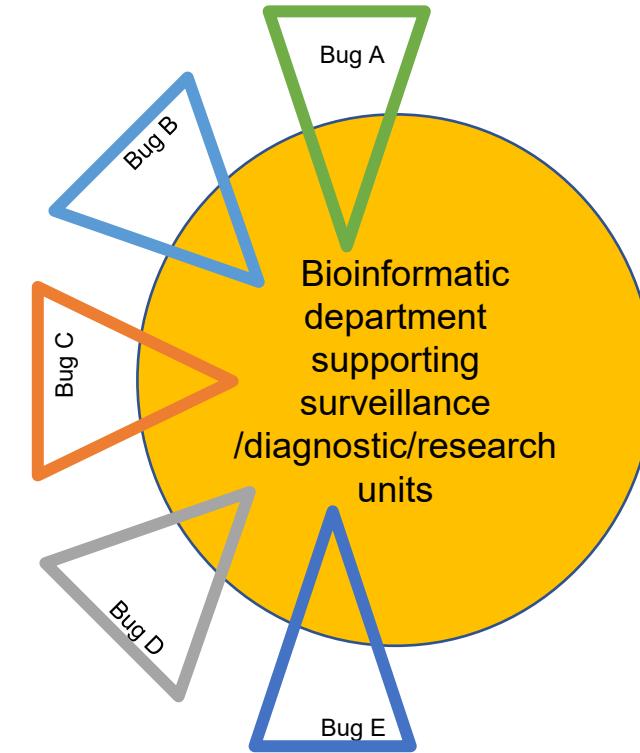
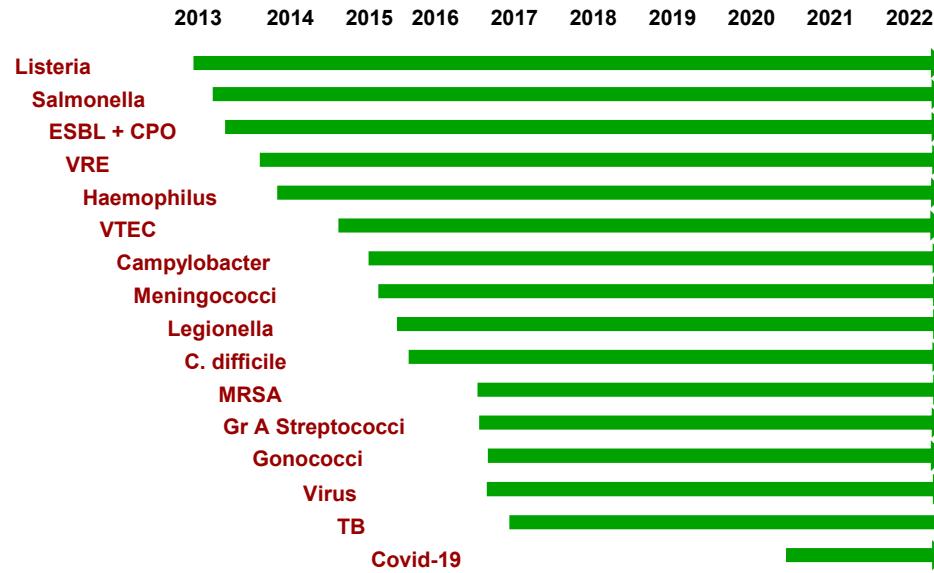


Statens Serum Institut (SSI), established in 1902, is a governmental Public Health Institut

- The national center for infectious disease control and national reference laboratory for both human and animal health
 - NRL- Antimicrobial resistance
 - Hospital Acquired infections
 - Preclinical development of antibiotics
 - (32 employees)

