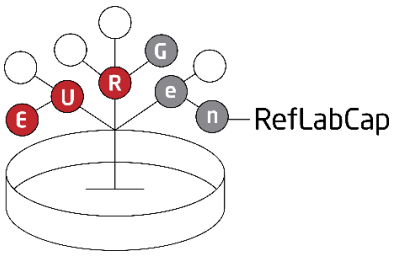

DATA-FOR-ACTION Workshop:

Date: September 17, 2024, from 9:00 to 16:45 CET.

Location: DTU, Kgs. Lyngby, Denmark

PRESENTATIONS

The purpose of the workshop is to continue building capacity for genomic epidemiology. It will focus on digital infrastructure and communication of whole-genome sequencing (WGS) data for national and international surveillance and outbreak detection. We will use the national WGS pilot projects of the priority countries as “cases” in break-out group discussions.

The objectives of these discussions will be to use the results including the genomic data as well as corresponding metadata to better understand the epidemiology of the organisms of the pilot projects. Questions such as "what does the data show" and "which actions to be taken by whom" will be addressed during the discussions but also in plenum sessions.

STATENS SERUM INSTITUT

DTU

EURGen-RefLabCap Workshop

EURGen-RefLabCap pilot genomic surveillance studies

17 September 2024

Ana Rita Rebelo

anrire@food.dtu.dk

Funded by the European Union

EURGen-RefLabCap pilot genomic surveillance studies

- The objective of the national WGS pilot studies was to build capacity at the NRLs for genomic surveillance and outbreak investigations of specific AMR priority pathogens.

- The WGS pilot studies aimed at supporting implementation of WGS for national AMR surveillance by providing a test case – in the priority and additional countries of EURGen-RefLabCap.

- The scope for the EURGen-RefLabCap WGS pilot studies included:
    * surveillance baseline studies of the epidemiology of defined pathogen(s)
    * investigation of ongoing or suspected outbreaks
    * retrospective and/or prospective epidemiological studies of strains of public health interest

Funded by the European Union

EURGen-RefLabCap pilot genomic surveillance studies

- Countries were encouraged to identify gaps and needs from their EURGen-RefLabCap action plans.

- Countries should define the target priority pathogens:

  WS1: carbapenem- and/or colistin-resistant Enterobacterales

  WS2: carbapenem- and/or colistin-resistant A. baumannii or P. aeruginosa

Funded by the European Union

Plan of the pilot studies

- The first step was to create a description of the pilot studies using a provided template (next slide).
- The target was to collect 25-30 strains in each country.
- The descriptions were discussed together with the countries, the EURGen-RefLabCap team and with input from ECDC.
- The pilot studies included financial support under the commitment of submitting a final report using a provided template (next slide).

Funded by the European Union

Plan of the pilot studies – the template for the description

Project description template

1. Objective and scope of the pilot study

Please describe the objective (including the WGS capacity building goal and general aim of the study):

2. Inclusion criteria

Please define the inclusion criteria of the pilot study (including the priority pathogens and phenotypes of interest, individuals/patients, sites/hospitals and time period):

3. *Collection of isolates for the pilot study*

*The **target** is to collect and sequence **25-30 isolates** in each country (**a minimum of 10 isolates is mandatory**). The collection may include isolates that have been previously sequenced and analysed by ECDC or other collaborators (e.g. isolates included in ECDC rapid risk assessments and in the CCRE survey). Please specify the number of isolates that will be included in the pilot study:*

4. *Collection of patient data (metadata)**

Please specify which patient data (or metadata) that you plan to include in the pilot study (e.g. age, gender, in/out patient, hospital location and sector, name/type of ward, etc.):

5. Collection of microbiology testing data

Please specify isolate collection date, laboratory testing dates, species identification results, phenotypic antimicrobial susceptibility testing results, location of pathogen (in organ or system), occurrence of infection or colonisation):

6. Collection of epidemiology data*

Please specify data relevant to the epidemiological investigations of the pilot study, including patient location, hospitalisation periods, hospital transfers, travel history, etc. (please note that some data may overlap data listed under patient metadata):

7. WGS setup and plans

Please specify the WGS technology (Illumina, MinIon, other) that will be used in the pilot study, number of isolates and WGS runs:

8. Bioinformatics analysis

Please specify your plans for bioinformatics analysis, including plans for identifying genetic determinants of AMR, phylogenetic relatedness, plasmids, virulence factors, etc.:

9. Data handling and storage

Please describe your plans for data storage, local computer and server capacity, secure handling of WGS and patient data and plans for uploading WGS sequence data in national or international WGS data repositories (incl. EpiPulse, ENA, other):

10. Timeline of the pilot study

Please describe your timeline, including details for the steps of collecting isolates and data, sequencing, bioinformatics analysis and preparing the report:

Funded by the European Union

Plan of the pilot studies – the template for the report

Description of sequence data

Please list the sequence data produced during the pilot study.

Nr.	Species	Sequence name	Sequencing platform	Accession number (if uploaded)
1				
2				
3				
4				
5				
6				
(…)				

Please provide the sequence quality control output(s) for these data (e.g. fastQC or MinKNOW file).

The QC outputs will only be used as confirmation that the materials were sequenced, and will not be evaluated further (i.e. the quality of data has **no impact** in the procedure).

Availability of sequence data

Please describe if sequence data were uploaded in national or international WGS data repositories (EpiPulse, ENA, other) including the respective project accession number. The accession numbers for the individual sequences should be added to the previous table. If sequence data have not been uploaded yet, please describe plans for the future.

Changes in relation to the project description template

In the following table describe any changes made in relation to the approved project description. If no changes were made and the approved project description was followed, please write "no changes" in those sections.

Table from the project description template
1. **Objective and scope of the pilot study**
2. **Inclusion criteria**
3. ***Collection of isolates for the pilot study***
4. ***Collection of patient data (metadata)****
5. **Collection of microbiology testing data**
6. **Collection of epidemiology data***
7. **WGS setup and plans**

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Timeline of the pilot studies

- October 2023 – Deadline for the project description
- December 2023 – EURGen-RefLabCap WGS training course at DTU
- March 2024 – Suggested timeframe for sequencing the isolates
- August 2024 – Deadline for the report of the pilot studies
- September 2024 - Deadline for submitting invoices for reimbursement (if report was approved)
- September 2024 – Discussion of pilot studies in EURGen-RefLabCap Workshop/Network Meeting

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Design of the pilot studies

Country	Pathogen	No of isolates
Priority country	CRE KPN	50-70
Priority country	CRE/CCRE KPN	25-30
Priority country	NDM-producing EC	40
Priority country	CCRE	40
Priority country	CRPa and CRAb harbouring NDM or VIM	300
Priority country	CCRE, CRAb, CRPa	250
Priority country	CRPa producing NDM-1	Up to 200
Priority country	CRE KPN, CRAb, CRPa	500
Priority country	CRE KPN	50
Priority country	CRE harbouring NDM-1 and OXA-48, COL-R KPN	25-30
Priority country	CRE KPN	20
Priority country	CRE EC harbouring NDM, OXA-48, VIM	Up to 200
Priority country	--	--
Additional country	Entrobacterales carrying IncL plasmids harbouring VIM-1 and OXA-48	50
Additional country	CRE EC and KPN, CRAb, CRPa	25-30
Additional country	CRE/CCRE	45
Additional country	CRE KPN	30

Mainly Enterobacterales

approx. 1500

Funded by the European Union

Completion of the pilot studies

- 15 / 17 countries committed to the pilot studies
  - 1 PC did not join the studies
  - 1 AC joined the studies but withdrew early

- Currently 11 / 15 countries have submitted their reports

Funded by the European Union

EURGen-RefLabCap@food.dtu.dk

Thank you on behalf of the EURGen-RefLabCap team

Funded by the European Union

Microbiological Diagnostic Unit
PUBLIC HEALTH LABORATORY

ISO accreditation for AMR genomics in clinical & public health microbiology labs

A/Prof Norelle Sherry

Deputy Director, MDU Public Health Laboratory,
University of Melbourne at The Doherty Institute

Co-Lead, Laboratory and Surveillance Stream
WHO Collaborating Centre for AMR, Doherty Institute

Infectious Diseases Physician, Austin Health

Doherty Institute | The University of Melbourne | The Royal Melbourne Hospital

A joint venture between The University of Melbourne and The Royal Melbourne Hospital

Background

Microbiological Diagnostic Unit PUBLIC HEALTH LABORATORY

Doherty Institute

THE UNIVERSITY OF MELBOURNE

Public health microbiology laboratory in Melbourne

Extensive pathogen genomics program for public health

- Surveillance – AMR, foodborne, STIs, invasive bacteria, water & environment
- Integrated wet lab, genomic epidemiology & bioinformatics teams
- Close links to public health units
- ISO accreditation (human & biological) for most workflows
- Co-located translational & basic science research teams

Strong links to hospitals and clinical micro labs

National programs for genomic data sharing & international capacity building

Outline

- Overview of what is needed for AMR genomics implementation
- The value and challenges of ISO accreditation
- How to perform validation and accreditation of genomic AMR
- Examples - abritAMR, tbtAMR
- Linking AMR genomic data to public health action

What do you need to perform AMR genomics?

