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PATH-SAFE Overview

Dr Ed Haynes

PATH-SAFE Science Fellow



**Pathogen Surveillance
in Agriculture, Food
and the Environment
(PATH-SAFE)**

**PATH-SAFE
Overview**

Dr Edward Haynes

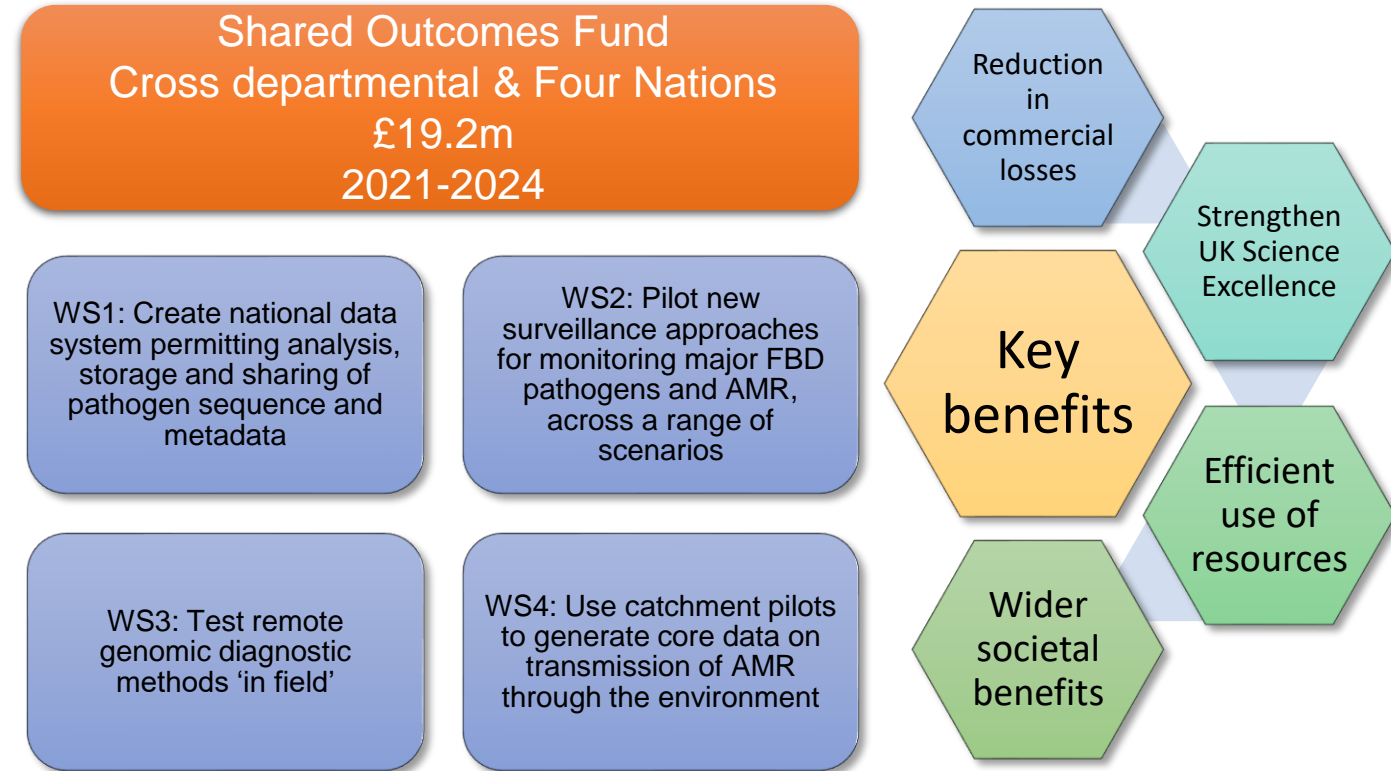
PATH-SAFE Science Fellow



Pathogen Surveillance in Agriculture, Food and the Environment (PATH-SAFE)

Aim:

To pilot a **better national surveillance system** for the monitoring and tracking of foodborne pathogens (**FBP**) and antimicrobial resistance (**AMR**) in the **agri-food system**.





Department for Environment Food & Rural Affairs



Animal & Plant Health Agency



UK Health Security Agency

Food Standards Scotland



Public Health Scotland



Centre for Environment Fisheries & Aquaculture Science



Veterinary Medicines Directorate



Department of Health & Social Care



Food Standards Agency



Environment Agency



Department of Health



Department of Agriculture, Environment and Rural Affairs



Department for Infrastructure





AIM

Pilot a national surveillance system that better monitors and tracks foodborne disease (FBD) and antimicrobial resistance (AMR) in the environment and agri-food system, taking a One Health approach



INPUTS



ACTIVITIES



OUTPUTS



OUTCOMES (2-5 years)



IMPACTS (5-10 years)