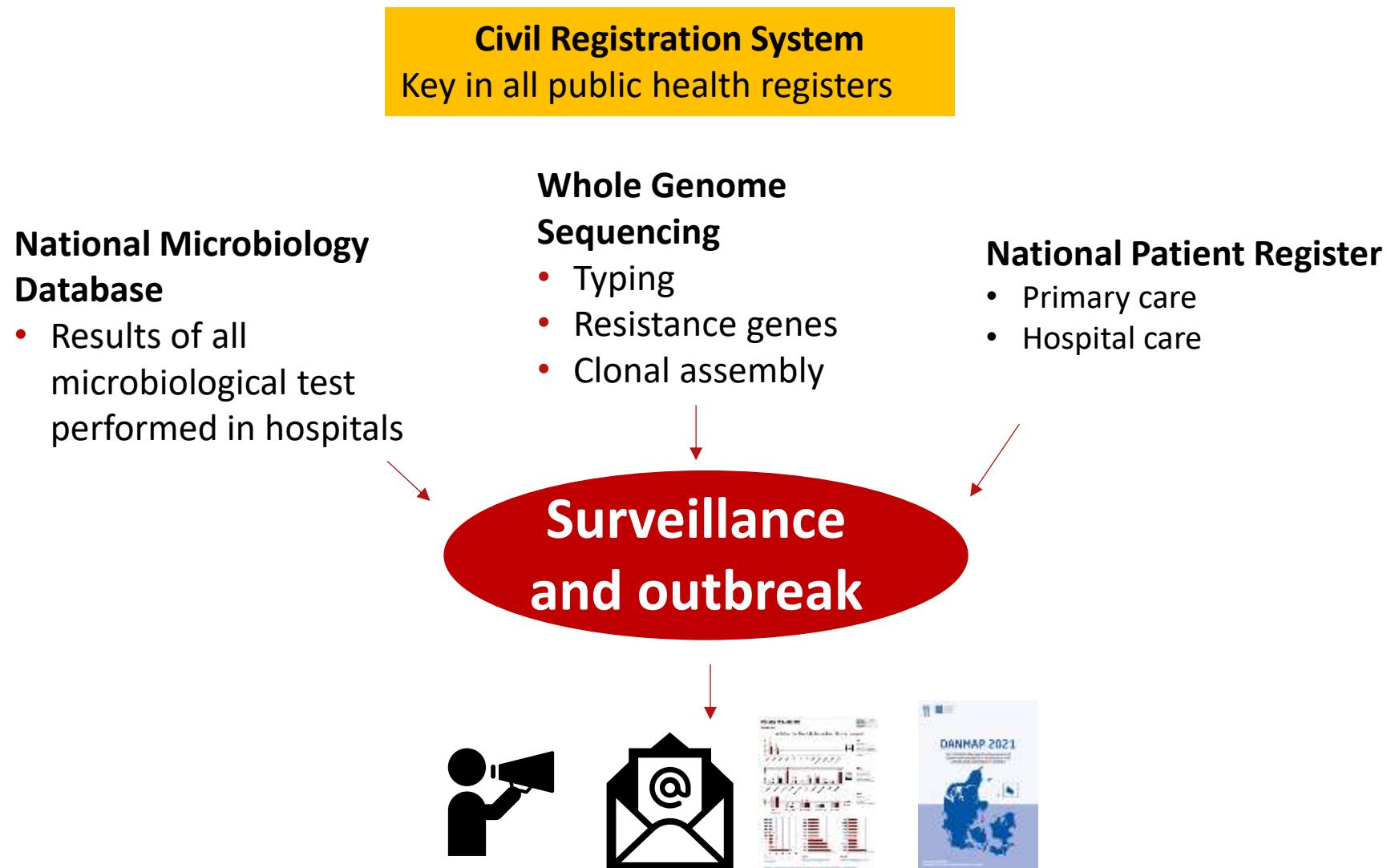


Implementation of WGS at Statens Serum Institut



- Approx. 12,000 bacterial genomes in 2024
- Up to 15,000 SARS-CoV-2 genomes per week- > 1,100,000 in total

Combining WGS with clinical and epidemiological data for surveillance and outbreak investigations



Ongoing support and capacity building programs- NRL-AMR

- HERA Incubator: Direct grant for National WGS infrastructure project: “Microbe-SEQ- Denmark”
- EURGen-RefLabCap: Increasing capacity in NRL functions, focus on implementing WGS for colistin and carbapenem resistant Enterobacterales, *P. aeruginosa*, *A. baumanii*
- GenEpi-BioTrain: Improving bioinformatic capacity and make WGS data useful in public health
- EURL-PH-AMR
- Fleming Fund -Fellows program in Bangladesh
- Strategic sector collaborations with
 - India CDC
 - UPC Ukraine
 - Tanzania