Requirements	Comments
Wet lab requirements • Molecular team with sequencing training • Short-read sequencing platform e.g. Illumina, OR • Long-read sequencing platform e.g. Oxford Nanopore	Many hospital labs already have sequencing platforms for human genomic sequencing
Bioinformatics requirements • Computing capacity (servers, secure data storage) • Personnel with bioinformatics training	Most bioinformatics pipelines are not (yet) user-friendly, e.g. command line and not GUI Relatively easy to get an 'answer' but not necessarily the right one
Governance and reporting • Medical microbiologist with genomics accreditation • Reporting mechanisms • NATA accreditation • Sequencing costs dropping but still relatively expensive	RCPA accreditation required for pathologists to report on genomics Databases not well set-up for clinical microbiology reporting Few labs currently have NATA accreditation

What makes an ideal tool for detecting AMR?

- Actively maintained by reputable organization
- Rapid to run with minimal computing resources required
- Detection methods suitable for your chosen sequencing workflow
- Interface should suit workflows in your lab (CLI/GUI)
- Reproducible results

- Able to run locally rather than upload (depending on volume)

What makes an ideal database for AMR?

- Actively maintained by reputable organization
- Comprehensive for your target species and antimicrobials
- Curated to include complete genes, minimize errors and duplications
- Consistent nomenclature of genes/mutations
- Classify AMR determinants by (clinically relevant) antimicrobial class
- Representative of global AMR populations
- Outputs compatible with your reporting needs

Implementing genomic AMR detection

1. **Identify aims of genomic AMR detection** with stakeholders
2. **Choose a tool and database** that suits your lab
3. **Implement locally** (e.g. containers) and get pipeline working
4. **Identify validation dataset**
   - Address the main species and AMR determinants to answer aims
5. **Test your pipeline**, identify discordances, attempt to resolve
6. **Design a report** including required elements
7. **Practical stuff** – LIMS, SOP/validation document, training, accreditation
8. **Re-verification** process

The value and challenges of ISO accreditation

—

Most public health & clinical micro labs work in an ISO-accreditation environment

- Ensure lab processes are robust and high-quality
- Accreditation requires extensive validation and reverification

Key ‘Slug-gate’ saga evidence left out of inquiry

ISO-accreditation for bioinformatic pipelines can be challenging

- ‘Gold standard’ validation datasets usually not available for genomics
- Robust, reproducible, user-independent, stable environment
- Re-verification with each major update to software or database

Most bioinformatics tools are not tailored for CPHM

- May not be directly fit-for-purpose ‘out-of-the-box’, especially reporting

Validation and accreditation of genomic AMR

Modular accreditation to ISO standards for genomics is usually best

- Validate and accredit wet lab workflows to sequence generation
- Then validate and accredit bioinformatics pipelines and reporting
- This means any changes won't affect the whole workflow and require reverification

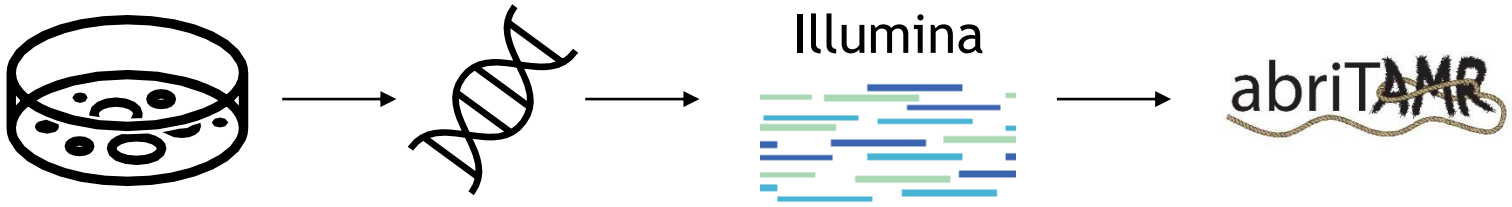
Assuming you've validated wet-lab sequencing workflows…

- Ideally validate against molecular assays for same AMR gene/mutation
- Few standardized external datasets currently available
- Validation against phenotype is complicated and best avoided unless validating inferred antibiogram
- Alternative – use synthetic genomic data to create a validation dataset where others are not readily available

ISO accreditation for genomic AMR – *abritAMR*

Kristy Horan

In-house

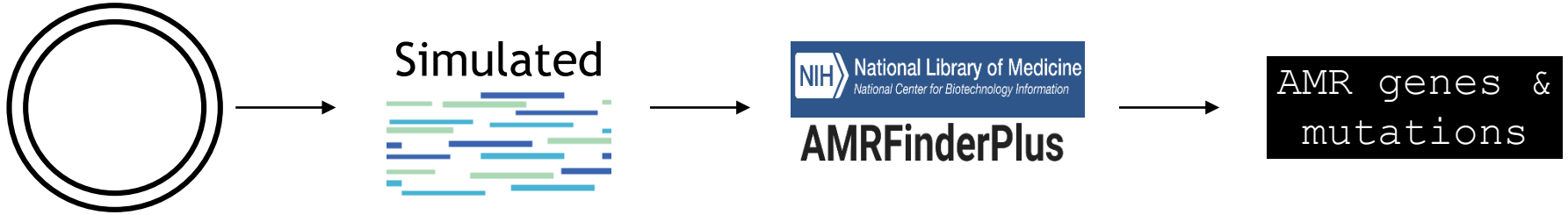


Compared to PCR where available

BUT many AMR mechanisms where no PCR validation data were available…

COMPARE

Synthetic data



Validation dataset and methods made publicly available (GitHub & by publication)

Sherry *et al.* Nature Comms 2023
Figure: Claire Gorrie
Code available on GitHub: github.com/MDU-PHL/abritamr (Kristy Horan)

What needs to be validated/verified?

- **Accuracy, sensitivity & specificity - detection of SNPs and AMR genes**
- **Limit of detection - minimal coverage**
- **Precision - repeatability and reproducibility (wet lab & bioinformatics)**

- **Validation dataset (or a subset) should be re-run after each major software or database update (re-verification)**
  - Version control very important!!
  - Ideally automate

Considerations when designing a report

1. What is the purpose of sequencing and reporting?
2. Who is the audience/client (and how much knowledge)?
3. What are the main question/s to be answered?
4. How long will they have to read the report?
5. Are you reporting on single isolates or multiple (line list)?
6. What are the uncertainties/caveats and comments required to accurately interpret the findings?
7. What are the obligations for reporting?

Importance of training reporting scientists

Unlike some other genomic tests, significant knowledge of AMR mechanisms, intrinsic resistance and phenotypic testing is required to integrate genomic AMR into reports

1. Check genotype fits with phenotype

e.g. CIM positive but no carbapenemase gene detected

2. Reporting requirements - notifiable (national or reportable to network)

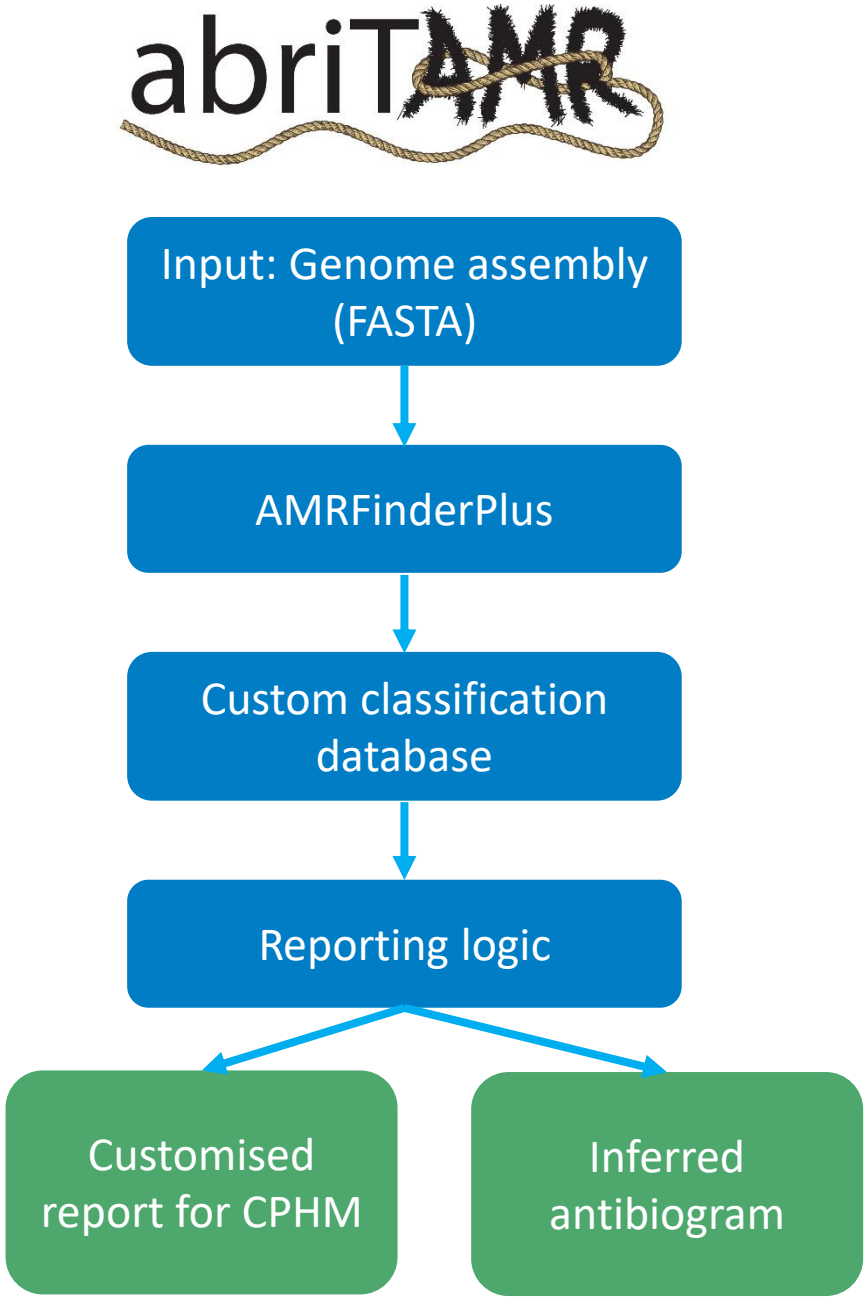
3. Identify when further wet lab or dry lab work might be required