Staff and researcher time



Laboratories



Consumables and equipment



Sampling sites and samples



Contractors



WGS technology



Novel and user-friendly tools for analysis and visualisation of microbial genomes



Collaborations with key stakeholders and partners such as DEFRA, UKHSA devolved nations, and academics and access to their expertise and facilities



Funding



WS1

Establish a curated and national FBP (and their AMR) genomic data platform with Salmonella as exemplar pathogen



WS2

Pilot new FBP and AMR surveillance approaches based on regular, multi-location sampling in a range of settings, combined with novel technologies (e.g. whole genome sequencing)



WS3

Map and test new and repurposed technologies for rapid onsite FBP testing in collaboration with end users



WS4

Develop a pilot AMR surveillance system based on mechanisms of AMR spread in the environment



WS1

Functional and scalable data platform that houses sequences of exemplar pathogens and their AMR genes

Data platform is interoperable and can interact with other systems like Enterobase and provide an interrogatable user interface



WS2

AMR and FBP curated sample data captured from multiple sources, and tested using novel analysis techniques

Combined evidence from the piloted FBP and AMR surveillance and modelling approaches



WS3

TRL assessment of rapid onsite FBP testing tools with end users Evidence on utilising COVID-19 testing technology (LAMP) for FBP detection in wastewater



WS4

AMR surveillance framework and suite of diagnostics monitoring of AMR across the environment within a catchment area



Key stakeholders can more easily share and access data across organisations for rapid identification and tracking of foodborne pathogens and AMR, bringing together multiple data sources



Predictive assessment of risk and threat is enabled when assessing a new isolate through access to a comparative repository of pathogen sequences and metadata



Improved understanding of source attribution and infection threat of FBP and AMR through various environments and international entry points



Additional knowledge of how to expand existing surveillance mechanisms to support a robust national surveillance infrastructure and improved monitoring



Guide the use of novel and existing/repurposed rapid onsite FBP testing technology with improved knowledge of where further development is needed



Informed consideration, based on evidence surfaced, on how proactive, rapid and efficient management can be used to reduce the risk of FBP and AMR introduction into the wider environment and food systems



Key stakeholders and decision makers are brought together to engage with evidence and take forward policy recommendations



Contributing to the One Health ambitions of reducing threats to public health and the ecosystem



Improved monitoring helps track spread of food borne pathogens and AMR across the agri-food system and wider environment



Knowledge and technology is added to the UK's capability to respond to and build resilience to AMR threats



Policy makers make informed, evidence-based decisions which improves efficient use of resources and strengthens cross-government collaboration in FBP and AMR surveillance and management



Detection of pathogen emergence and spread supports development of mitigation strategies to stop increased incidence of foodborne illness



Reduced incidence of foodborne illness



Innovations enable step change in approach to FBP/AMR surveillance and decision making promoting UK's food sector reputation internationally in FBP and AMR surveillance



Reduction of commercial losses from reduced food waste through prevention of FBP contamination

AMR: Antimicrobial resistance
FBP: Foodborne pathogen

TRL: Technology readiness level
WGS: whole genome sequencing

Inputs



Staff and researcher time



Laboratories



Consumables and equipment



Sampling sites and samples



Contractors



WGS technology



Funding



Novel and user-friendly tools for analysis and visualisation of microbial genomes



Collaborations with key stakeholders and partners such as DEFRA, UKHSA devolved nations, and academics and access to their expertise and facilities

Outcomes (2-5 years)

WS1

WS2

WS3

WS4



Key stakeholders can more easily share and access data across organisations for rapid identification and tracking of foodborne pathogens and AMR, bringing together multiple data sources



Predictive assessment of risk and threat is enabled when assessing a new isolate through access to a comparative repository of pathogen sequences and metadata



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Informed consideration, based on evidence surfaced, on how proactive, rapid and efficient management can be used to reduce the risk of FBP and AMR introduction into the wider environment and food systems



Key stakeholders and decision makers are brought together to engage with evidence and take forward policy recommendations



Contributing to the One Health ambitions of reducing threats to public health and the ecosystem



Continuation funding

- Data Sharing & Analysis theme
 - Additional pathogens and functionality
- Foodborne Disease theme
 - Further surveillance pilots and extension of models
- AMR theme
 - Novel surveillance methods and sources
- Onsite Diagnostics theme
 - Develop a framework for deployment of onsite diagnostics



Thank you for listening!