GenEpi- BioTrain

**Site visit
possibilities in
Finland**

Finnish Institute for
Health and Welfare

28/10/2025



Duties and roles

- Finnish Institute for Health and Welfare (THL)
 - State-owned expert and research institute
 - Promotes welfare, health, and safety of the population
 - Operates and serves at national level
- Department of Public Health
 - Monitoring health and wellbeing
 - Preparedness for national and cross border health threats
 - Expertise in planetary health
- Microbiology Unit
 - Expertise on bacterial, viral, and parasite infections, AMR, and microbiological water analysis
 - Coordination of laboratory-based surveillance of infectious diseases
 - Offers microbiological analysis
 - Participates in outbreak investigations
 - Reference laboratory for polio, influenza, measles, and rubella
 - Accreditation for several methods



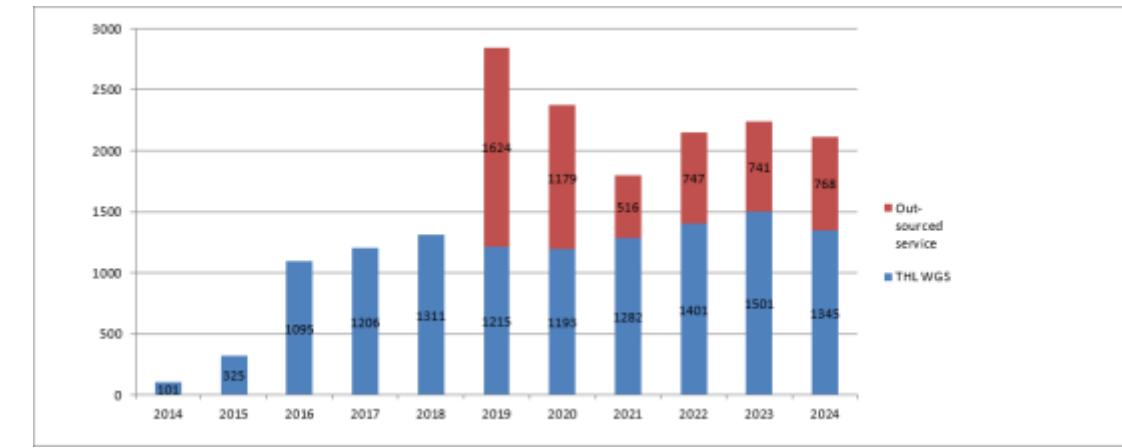
TIETOA TESTAUSLABORATORIOSTA



WGS-based surveillance

- WGS started in 2014 for bacteria
 - ~2200 sequenced strains/year
 - sequencing in-house and outsourced
- WGS started in 2021 for viruses
 - Influenza A and B
 - since 2021, ~ 60-240 genomes /year
 - SARS-CoV-2
 - in house since 2022
 - 2000-12 000 genomes/year
 - currently about 1 000 – 1 200 genomes/year
 - Other respiratory viruses
 - adenovirus in 2024, ~ 50 genomes
- Illumina (MiSeq, NextSeq) and Nanopore (MinION) technology

WGS, Bacteria



Site-visit at THL

- Planned for autumn 2026, one week
- For early career bioinformaticians
- Objectives
 - To present bioinformatic tools and pipelines used in THL
 - To discuss how genomic data is integrated in infectious disease surveillance in Finland
- Suggested program
 - One Health approach
 - Topics: FWD, (AMR), avian influenza, waste-water surveillance, legionella, vibriosis
 - Also covered: reporting, standardization, laboratory infrastructure
 - Program to be adjusted according to needs
- Experts:
 - Bioinformatics: Jani Halkilahti, Anastasia Karaeva; Heidi Putkuri, Outi Nyholm
 - Bacteriology: Anni Vainio, Saara Salmenlinna
 - Virology: Erika Lindh, Niko Tervo, Niina Ikonen
 - Water microbiology: Elisa Salmivirta, Eveliina Nurmi, Outi Zacheus