e.g. bioinformatic analysis identifies partial genes

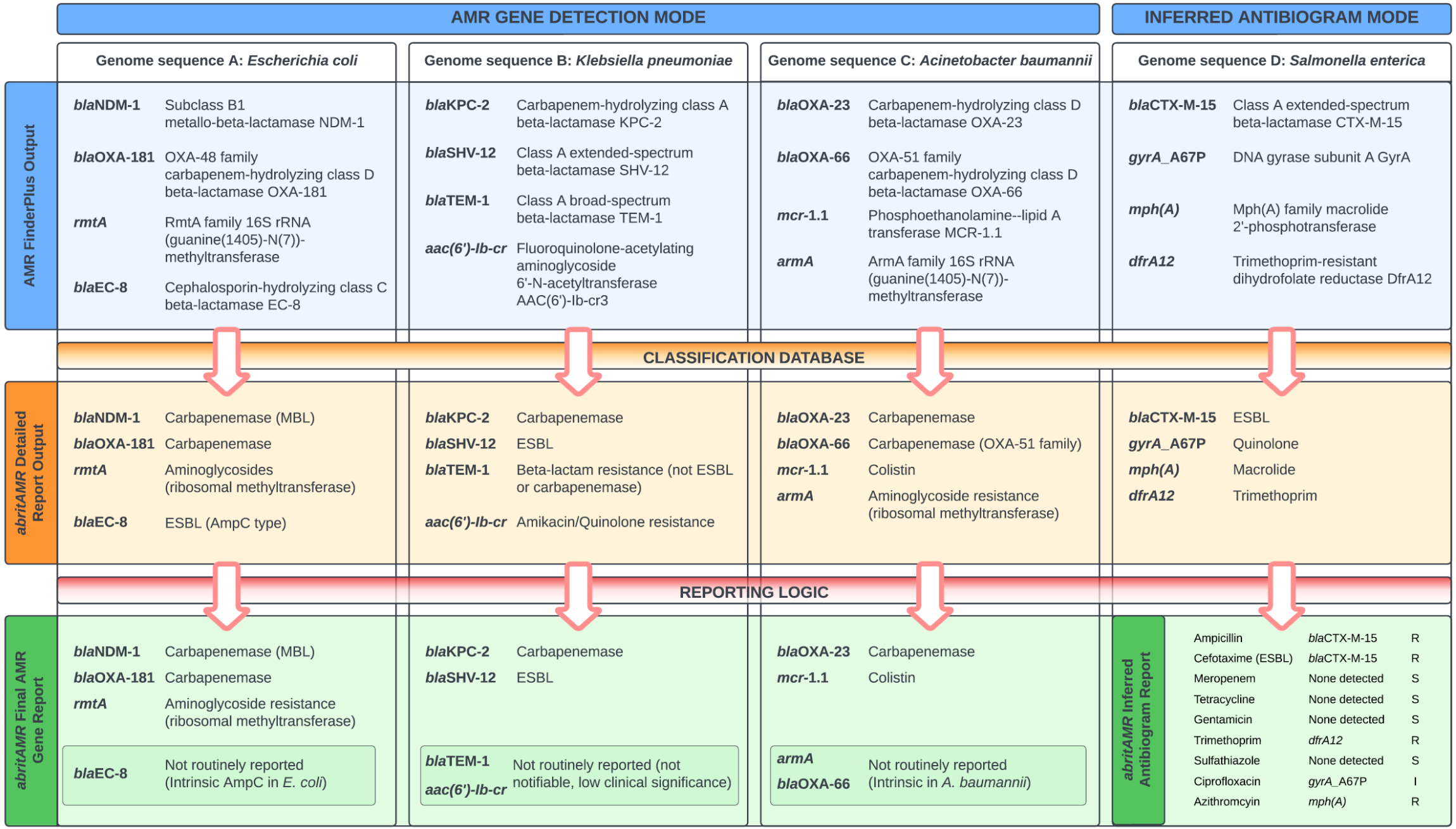
e.g. plasmid dropout in culture

Example: Tailoring reporting of AMR determinants for CPHM

- **Aimed to design AMR pipeline optimised for CPHM reporting**
- **Additional modifications required for use in these settings**
- **Examples:**
  - Exclude intrinsic AMR genes
  - Separate carbapenemase classes
  - Separate out cephalosporin resistance mechanisms
  - Tailor for local reporting requirements

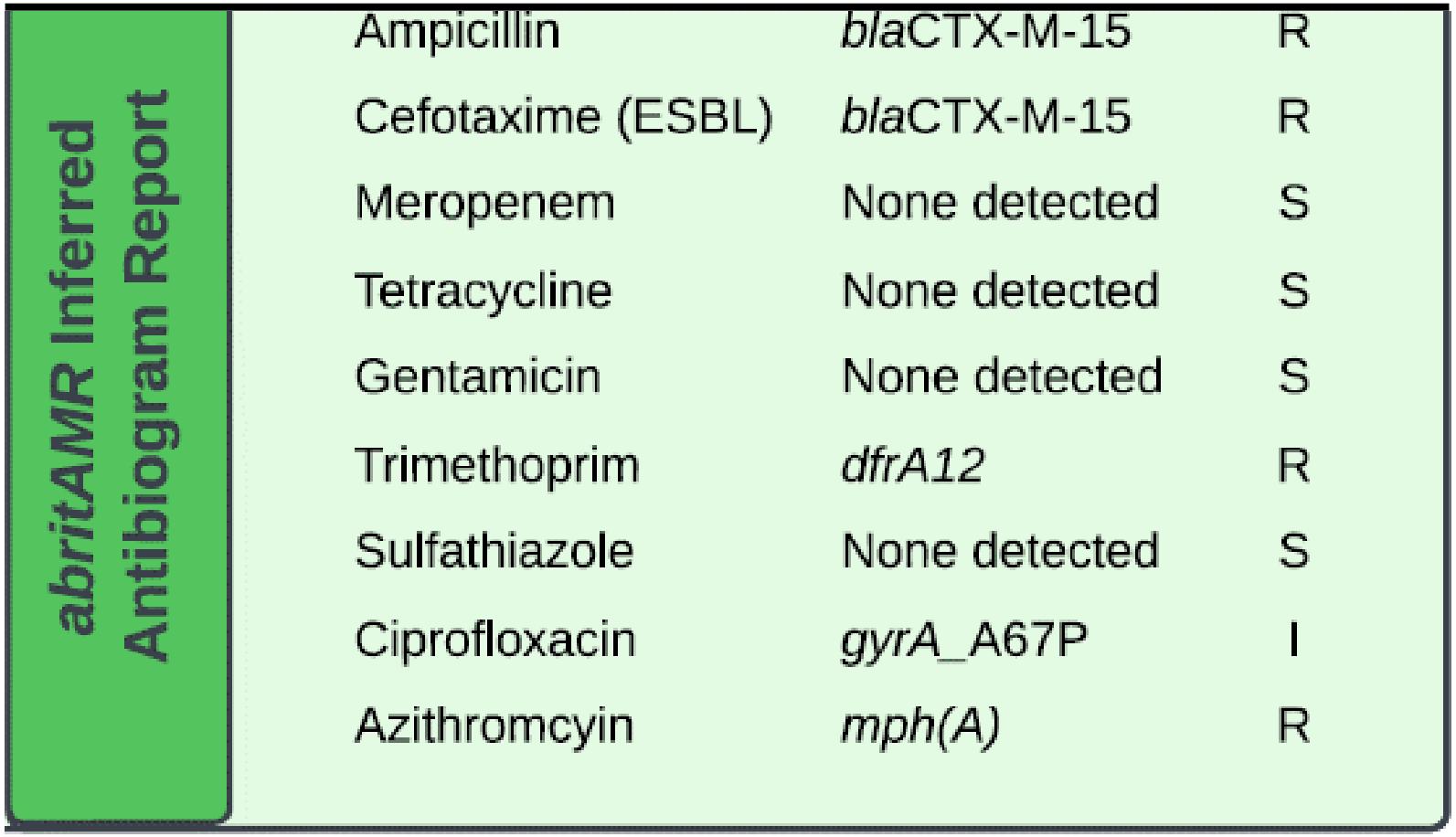


Norelle Sherry, Kristy Horan et al., Nature Comms 2023
Code available on GitHub:
github.com/MDU-PHL/abritamr (Kristy Horan)



Norelle Sherry, Kristy Horan et al., Nature Comms 2023

Inferred antibiogram: *Salmonella spp.*



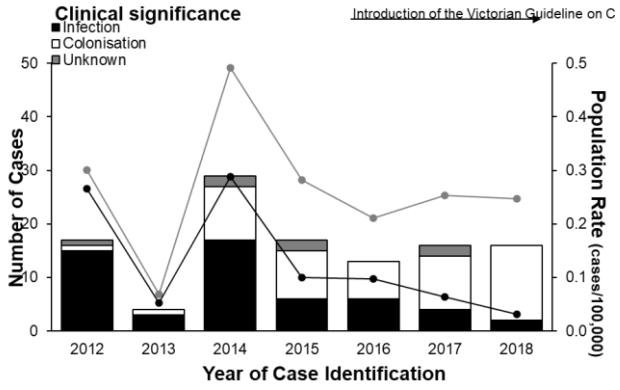
Note – for some classes, AMR determinants are additive
e.g. quinolones in *Salmonella*