PATH-SAFE Programme

Email: PATHSAFE@food.gov.uk

Webpage: [PATH-SAFE](#)



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Session 1

Developing

Biosurveillance Data

Systems

Development of a National Foodborne Disease Genomic Data Platform - PATH- SAFE WS1a efforts

Aim: to provide genomic interpretation linked to core minimal contextual data for decision makers within PATH-SAFE partner organisations - initially with a focus on Salmonella

Key Benefits

Rapid cluster identification

Standardised analysis

Easier communication

Multi-agency genomic surveillance

Easy to use interface

Trigger cross agency investigations

Project workstreams

WP1: **Project management & Administration**

WP2: **Platform development**

WP3: **Consortium partners**
(CLIMB-BIG-DATA, PubMLST, EnteroBase)

WP4: **Community Input Advisory Groups:** Technical, AMR, FBD Data Standards, International Interaction

2022

Discovery 1: General overview of foodborne infrastructure in the UK

Discovery 2: Salmonella specific investigation

January 2023-March 2024

Consortium efforts

Platform development



**CLIMB
BIG DATA**

<https://www.climb.ac.uk/>



- Established 2014, multi-site cloud infrastructure dedicated to microbial bioinformatics, established sustainability model through user and institutional contributions
- Multiple rounds of investment in hardware specific for microbial big data analysis, upgraded and refreshed in 2020-2022 in Birmingham and Cardiff. Each site:
 - Very large storage capacity, fast (>1PB SSD) and slow (>10PB spinning disk)
 - GPU server farm for machine learning applications (>40 Nvidia A100s)
 - Very large memory machines for genome assembly (1-3Tb)
- Scalable cloud hosting and containerised analytic pipelines



**UK Research
and Innovation**



<https://enterobase.warwick.ac.uk/>

- Years of experience hosting and providing research interface for multiple pathogens (Salmonella, Escherichia/Shigella etc.)
- Conducted assembly pipeline comparisons to inform decision making and sign-off by PATH-SAFE governance.
- Worked with the development team to ensure API utility to deliver analytics and where possible pull data into the data platform

PubMLST



<https://pubmlst.org/>

- Providing gold-standard typing (MLST/cgMLST) for the research and public health communities for multiple pathogens
- Ensured maximal utility of APIs to deliver typing and where possible enhanced usage of data for the data platform
- Additional retrospective sequencing and analysis of Campylobacter is being undertaken across the UK in order to gather baseline data

Exemplar End User Group

Aim: understand user needs and organisation requirements as well as discussions on policy, data and analytics

- Questionnaires
- Metadata requirements
- Risk factors (analytics)
- User personas
- Platform use cases



Animal &
Plant Health
Agency



UK Health
Security
Agency



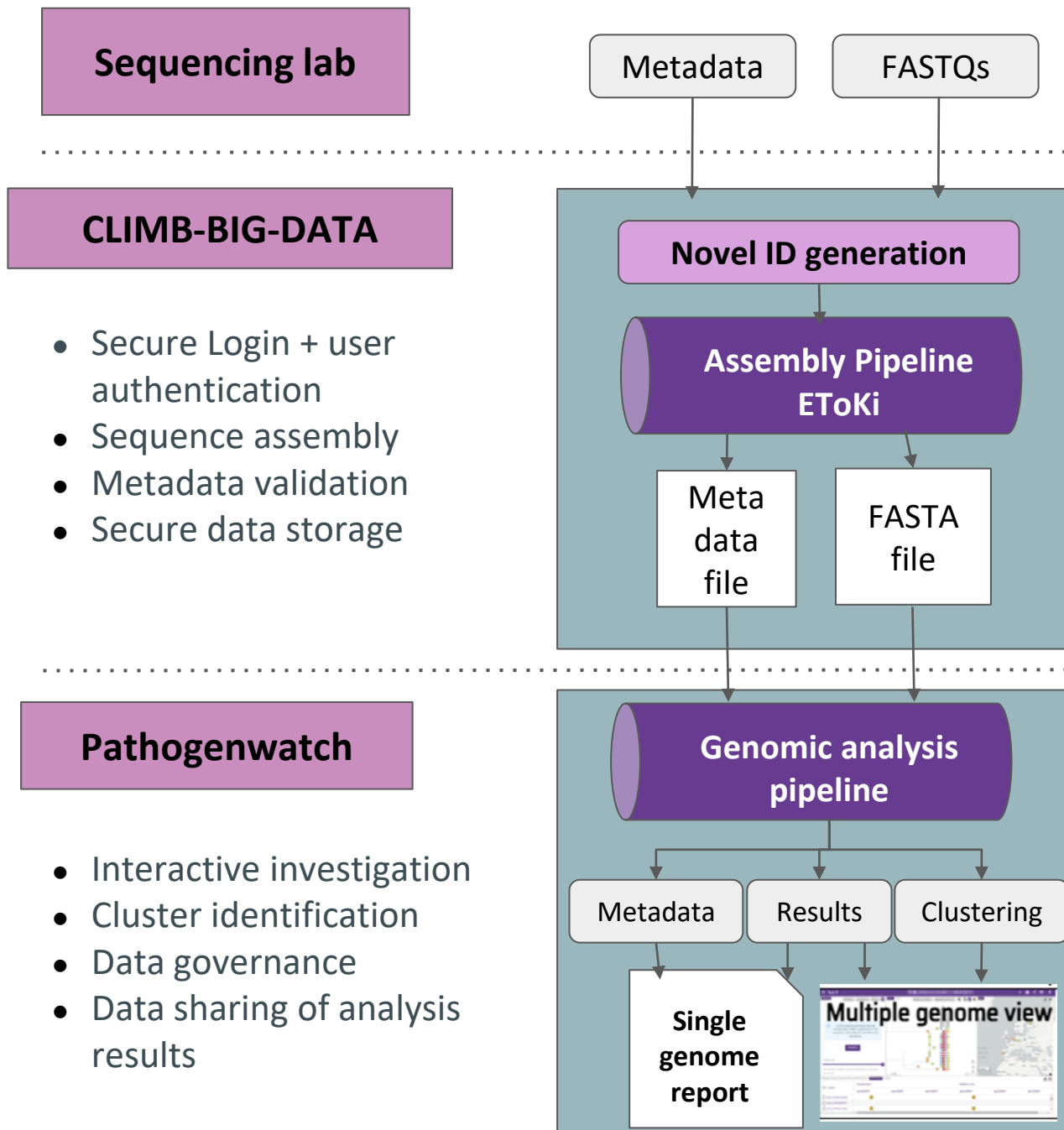
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Scotland