Karolinska University Hospital

Christian G. Giske, Professor Clinical Bacteriology

Jan Albert, Professor Clinical Virology

Robert Dyrdak, Specialist in Clinical Microbiology/PhD

Annika Tiveljung Lindell, Head of Department/PhD

24 October 2025

Karolinska University Hospital

- One of the largest university hospitals in Europe with 1.35 million patient visits annually
- Covers almost a quarter of the population in Sweden
- Clinical microbiology has 320 employees and offers a very broad range of diagnostic areas
- Clinical microbiology also has national reference function for a number of areas such as retroviruses, enteroviruses, TBE virus, respiratory viruses (except influenza), *M. tuberculosis* (primary diagnostics), atypical bacterial pneumonia, susceptibility testing of anaerobes, mycology, and metagenomics
- Available trainers in bioinformatics
 - Sofia Stamouli, bioinformatician with expertise on viruses and metagenomics
 - Lili Li, bioinformatician with expertise on viruses
 - Samuel Lampa, bioinformatician with expertise on workflow systems and bacterial typing
 - Mohammad Razavi, bioinformatician with expertise on bacteria and metagenomics
 - Patrik Jonsson, biomedical analyst with extensive experience on analysis of data from epidemiological typing of bacteria
 - Martin Vondracek, molecular biologist with long experience regarding metagenomic diagnostics

Which areas of interest do we offer?

- Whole genome sequencing of *S. aureus*, *Enterococcus* spp., *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *A. baumannii*, *N. gonorrhoeae* and *M. tuberculosis*
 - For *M. tuberculosis* we also offer genomic AST, for others mostly epidemiological characterisation
 - For *Candida* spp. work is ongoing to establish assays
- Molecular susceptibility testing of HIV and hepatitis B virus, and herpes simplex-virus; CMV in development
- Subtyping of SARS CoV-2, enteroviruses, and hepatitis C and D viruses
- Metagenomics (16S, ITS, shotgun metagenomics)

- 3-day on-site workshop (Block 3/Wave1) SARS-CoV-2 and influenza held 7-9 Nov 2023

Workshop proposal 2026

NGS clinical diagnostics, 3-day on-site workshop

(nominations will only start in 2026, not open for pathogen wave 7)

Aim: to provide the skills necessary to implement bioinformatics pipelines into routine clinical diagnostics

Objectives:

- To provide knowledge on existing pipelines:
 - metagenomics: 16S and shotgun
 - HIV resistance typing
- To provide knowledge on quality assurance and accreditation of bioinformatics pipelines

Training programme in genomic epidemiology and public health bioinformatics –
“GenEpi-BioTrain”

Nomination and selection of training participants

Theresa Enkirch, ECDC (Microbiology and Bioinformatics Section, ECDC)
24 October 2025

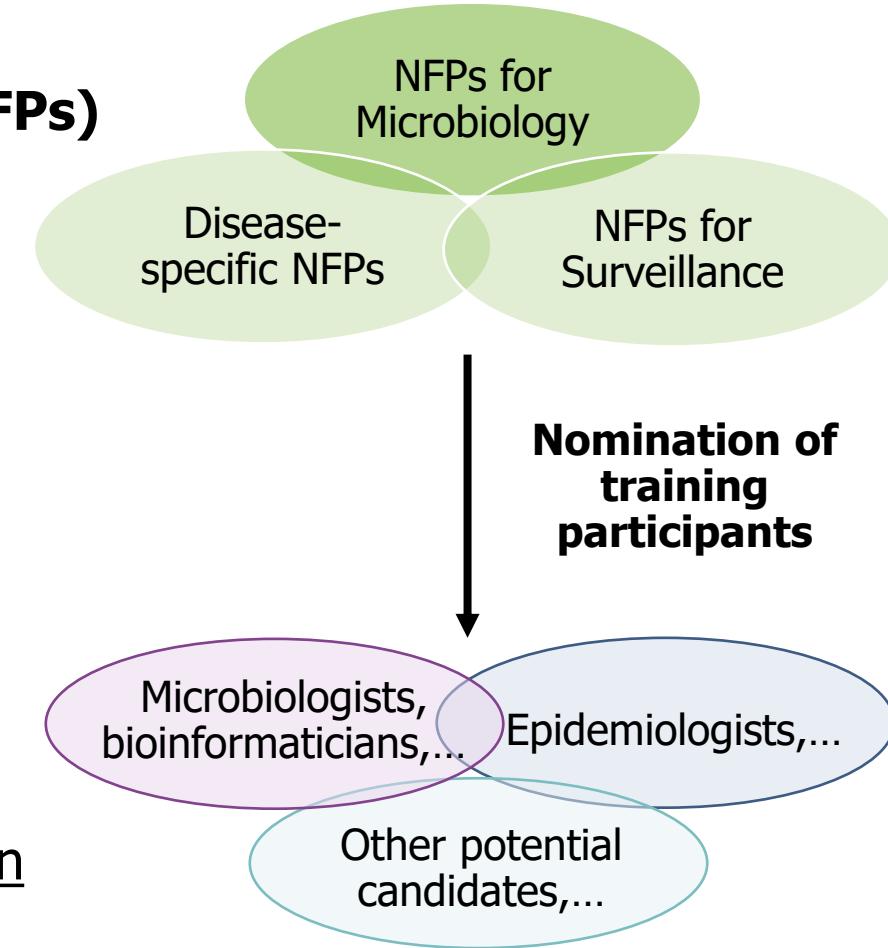
Who did we invite for this meeting and why