- 1 mutation/gene – Intermediate
- >=2 mutations/genes – Resistant

Sherry *et al.* Nature Comms 2023

Implementation into practice: Genomic surveillance for carbapenemase-producing organi (CPOs)

Courtney Lane



Early implementation of statewide genomic surveillance program for CPOs

- Notifiable disease, all suspected CPOs sent for testing WGS
- Phenotypic AST, WGS (reported with abritAMR) and phylogenetic analysis
- Integrated with public health response and hospital IPC teams

Pathogen genomic data

Epi data

Bioinformatic analysis

Internal discussions & clinical

Incident Management Team
Hospital/IPC, Public Health & Ref Lab

Required interventions designated

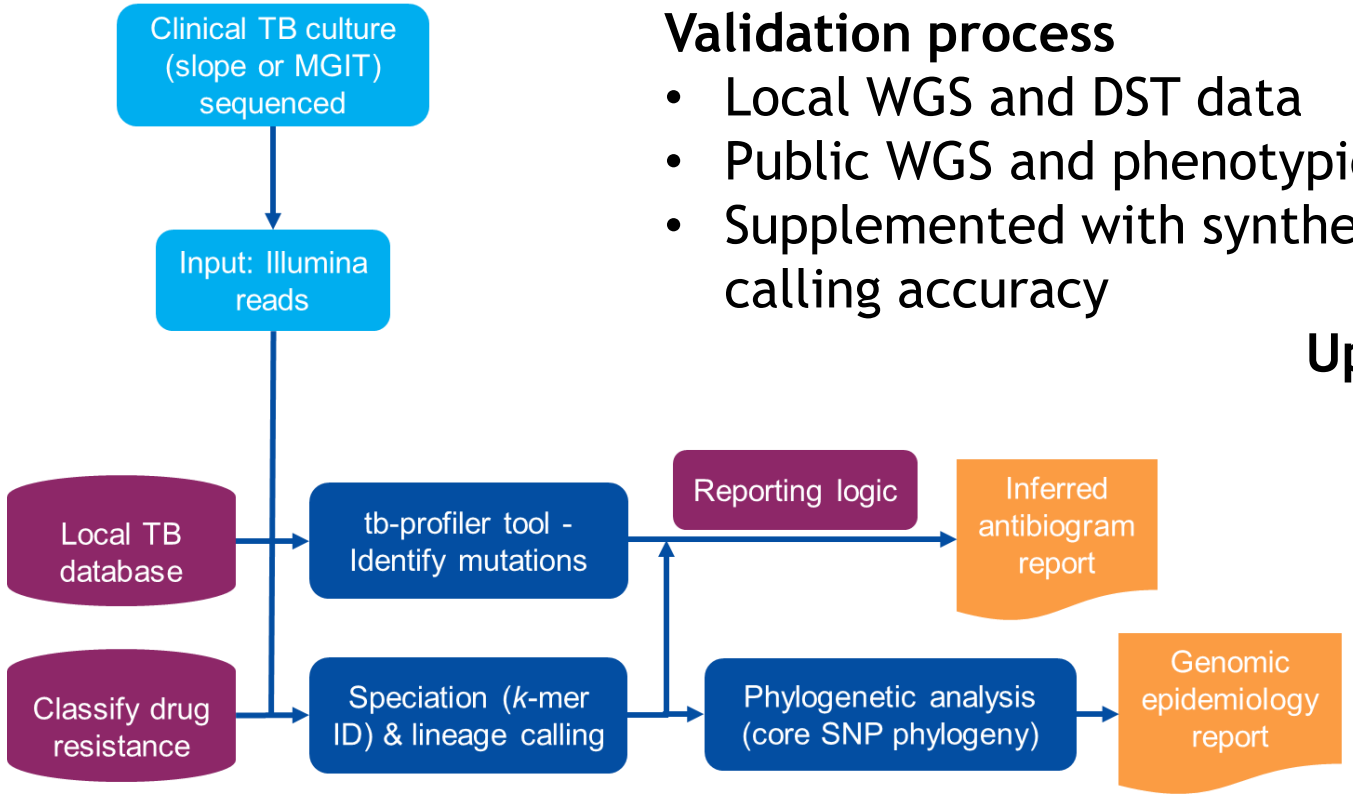
- Screening
- Patient alerts
- Letters to patients
- Other hospitals notified

Lane *et al* ***CID*** 2020
Sherry et al. ***JCM*** 2020

Pipeline for Mtb AMR suitable for clinical & PH microbiology

tbtAMR

Kristy Horan



Validation process

- Local WGS and DST data
- Public WGS and phenotypic datasets – cover all drugs
- Supplemented with synthetic dataset to establish LOD and SNP calling accuracy

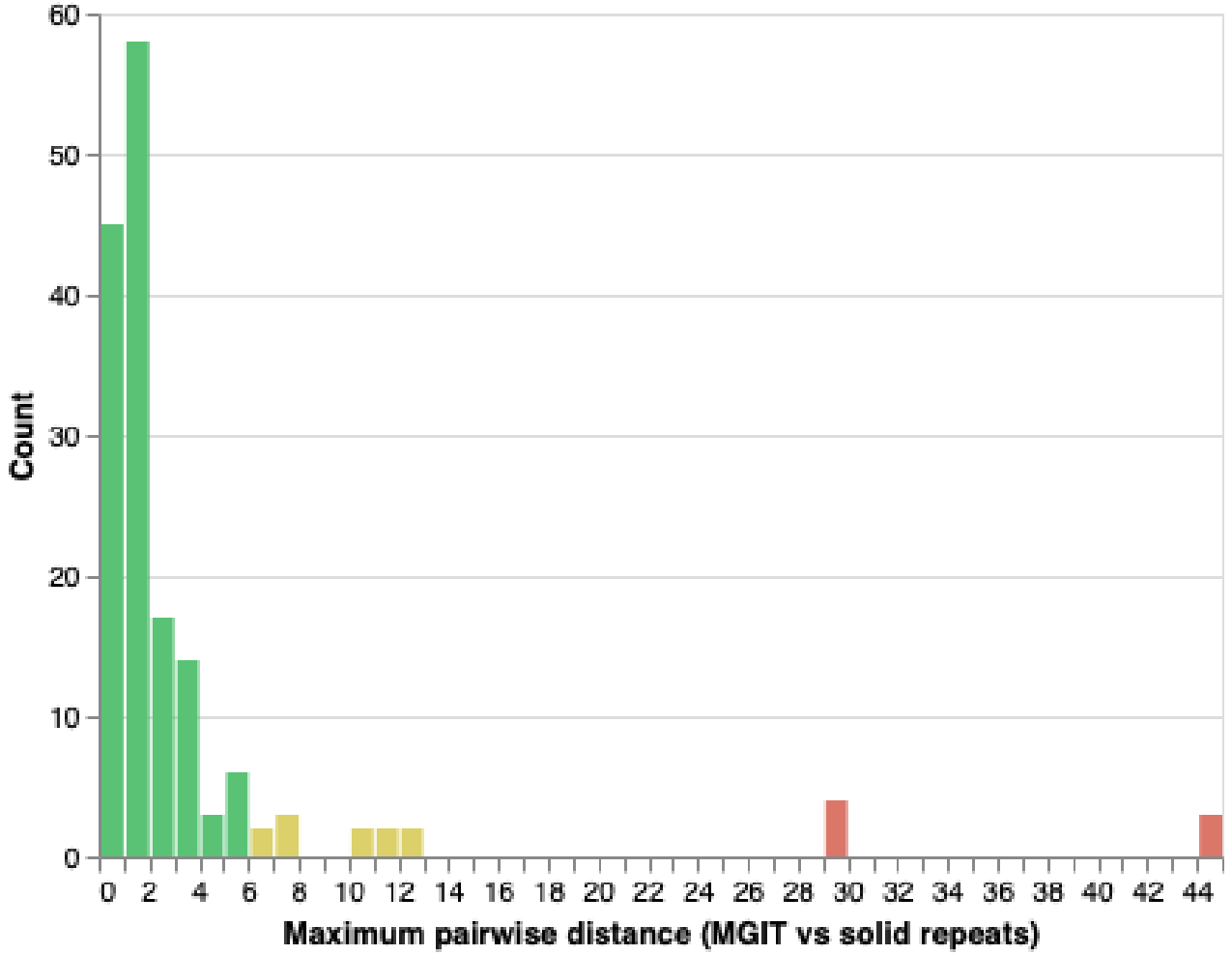
Updated tool and pre-print coming soon

Drug	Mutations detected	Predicted phenotype	Resistance level	Confidence
Rifampicin	*rpoB* (p.Ser531Leu)	Resistant	High	High
Isoniazid	*fabG1* (c.-15C>T)	Resistant	Low	High
Ethambutol	*embB* (p.Met306Val)	Resistant		Uncertain
Pyrazinamide	No mutation detected	Susceptible		
Moxifloxacin	No mutation detected	Susceptible		

Horan et al. biorXiv Nov 2023
GitHub: https://github.com/kristyhoran/tbtamr

Validating Mtb AMR from broth culture (MGIT)

vs



Pairwise distances between sequences from matched MGIT and solid culture

- 66 matched pairs which passed QC
- 64 (97%) matched pairs have concordant reportable variants detected

- New quality control criteria added
- Some issues with 23S rRNA mutations (linezolid resistance)

Bringing it all together: AMR genomics for *M. tuberculosis*

Clinical arm – patient treatment

Expert review panel for discrepancies

- WGS
- Phenotypic DST
- PCR (GeneXpert Ultra/XDR)