Public Health
Scotland

Community Input Advisory Groups

1. **Technical Advisory Group:** Best practice analytics and QC – assembly recommendations, typing, clustering, additional (eg serotyping)
1. **AMR Advisory Group:** Define markers of risk (e.g. genes, SNPs, mechanisms) to be reported for genotypic resistance and tools used
1. **FBD Data Standards Group:** Adherence to, and extension of data standards to improve interoperability and QC
1. **International Interaction Advisory Group:** Liaise with international stakeholders regarding best practice standards, challenges and learnings



Important to consider:

- De-centralised sequencing capacity
- Standardised analytical pipeline needed to be able to compare genomes
- Value provided to genomic information by providing context to publicly available genomes
- Linkage to minimal associated data (time, place, organism, sample type)



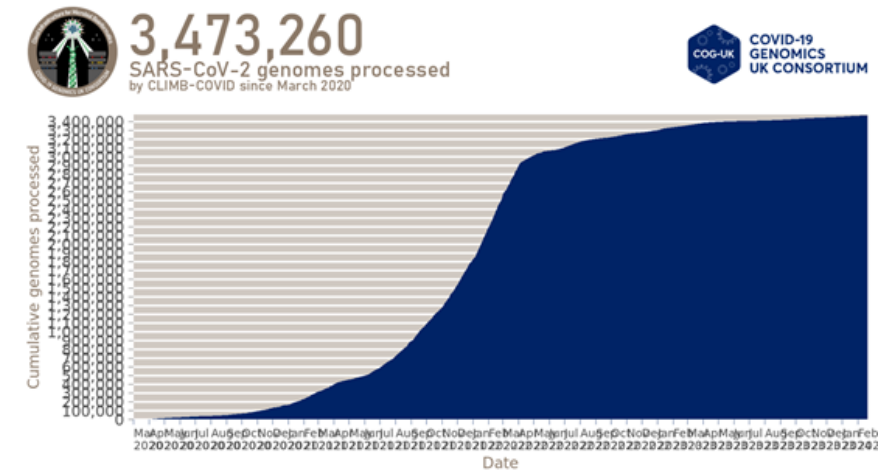
**CLIMB
BIG DATA**

<https://climb-tre.github.io>

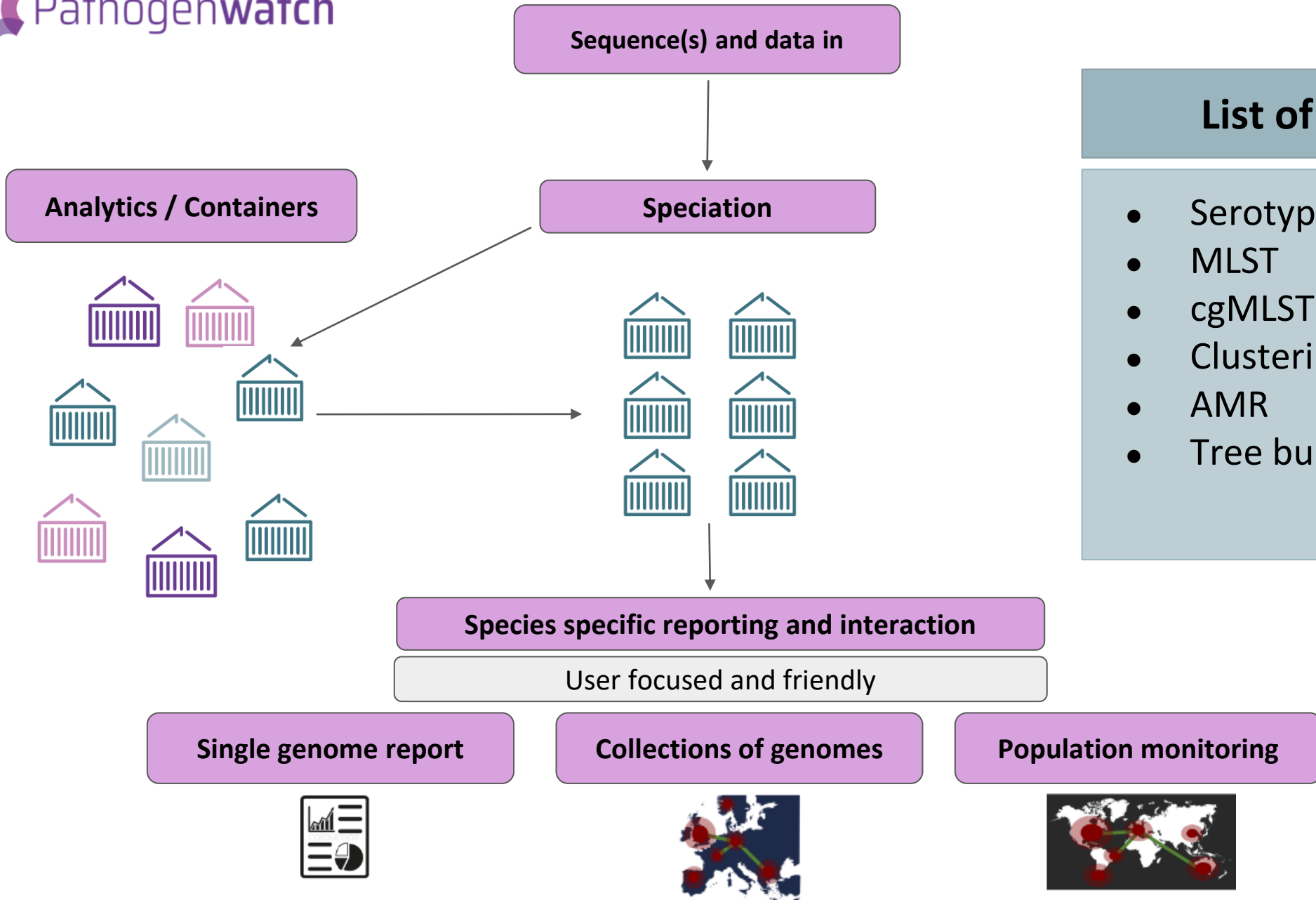


CLIMB-TRE: Trusted Research Environment

- Specialised TRE for pathogen genomic surveillance
- Base platform utilised for COG-UK & UK COVID-19 genomics response, ~3.5m genomes processed
- Decentralised sequencing – centralised real-time analytics - decentralised delivery to public health agencies and academics
- Web upload/authentication and ID generation