- National Focal Points (Observer) for
 - Microbiology
 - Surveillance
 - FWDs and Zoonoses
 - AMR
 - HAIs
 - Legionnaires' disease
 - Training
- National Coordinators
 - Operational Contact Points for Bioinformatics
 - Operational Contact Points (Microbiology & Epidemiology) for
 - Antimicrobial-resistant isolates
 - Diseases Caused by Antimicrobial-Resistant Microorganisms
 - Healthcare-Associated Infections: Clostridium difficile Infections & All
 - Campylobacter isolates
 - Campylobacteriosis
 - E. Coli isolates, Shigellosis, Verotoxigenic Escherichia Coli Infection (VTEC)
 - Legionellosis
 - Listeria isolates, Listeriosis
 - Salmonella isolates, Salmonellosis

→ To ensure the information reaches ALL relevant stakeholders

How can I apply for the training programme?

- Training participants should be nominated
- Nomination of participants should be done by the (Observer) **National Focal Points for Microbiology (NMPFs)**
 - GenEpi-BioTrain is a microbiology capacity building activity
 - NMPFs have contacts to the National and sub-national laboratories
 - NMPFs know where training and capacity building is needed most
- Disease-specific NFPs and NFPs for Surveillance can contact the NFPs for Microbiology to coordinate the nominations
- NFPs for Microbiology lead the coordination of the nomination process in their country



How does the nomination process work?

- Each country will receive a separate email containing an invitation letter to nominate potential candidates for the GenEpi-BioTrain
- A survey link will be provided in the email which can be distributed to potential candidates
- Interested candidates should contact their National Focal Point for Microbiology to receive the survey link
- The email will be sent:

To: (Observer) National Focal Points for Microbiology & Alternates

CC: National Focal Points for Surveillance, Disease-specific NFPs, Disease-specific OCPs, NFPs for Training, National Coordinators

How does the nomination process work?

- Potential candidates are asked to fill the survey
 - Choose the pathogen wave and training block of interest
 - Contact details
 - Short CV
 - Short statement why they chose the training and how they can benefit from it
 - Short questionnaire about bioinformatics skills
- **NMFP should write a short paragraph** (word document/pdf; signed) to be attached to the survey before submission
 - To justify why this individual should be chosen for the training
 - How the host institute can benefit from their participation

Example: Survey for nomination

☒ EUSurvey

Nomination for the training programme in genomic epidemiology and public health bioinformatics – “GenEpi-BioTrain” focused One Health pathogen wave

Nomination for GenEpi-BioTrain, Wave 7, One Health wave

Instructions

- Select your current level of bioinformatic skills
- Block 2 focuses on Foodborne pathogens such as Campylobacter, Salmonella, Listeria and AMR-related issues
- **Please apply to the blocks based on your experience in Bioinformatics to benefit with the training**
 - Block 1 (Target group - Beginners in Bioinformatics)
 - Block 2 (Target group - Country team of 3 people - Bioinformatician (with some experience), Epidemiologist / Food safety Expert and Microbiologist)
 - Block 3 (Target group - Advanced Bioinformaticians, familiar with command-line interface and experience analysing genomic data)
- Provide a short CV (max. one page) and a justification for training (max. 200 words each)
- Provide your contact information
- For further details on the training programme, please check the invitation letter and presentations
- **To be filled by the NFP for Microbiology:** Provide a short paragraph to justify why this person should be chosen for the training and how the host institute can benefit from their participation (max. 200 words), and send the signed letter to the candidates
- **Deadline for nomination: Wednesday, 26 November 2025**

Example: Survey for nomination

* One Health Training Block

- Block 1 (Beginners in Bioinformatics)
- Block 2 (Country teams - Bioinformatician, Epidemiologist / Food safety Expert and Microbiologist)
- Block 3 - Plasmid analysis (Advanced Bioinformaticians)
- Block 3 - Legionella training (Advanced Bioinformaticians)

Choose the training block of interest

Bioinformatics skills

* Do you have experience working from the command-line UNIX?