Urgent collaboration for new cases of MDR/XDR TB

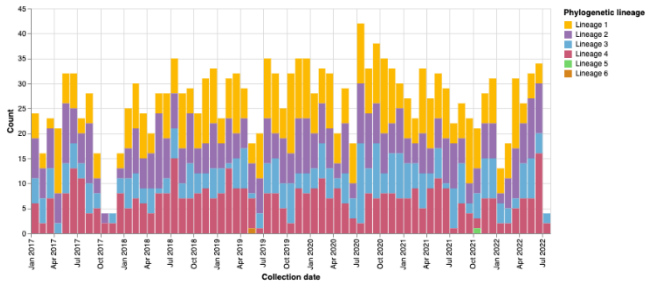
Drug	Xpert Ultra/XDR	Phenotypic AST	Genome sequencing	
			Resistance mechanism	Confidence level
Rifampicin	Resistance NOT detected	R	*rpoB* (1292 1294dupGCC)	Uncertain
Isoniazid	HL Resistance DETECTED	R	*katG* (Ser315Thr) *fabG1* (-15C>T)	High
Pyrazinamide	N/A	R	*pncA* (Gly24Arg)	Uncertain
Ethambutol	N/A	(S/R) pending	*embB* (Met306Ile)	High
Moxifloxacin	LL Resistance DETECTED	LL R	*gyrA* (Asp94Ala)	High
Amikacin	Resistance DETECTED	R	*rrs* (1401A>G)	Uncertain
Ethionamide	Resistance DETECTED	S	*fabG1* (-15C>T)	High

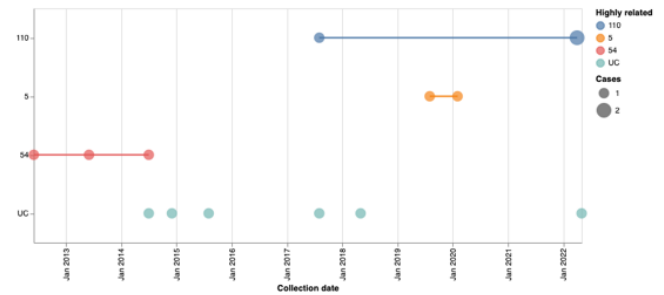
Public health arm – transmissions

Fortnightly phylogenetic analysis report & meeting

- TB program nurses, epidemiologists & clinicians
- Mycobacterial reference lab
- Bioinformatics & genomic epidemiology

Identify unexpected epi links – targeted enquiries





Conclusions

Genomics for AMR can be complex, but manageable if you follow logical steps

- Identify aims and stakeholders/clients
- Implement a workflow that suits your lab and needs
- Validate with a variety of datasets and methods as required
- Work towards accreditation to ISO standards where you can
- Design a report with the clients and questions clearly in mind – and test it!

Open communication channels with stakeholders/clients when implementing a new AMR test, consider education

Remember re-verification/re-validation and version control (tool/dbs) and training of reporting scientists

Acknowledgements

MDU PHL
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Kristy Horan
Courtney Lane
Susan Ballard

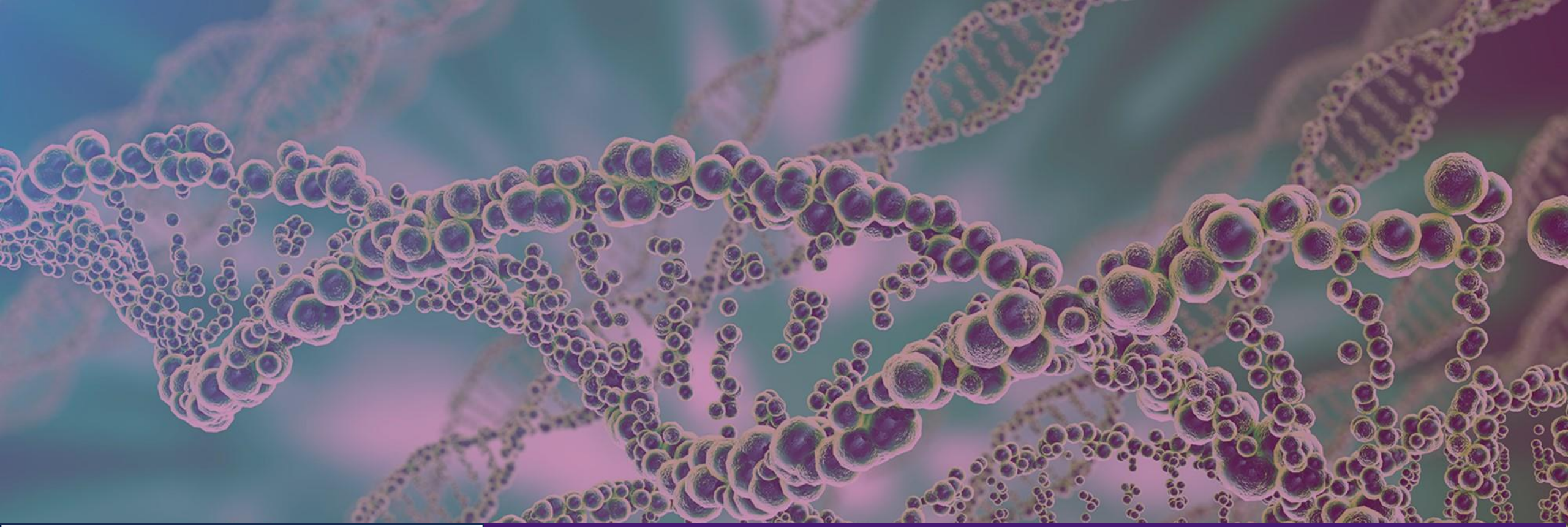
MDU Bioinformatics:
Kristy Horan
Torsten Seemann
Anders Goncalves da Silva & others
Wet lab & epidemiology teams

Research teams

VIDRL - Mycobacterial Reference Lab

Victorian Dept of Health & TB Program

Creators of open-source bioinformatic tools & databases everywhere!



MicrobeSeq
Denmark

Strengthened capacity and Sustainable Infrastructures for Sequencing-based diagnostic preparedness

Berit Lilje

MicrobeSeq Denmark

STATENS SERUM INSTITUT

Mission:
Lift the quality of WGS (whole genome sequencing) based surveillance in Denmark

Facts:

- Co-funding from the European Union's EU4Health programme
- Budget of 3,7/6,2 mio. euro (27,8/46,3 mio. kr.) (60% covered by EU)
- 2022-2026 (36 months)

Output:

- Standardized and publicly available lab protocols
- New computer system on a supercomputer
- Standardized and open-source computer code
- Teaching and workshops for knowledge sharing.

MicrobeSeq Denmark

SSI-Seq is supported by co-funding from the European Union's EU4Health programme under Grant Agreement Nr 101111879. Views and opinions expressed do not necessarily reflect those of the European Union or HaDEA. Neither the European Union nor the granting authority can be held responsible for them.

Background

- Be better prepared for potential pandemics.
- Non-covid surveillence down-prioritized.
- Have to move away from our current data system.
- Restructure code.

- Departments of Clinical Microbiology (DCMs) are doing more and more sequencing, need for a common QC and a way to easily transfer data to us, and get results back.

MicrobeSeq Denmark

- 5 regions in Denmark, 10 DCMs
- Varying WGS capability, some are very good.
- Want to send us sequence data instead of isolates.
- MiBa/EpiMiBa country-wide database of microbiological test results