**UK Research
and Innovation**



List of analytics

- Serotyping
- MLST
- cgMLST
- Clustering
- AMR
- Tree building

Clustering

Folders Locations Time

Tree 1

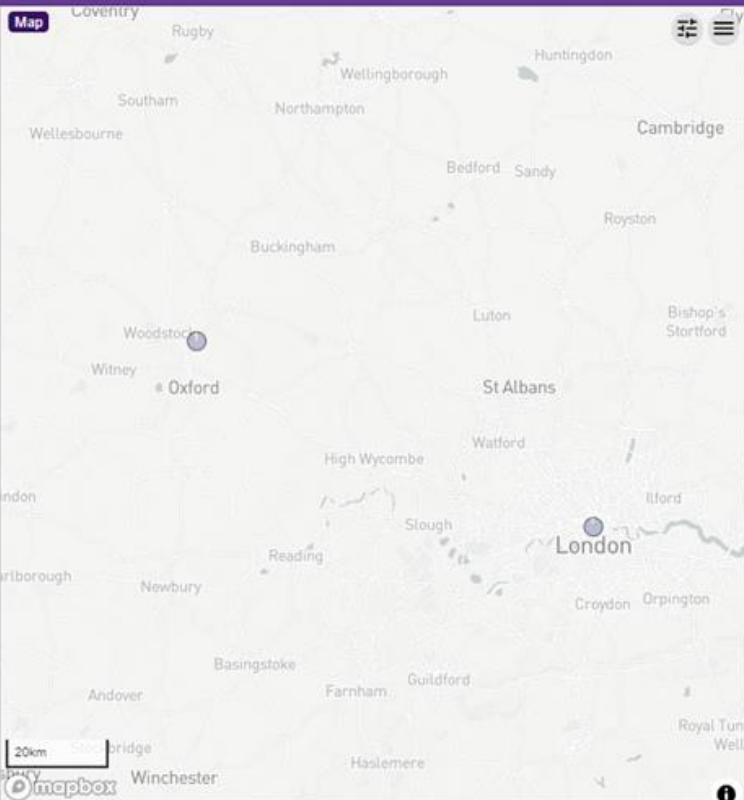
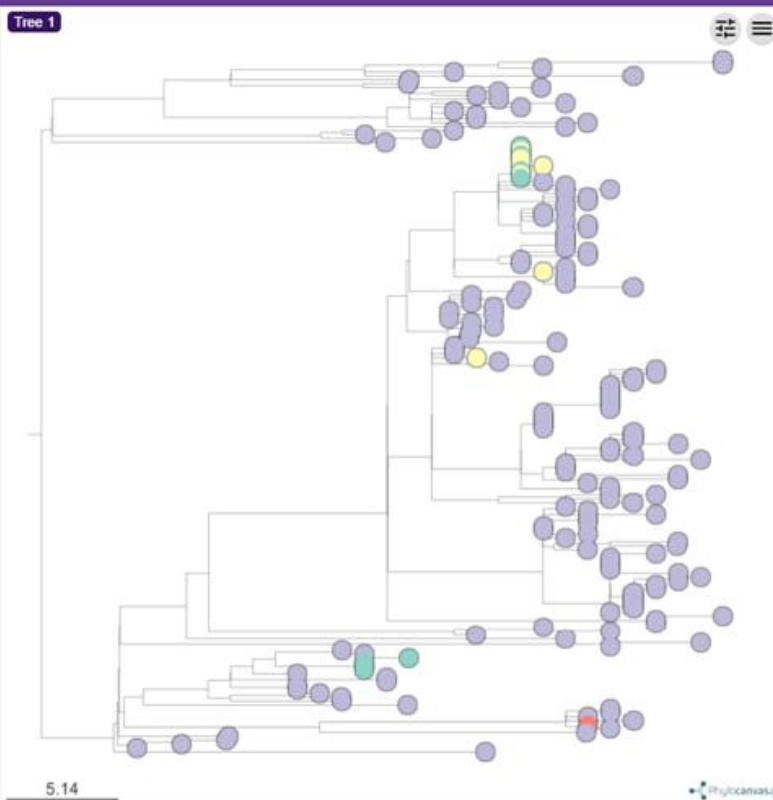
Map

To find existing genomes that are contextually linked to genomes in this view, optionally set the filters and hit search.

SEARCH

Threshold

The maximum alleles distance of genomes to include in the context



Legend
 Colours by metadata/source_type
 animal (green)
 food (yellow)
 human (purple)
 other (red)
 Shapes by source
 folder (circle)

Metadata Typing Assembly stats Antibiotics Genes AMR Variants Timeline

| Name | month | county | country | latitude | run_name | BioSample | longitude |
|-----------------|-------|-------------|----------------|------------|-----------------|--------------|-----------|
| GCA_016332755.1 | 1 | London | United Kingdom | 51.5073359 | GCA_016332755.1 | SAMN08796253 | -0.12765 |
| GCA_016301785.1 | 1 | Oxfordshire | United Kingdom | 51.833333 | GCA_016301785.1 | SAMN10067832 | -1.25 |
| GCA_011613645.1 | 1 | Oxfordshire | United Kingdom | 51.833333 | GCA_011613645.1 | SAMN08823121 | -1.25 |
| GCA_011611875.1 | 1 | London | United Kingdom | 51.5073359 | GCA_011611875.1 | SAMN08826519 | -0.12765 |