- A lot
- Some
- Not at all

(10 questions in total)

* Do you have experience with coding in python?

- A lot
- Some
- Not at all

Example: Survey for nomination

CV, Motivation letter and Justification for nomination

- * CV (required, to be filled by candidates). Indicate your Education, Working experience. Max. 1 page.

Select file(s) to upload



[Click here to upload your short CV \(word, pdf\)](#)

- * Why do you think you are the appropriate applicant to this training? Maximum 200 words



Free text fields to be filled

- * Elaborate on how do you see the application the newly acquired skills and knowledge in your everyday work? Maximum 200 words



- * Justification for nomination (required, and should be filled by NFPs). Please upload the signed pdf document from NFPs. Instructions for NFPs: Short paragraph (Maximum 200 words) to justify why this person should be chosen for the training and how the host institute can benefit from their participation. Please note, only signed documents from NFPs are accepted.

Select file(s) to upload



[Click here to upload the justification letter from your NFP](#)

Training “blocks” per pathogen wave

Block 1:

- “Bridging the gaps”
- Exchange visits
- Specific topics

Level:

BEGINNER LEVEL

Target group:

Bioinformaticians or
“bioinformaticians-to-be”

Further info:

Candidates should work/plan to work directly with public health sequencing-related activities

Block 2:

- Interdisciplinary training (“Country teams”)

BEGINNER/
ADVANCED LEVEL

Per country:
1 Bioinformatician
1 Microbiologist
1 Epidemiologist

Bioinformaticians should have some experience;
No bioinformatic experience needed for microbiologists or epidemiologists

Block 3:

- Specific topics

BEGINNER/
ADVANCED LEVEL

Bioinformaticians, others
(Microbiologists, epidemiologists,...)

Candidates should already have some experience in bioinformatics

Block 4:

- Virtual training sessions

BEGINNER/
ADVANCED LEVEL

Anyone who is interested

These activities will be announced separately

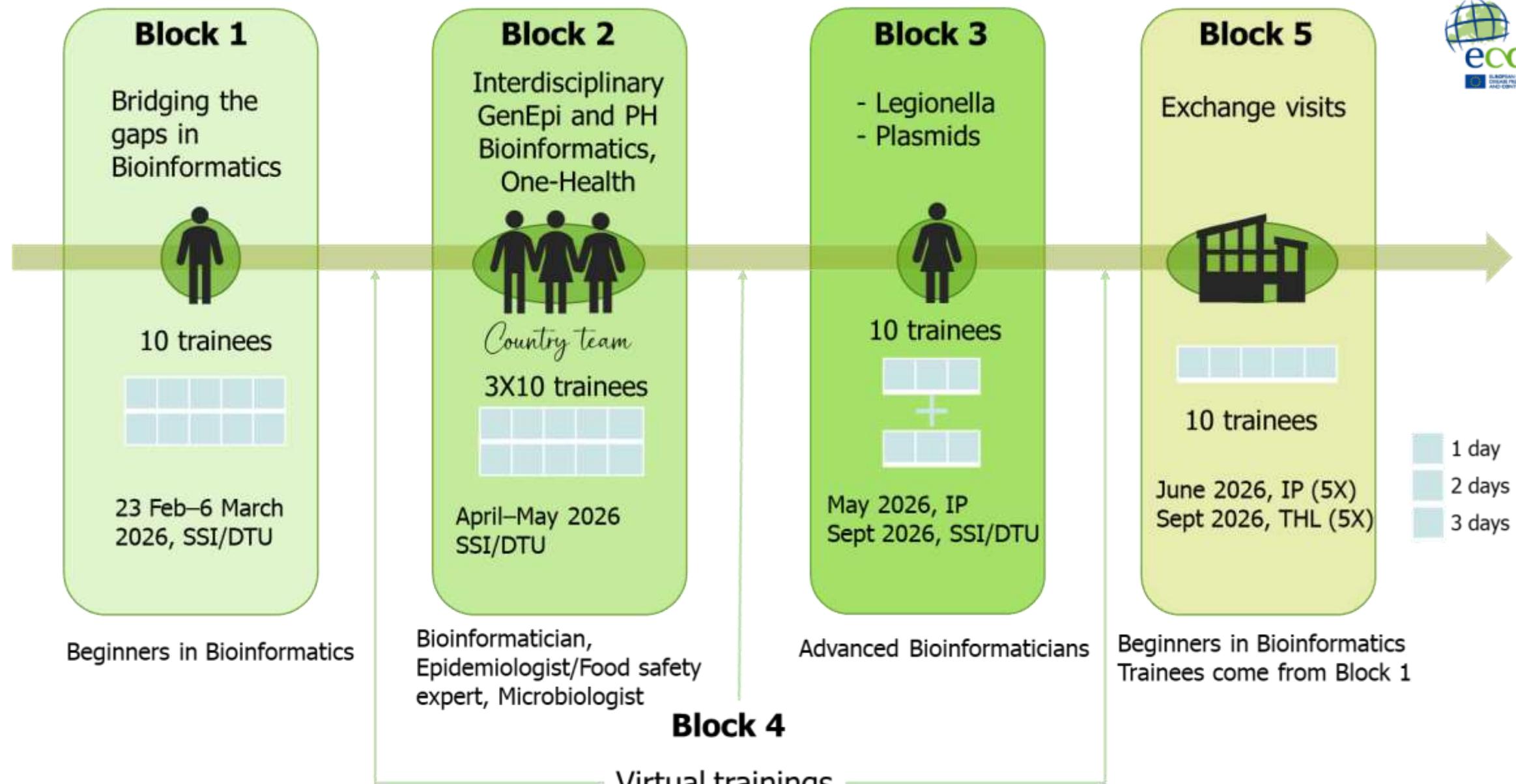
Block 5:

- Exchange visits

BEGINNER/
ADVANCED LEVEL

TBD

These activities will be announced separately



Nominations per country

- For each pathogen wave, each country can nominate up to two potential participants per training block
 - One person as backup in case someone drops out
- Nominees should be selected by the NFPs in an effort to ensure maximum impact of the training on the public health sector they serve, taking into consideration:
 - their projected period of implementation of skills at the institute
 - possibilities of cascading training nationally
 - direct use of the acquired skills

Nominations per country – “InterD course”

- F2F workshop “Interdisciplinary genomic epidemiology and public health bioinformatics” (Block 2)
 - Only one country team should be nominated
 - But good to have a backup person
 - Country team: 1x bioinformatician, 1x microbiologist, 1x epidemiologist/**food safety expert**
 - Professionals working in the food sector are also eligible to be part of the country teams, and it is recommended to consider including such a role, which can replace the epidemiologist one.
 - If this is not possible, the team will receive an additional assignment to ensure that all One Health aspects are fully covered and that participants can maximize the benefit of the training.
 - Epidemiologists/food specialists should be nominated in coordination with the NFPs for Surveillance/Disease-specific NFPs/Food Authority (if applicable)
 - Only complete country teams will be considered!



Eligibility and selection criteria

- Nominees must currently be employed **in the public health sector** in one of the EU/EEA countries
- ECDC will review applications and select candidates based on
 - professional background
 - training needs
 - maximum impact
 - course availability

Further information on the nomination and selection process

- ECDC will send out invitations to the NFPs to select nominees on **27/28 October 2025**
- Deadline for nominations/submitting the survey is Wednesday, **26 November 2025**
- ECDC will send an email to NMFPs, acknowledging the receipt of the nominations
- NMFPs then have the possibility to rank potential candidates
- Review of applications: 27 November – 12 December 2025
- Notification letter to successful candidates latest 19 December 2025
 - Please send your acknowledgement and confirmation of attendance by 15 January 2026
- ECDC will select one participant/country/training block/pathogen wave
- For the Interdisciplinary genomic epidemiology and public health bioinformatics workshop, ECDC will select one country team/country per pathogen wave
- If a selected participant is not able to join an activity, another person (backup) from the respective country can attend

Additional information

- There is a dedicated space on ECDCs Learning Portal for GenEpi-BioTrain:
[Course: GenEpi-BioTrain - Genetic Epidemiology and Bioinformatics Training Programme](#)
- Information about the training programme
 - Minutes and recording of this meeting
 - Virtual trainings
 - Training material from the different courses

If you have any further questions, please contact us!

ECDC.Microbiology@ecdc.europa.eu