MicrobeSeq Denmark

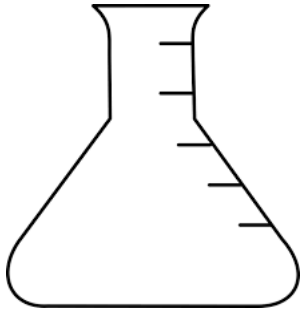
Digitalization at several steps

Move our system to a super computer

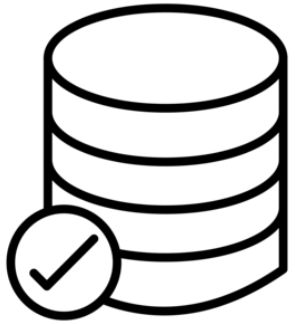
Modernize WGS QC pipeline

computerome

New LIMS system in the lab

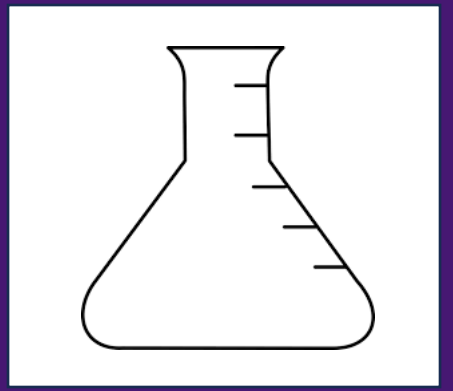


New surveillence database



MicrobeSeq Denmark

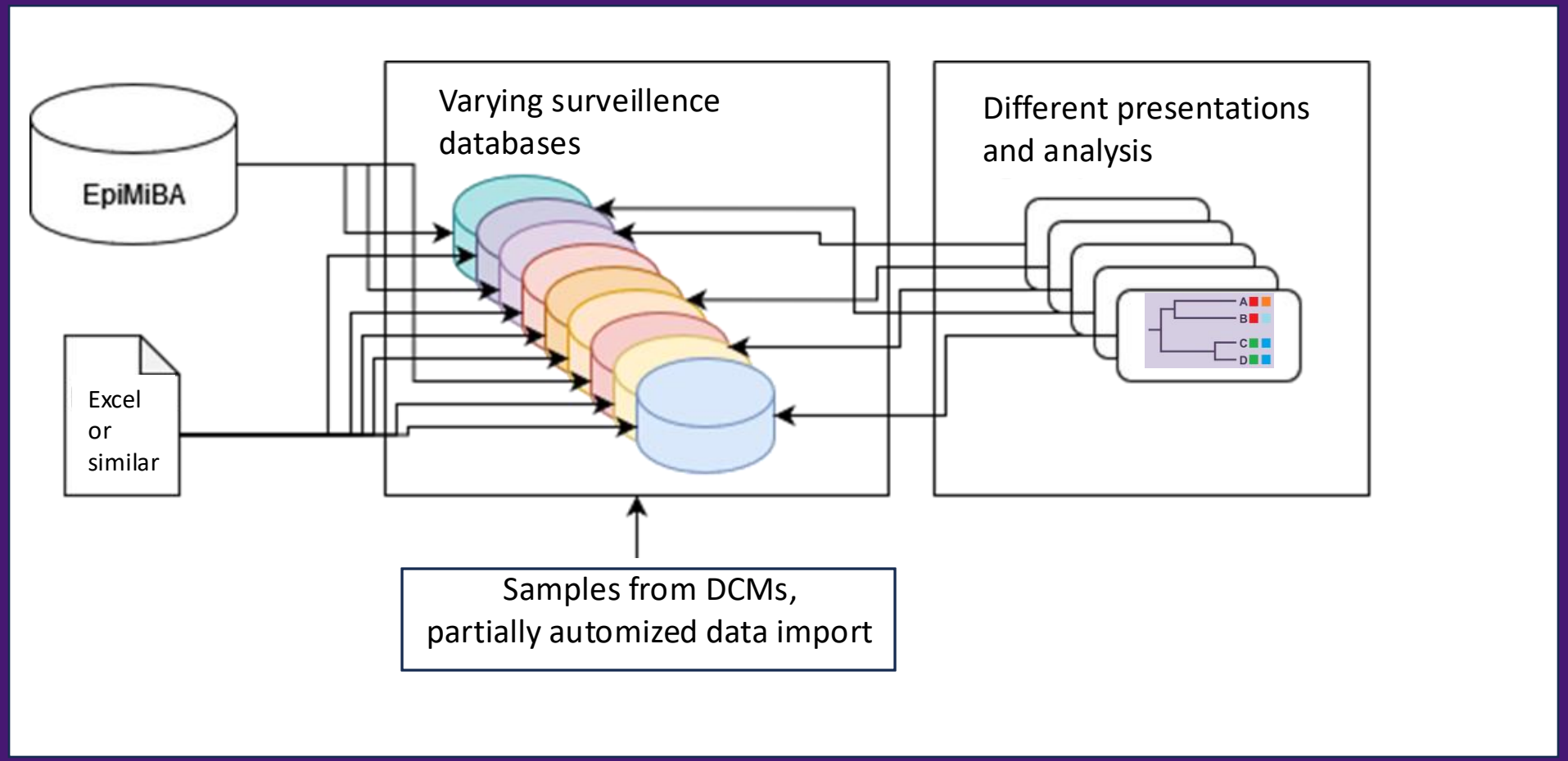
Laboratory improvements



- LIMS
- Standardized protocols on protocols.io
- New technology + data analysis:
  - Alternative technology
  - Rapid sequencing
  - Complex samples
  - PCR

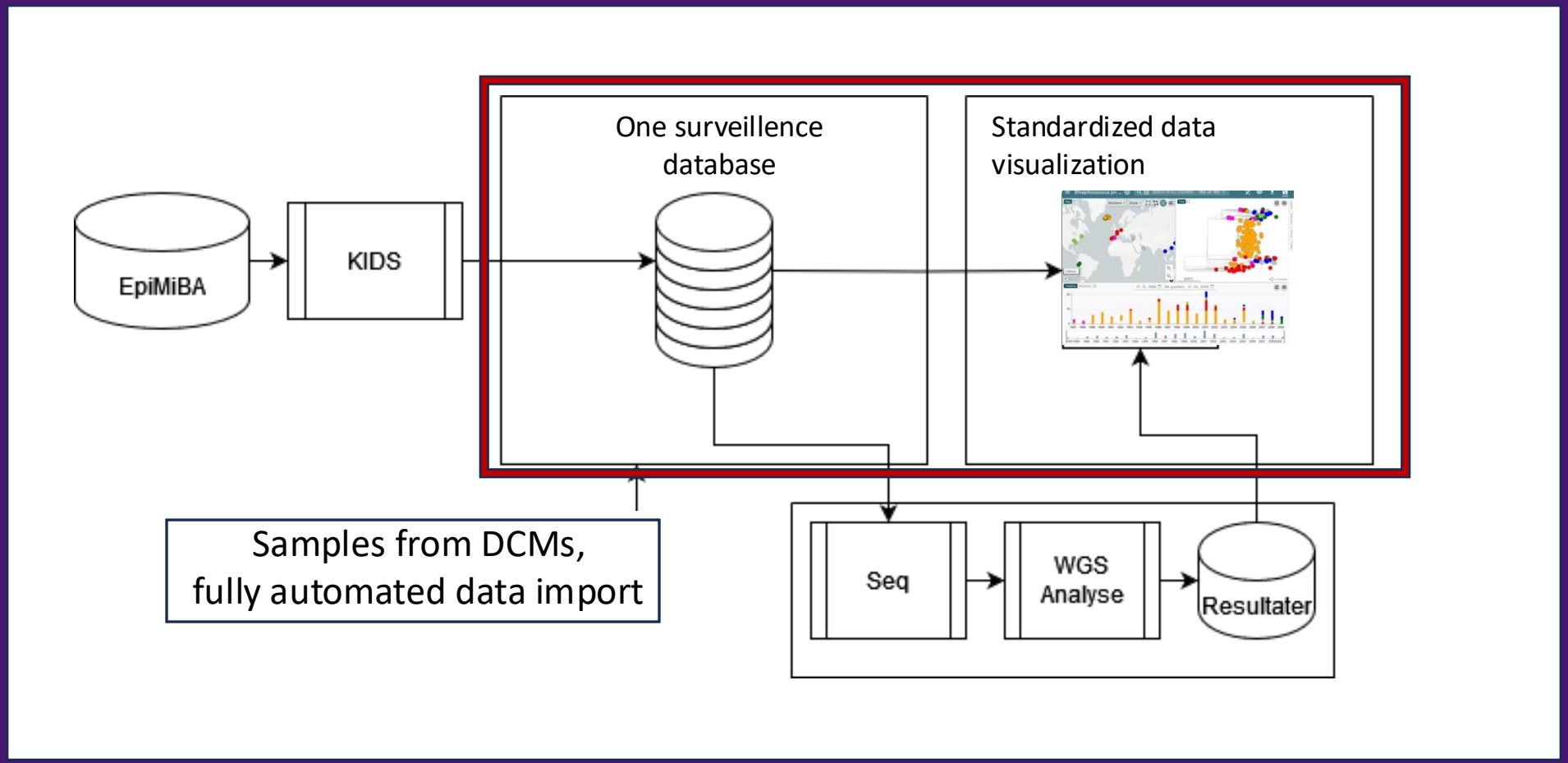
MicrobeSeq Denmark

New surveillence database



MicrobeSeq
Denmark

New surveillence database



MicrobeSeq Denmark

Move our system to a super computer
Modernize WGS QC workflow

SUNDHEDSDATA-STYRELSEN

STATENS IT

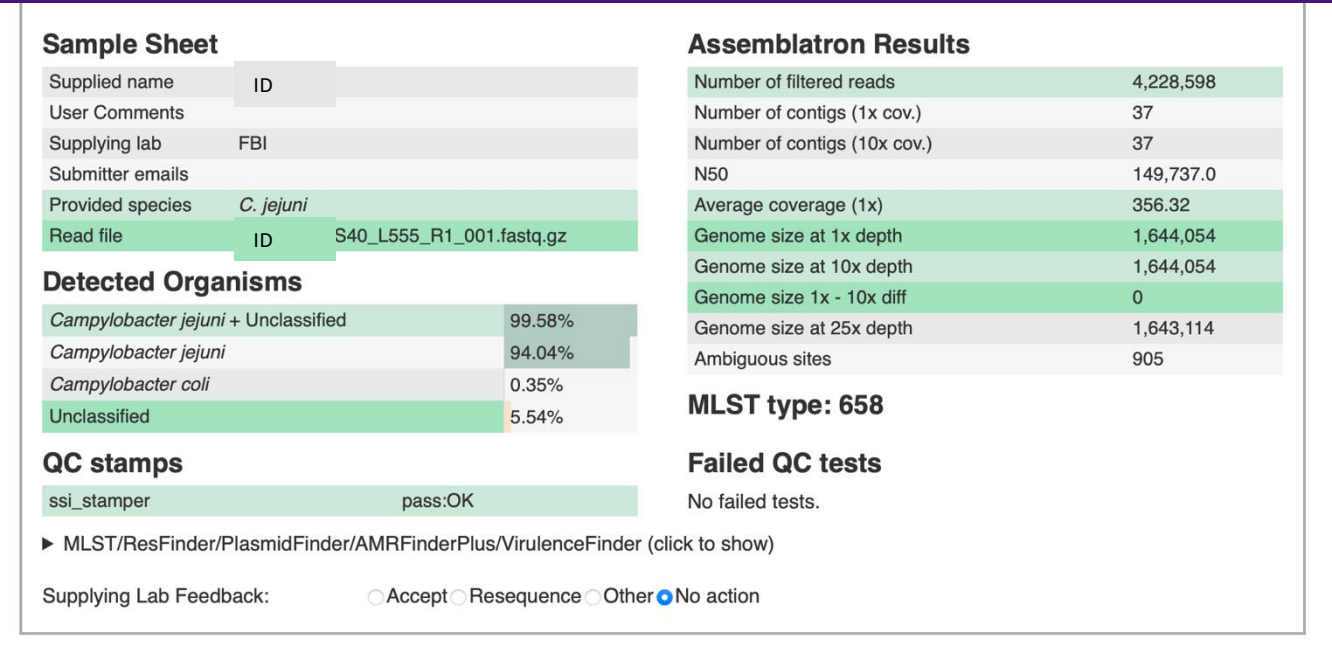
computerome

NATIONALT GENOM CENTER

MicrobeSeq Denmark

Status now

- Bifrost QC pipeline
- Ad-hoc scripts, not meant for sharing, not many people can do further development, learn a lot from this system.
- No integration to species specific tools.