| GCA_011587245.1 | 1 | Oxfordshire | United Kingdom | 51.833333 | GCA_011587245.1 | SAMN08797883 | -1.25 |
| GCA_011587165.1 | 1 | London | United Kingdom | 51.5073359 | GCA_011587165.1 | SAMN08797797 | -0.12765 |
| GCA_011586725.1 | 1 | London | United Kingdom | 51.5073359 | GCA_011586725.1 | SAMN08797846 | -0.12765 |
| GCA_011571905.1 | 1 | London | United Kingdom | 51.5073359 | GCA_011571905.1 | SAMN08797999 | -0.12765 |
| GCA_011560045.1 | 1 | London | United Kingdom | 51.5073359 | GCA_011560045.1 | SAMN08795876 | -0.12765 |
| GCA_011544855.1 | 1 | Oxfordshire | United Kingdom | 51.833333 | GCA_011544855.1 | SAMN08823449 | -1.25 |

Single genome report

GCA_016332755.1

Salmonella



Metadata

| | | |
|---------------------|------------------|-----------------|
| day | Host | NAME |
| 22 | Homo sapiens | GCA_016332755.1 |
| file | year | month |
| GCA_016332755.1.fna | 2024 | 1 |
| county | country | latitude |
| London | United Kingdom | 51.5073359 |
| run_name | BioSample | longitude |
| GCA_016332755.1 | SAMN08796253 | -0.12765 |
| data_owner | submit_org | source_type |
| UKHSA | UKHSA | human |
| Isolation type | sample_accession | |
| clinical | SAMN08796253 | |

Typing

MLST - Multilocus sequence typing

<http://mlst.warwick.ac.uk/mlst/dbs/Senterica>

Sequence type 11

| | | | | | | |
|------|------|------|------|------|------|------|
| aroC | dnaN | hemD | hisD | purE | sucA | thrA |
| 5 | 2 | 3 | 7 | 6 | 6 | 11 |

Serotype

[Salmonella In Silico Typing Resource \(SISTR\)](#)

| | |
|------------|-------------|
| Subspecies | Serovar |
| enterica | Enteritidis |

AMR - Anti-microbial resistance

ResfinderPlus AMR

| Agent | Inferred resistance | Known determinants |
|-------------------------|---------------------|--------------------|
| Imipenem | None | - |
| Piperacillin+Tazobactam | None | - |
| Azithromycin | None | - |
| Ciprofloxacin | Resistant | gyrA_S83Y |
| Trimethoprim | None | - |

Plasmid Inc Types

<https://cge.food.dtu.dk/services/PlasmidFinder/>

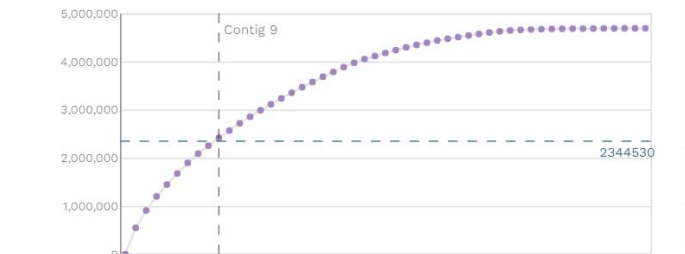
No matches reported

Core Stats

| | | |
|------------------|------------------|--------------------------------------|
| Core matches | Core families | Non-core |
| 2830 | 99.8% | 32.6% |
| Complete alleles | Families matched | Pathogenwatch reference |
| 2722 | 2830 | GCF_020714645.1_ASM2071464v1_genomic |

Assembly Stats

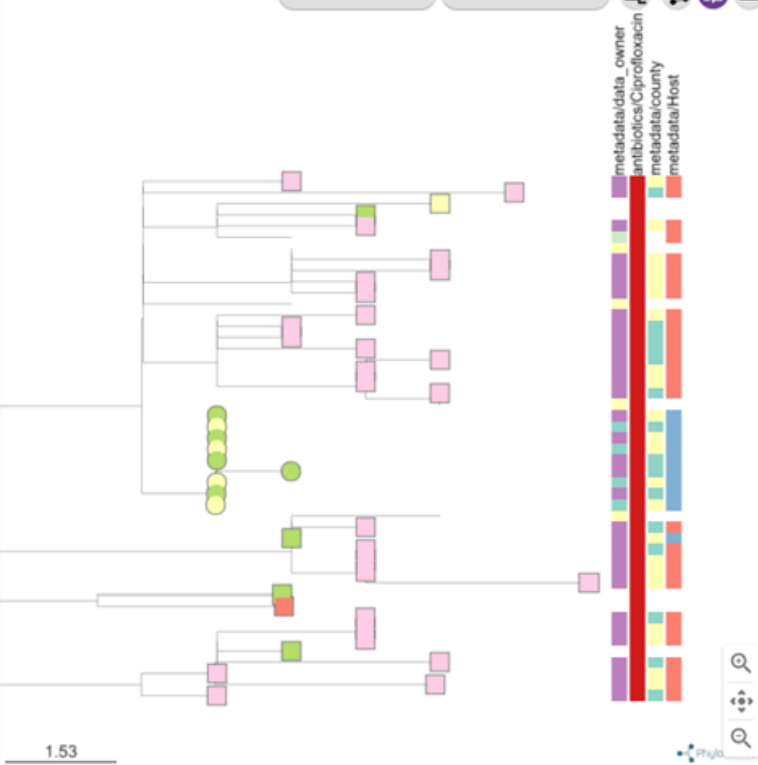
| | | |
|----------------|-----------------------|-----------------|
| Genome length | No. contigs | Smallest contig |
| 4689060 | 50 | 446 |
| Largest contig | Average contig length | N50 |
| 546173 | 93781 | 162472 |
| Non-ATCG | GC content | |
| 0 | 52.1% | |



Clustering [Folders] [Locations] [Time]

Tree 1 Tree 2 [Nodes & Labels] [Metadata blocks] [Map]

✔ We temporarily added 311 genomes to this snapshot. To persist the genomes, please save a snapshot. You can search again by modifying the filters.