Sample Sheet

Supplied name	ID	
User Comments		
Supplying lab	FBI	
Submitter emails		
Provided species	*C. jejuni*	
Read file	ID	S40_L555_R1_001.fastq.gz

Detected Organisms

Campylobacter jejuni + Unclassified	99.58%
Campylobacter jejuni	94.04%
Campylobacter coli	0.35%
Unclassified	5.54%

QC stamps

ssi_stamper	pass:OK

Assemblatron Results

Number of filtered reads	4,228,598
Number of contigs (1x cov.)	37
Number of contigs (10x cov.)	37
N50	149,737.0
Average coverage (1x)	356.32
Genome size at 1x depth	1,644,054
Genome size at 10x depth	1,644,054
Genome size 1x - 10x diff	0
Genome size at 25x depth	1,643,114
Ambiguous sites	905

MLST type: 658

Failed QC tests

No failed tests.

▶ MLST/ResFinder/PlasmidFinder/AMRFinderPlus/VirulenceFinder (click to show)

Supplying Lab Feedback: ○ Accept ○ Resequence ○ Other ◉ No action

MicrobeSeq Denmark

Current work

- New pipeline:

  Data from machine -> internal SSI server -> demulitplex -> data on uGerm cloud ->split into projects -> general QC -> species specific analysis -> results into surveillence database and sample status to lab LIMS + semi-automatic upload of data

MicrobeSeq Denmark

Current work

- New pipeline:

  Data from machine -> internal SSI server -> demulitplex -> data on uGerm cloud ->split into projects -> general QC -> species specific analysis -> results into surveillence database and sample status to lab LIMS + semi-automatic upload of data
- Common coding standards
- Nbdev (jupyter notebooks to packages)
- Modular
- Easy to install and use programs
- Publically available on github
- Integration to species specific tools.

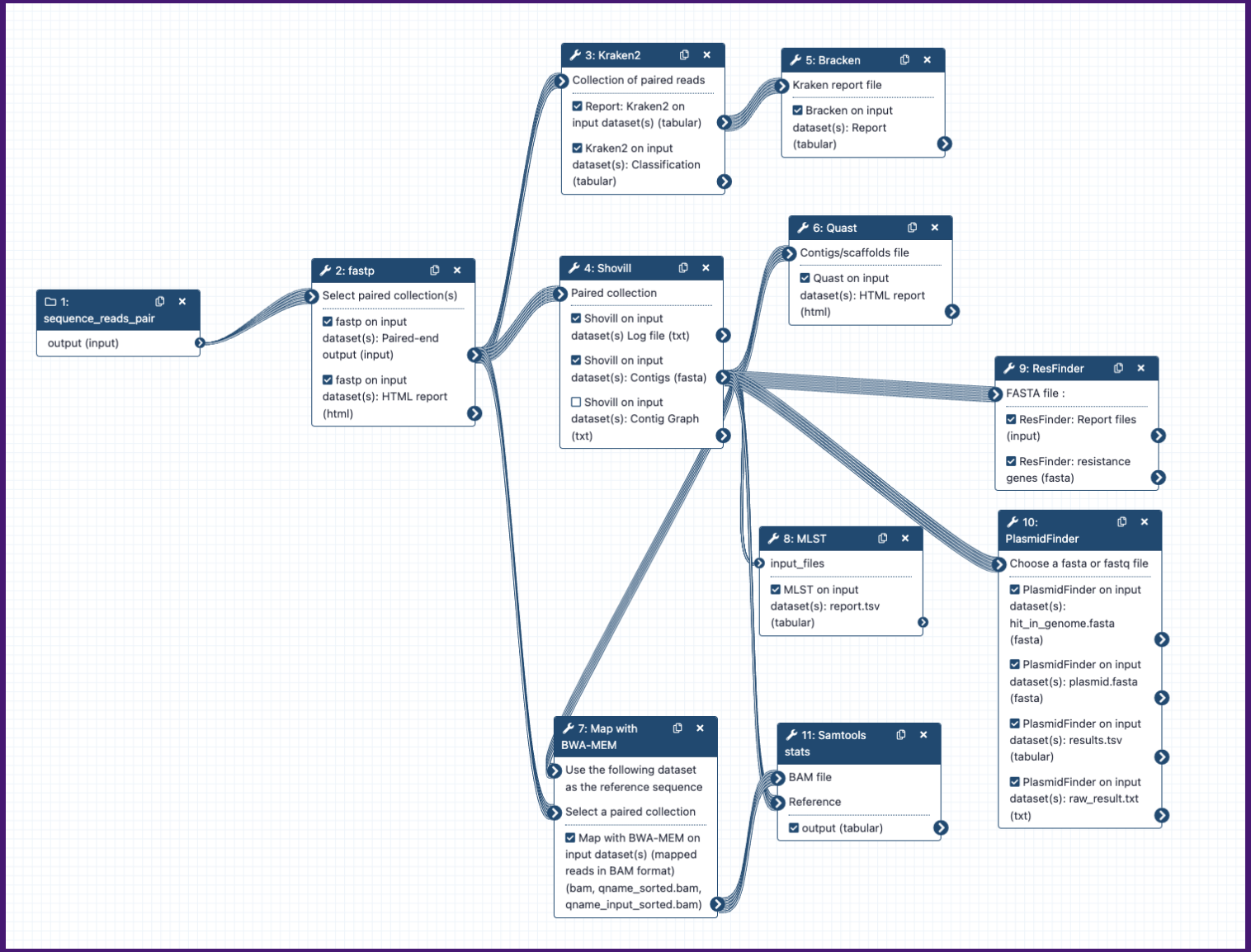
MicrobeSeq Denmark

QC

- Irida (db,

INTEGRATED RAPID INFECTIOUS DISEASE ANALYSIS)

- Galaxy (analysis)
- Microreact (visualization)



MicrobeSeq Denmark

Data sharing

Current status

- Share reports with DCMs, emails
- SOFI to share data with food authorities.
- Upload data to ECDC and public repositories manually

Vision

- Allow DCMs access to computerome private cloud.
  - See all seuqnecing data from national surveillence and use our tools.
- Automatic upload to ECDC and public repositories, when samples have passed QC. Data for action.

MicrobeSeq Denmark

Status

computerome

	Q1.1	Q1.2	Q1.3	Q1.4	Q2.1	Q2.2	Q2.3	Q2.4	Q3.1	Q3.2	Q3.3	Q3.4	After project
Lab LIMS development													
Lab LIMS testing													
Sureveillende DB planning													
Prototype development													
Integration with other systems													
Inclusion of more DB, finalized version													
Transfer to uGerm													
Development of new QC pipeline													
Species specific tools													
Improved functionality													

- Lab protocols and computer code are/will be available online on protocols.io and github (ssi-dk.github.io/MicrobeSeq-Denmark/)
- See our web-page https://microbeseqen.ssi.dk

Contact: lvp@ssi.dk

www.microbeseqen.ssi.dk

MicrobeSeq Denmark

Thanks

Work Package leads







50+ people at SSI who are working on this project

SSI-Seq is supported by co-funding from the European Union's EU4Health programme under Grant Agreement Nr 101111879. Views and opinions expressed do not necessarily reflect those of the European Union or HaDEA. Neither the European Union nor the granting authority can be held responsible for them.

MicrobeSeq Denmark

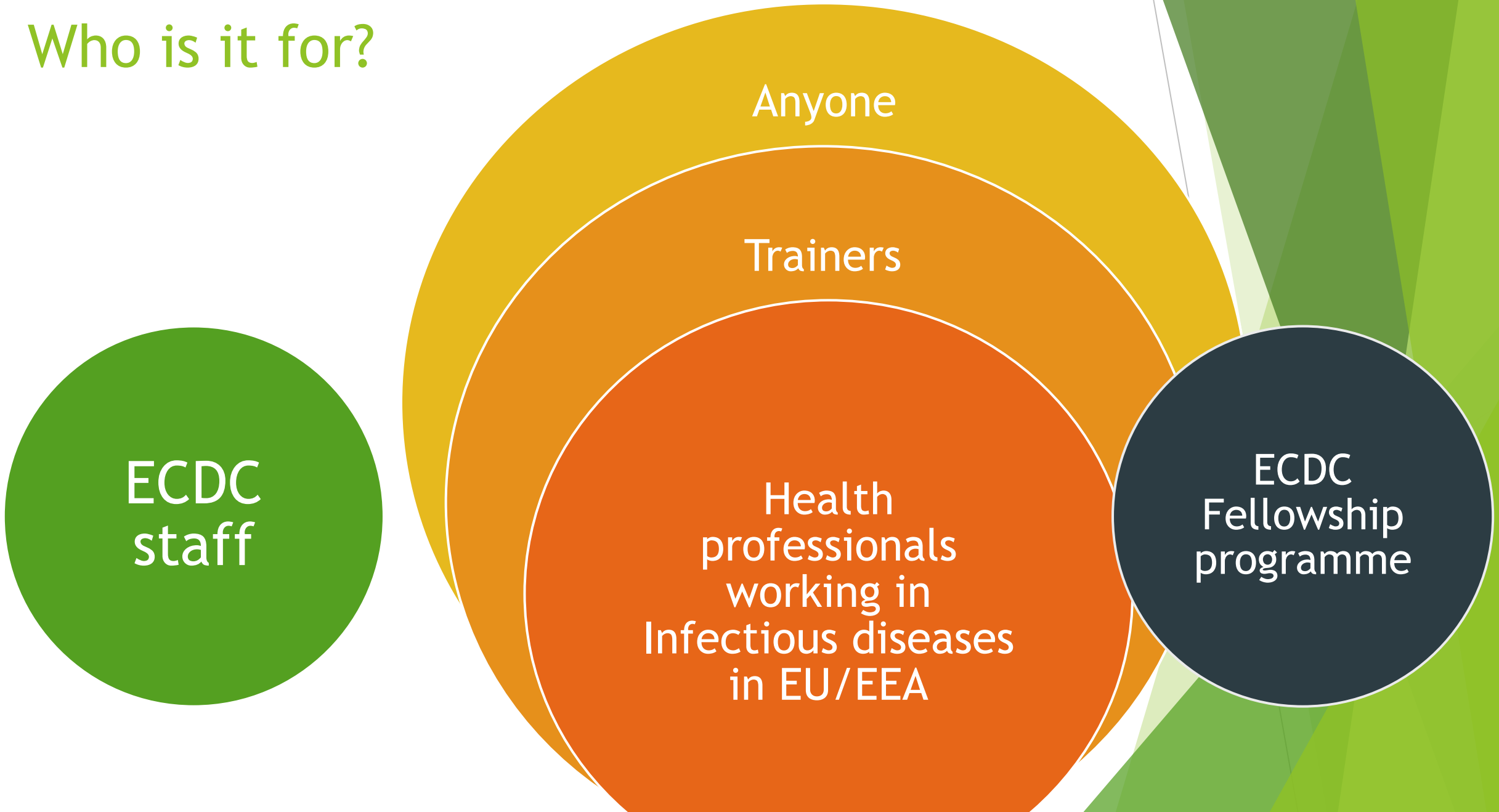
Learning Portal
for infectious diseases

Rodrigo Filipe, 17 September 2024

What is the Learning Portal?

- It’s the ECDC Learning Management System (LMS), built using Totara learn, a Moodle based LMS.
- It is a platform hosting virtual environments to support every training activity delivered by ECDC.
- It’s a structured place to teach and evaluate training.
- It’s protected safe space for people to learn.

Who is it for?


Anyone
Trainers
Health professionals working in Infectious diseases in EU/EEA
ECDC staff
ECDC Fellowship programme

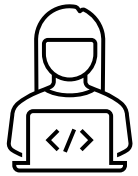
Types of content

Instructor-led training events

- Online or face-to-face

Self-paced training materials

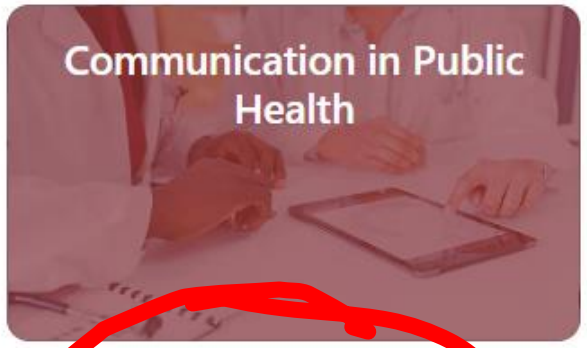
- Video, podcast, e-learning

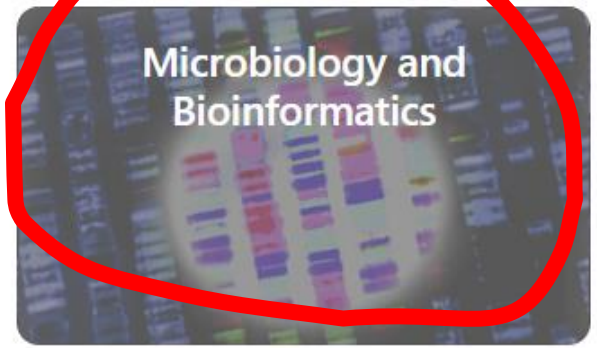


Training materials for trainers

- Facilitator guides, presentations, case-studies

Content areas covered



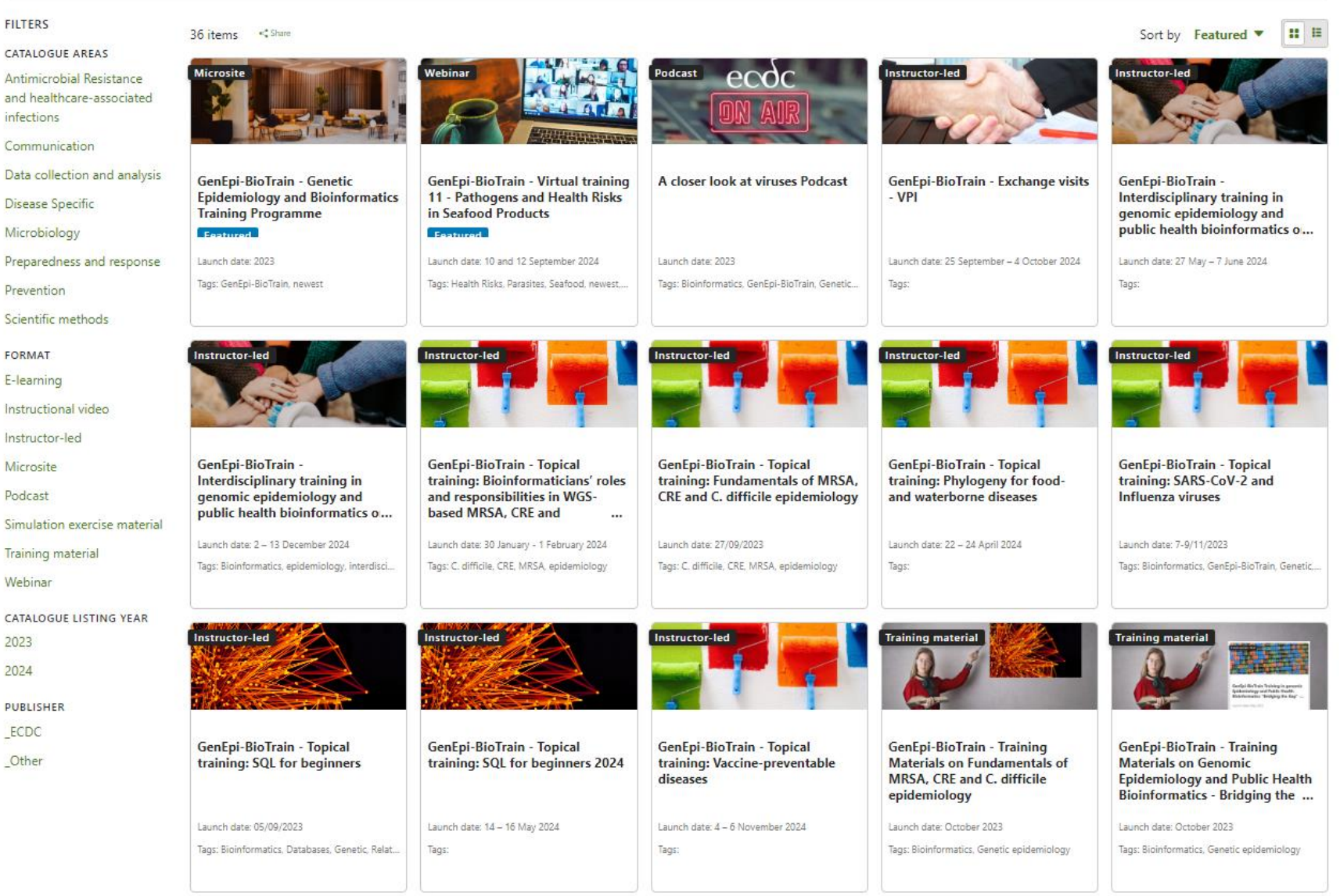


Explore our chronological list of trainings

Search courses on EVA

Search...

GenEpi-BioTrain



Wave 2 - Antimicrobial resistant pathogens (late 2023)

Training in genomic epidemiology and PH bioinformatics "Bridging the gap"

May 2023

Training material

Interdisciplinary training (Epidemiology, Microbiology, Bioinformatics)

November 2023

Training material

Topical trainings

September 2023 SQL for beginners

Training material

September 2023 Fundamentals of MRSA, CRE and C. difficile epidemiology

January 2024 Fundamentals of MRSA, CRE and C. difficile epidemiology - 2nd Edition

Training material

Open virtual trainings

4 and 8/09/2023 WGS based detection of AMR in bacteria

12 and 14/09/2023 From sequencer to polished reads for bacteria

4 and 7/12/2023 Bacterial genome assembly and quality control

19/03/2024 - Phylogenetics and alignments

Events are accessible only to nominated participants.

Trainings materials are available to all after the training events.

Live virtual trainings -> Recorded self-paced videos

Session 1 - 19 March