Legend

- Colours by metadata/source_type
 - animal
 - environment
 - food
 - human
 - (blank)
- Shapes by source
 - cluster
 - folder
- Colours by metadata/data_owner
 - APHA
 - CDC
 - UKHSA
 - (blank)
 - University Hospital Galway
- Colours by antibiotics/Ciprofloxacin
 - RESISTANT
- Colours by metadata/county
 - London
 - Oxfordshire
 - (blank)
- Colours by metadata/Host
 - Homo sapiens
 - Not available
 - (blank)

Threshold [Slider] 1.53
The maximum alleles distance of genomes to include in the context

Metadata [Typing] [Assembly stats] [Antibiotics] [AMR Variants] [Timeline]

| <input type="checkbox"/> | Name | file | year | month | county | country | latitude | run_name |
|--------------------------|-----------------|---------------------|------|-------|-------------|----------------|------------|-----------------|
| <input type="checkbox"/> | GCA_007013205.1 | GCA_007013205.1.fna | 2024 | 1 | Oxfordshire | United Kingdom | 51.833333 | GCA_007013205.1 |
| <input type="checkbox"/> | GCA_007269695.1 | GCA_007269695.1.fna | 2024 | 1 | Oxfordshire | United Kingdom | 51.833333 | GCA_007269695.1 |
| <input type="checkbox"/> | GCA_007276235.1 | GCA_007276235.1.fna | 2024 | 1 | London | United Kingdom | 51.5073359 | GCA_007276235.1 |
| <input type="checkbox"/> | GCA_007286535.1 | GCA_007286535.1.fna | 2024 | 1 | London | United Kingdom | 51.5073359 | GCA_007286535.1 |
| <input type="checkbox"/> | GCA_007685605.1 | GCA_007685605.1.fna | 2024 | 1 | Oxfordshire | United Kingdom | 51.833333 | GCA_007685605.1 |
| <input type="checkbox"/> | GCA_007608355.1 | GCA_007608355.1.fna | 2024 | 1 | Oxfordshire | United Kingdom | 51.833333 | GCA_007608355.1 |
| <input type="checkbox"/> | GCA_007608715.1 | GCA_007608715.1.fna | 2024 | 1 | London | United Kingdom | 51.5073359 | GCA_007608715.1 |
| <input type="checkbox"/> | GCA_007685385.1 | GCA_007685385.1.fna | 2024 | 1 | London | United Kingdom | 51.5073359 | GCA_007685385.1 |
| <input type="checkbox"/> | GCA_003896935.1 | GCA_003896935.1.fna | 2024 | 1 | Oxfordshire | United Kingdom | 51.833333 | GCA_003896935.1 |
| <input type="checkbox"/> | GCA_016382045.1 | GCA_016382045.1.fna | 2024 | 1 | | USA | 39.7837304 | GCA_016382045.1 |

Challenges

- Data release
- Standardisation
- Policy and Governance going forward
- Measuring impact and value provided

What's next?

- Build trust in the platform
- Increase level of data uploaded to the platform
- Measure impact and value
- Continuation bid
- Scale up to additional pathogen(s)

Acknowledgements

Special thanks to all members of our end user group, advisory groups, international collaborators, and everyone that has contributed and helped develop this data platform.

EUG Leads:

Dr Lesley Larkin
Dr Marianne James
Dr Katy Moran
Dr Kathryn Callaghan
Dr Anthony Wilson
Dr Sarah Evans
Dr Liljana Petrovska
Dr Janine Thoullass

Consortium Leads:

Prof Nick Loman
Prof Sascha Ott
Prof Martin Maiden

PATH-SAFE programme team:

Dr Elaine Kinsella
Dr Shona O'Rourke
Dr Rick Mumford
Prof Robin May

CIAG Chairs:

Prof Kat Holt
Prof Tom Connor
Dr Tim Dallman
Dr Matthew Gilmour

The team at DES and CGPS



UK Health
Security
Agency

Developing an exemplar One Health Data System for a pilot Environmental AMR surveillance

Olisaeloka Nsonwu - Project manager

Principal Scientist / Project Manager

HCAI, Fungal, AMR, AMU & Sepsis Division

UK Health Security Agency

Objectives

One Health Surveillance System (OHSS)



Objective

- ✓ to complete discovery for target vision & feasibility of creating a UK wide One Health AMR Surveillance System

Environmental Surveillance System (ESS)



Objective

- ✓ to design and develop a shared data environment for environmental AMR

Epics development

For each source,
what resistance
is present and
in what
organisms?

1

What is the
level of
resistance?

2

What is the
context of
resistance?

3

How is
resistance
distributed?

4

What is the
risk?

5

Has the
resistance been
investigated
and acted
upon?

6

User Groups



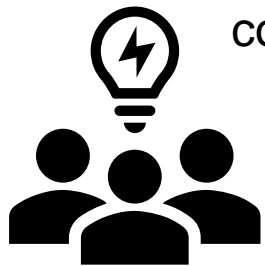
Data providers

Clinicians | Environmental scientists | Public health specialists | Veterinarians | Water suppliers | Sewage/wastewater treatment plants | Government agencies* | Academia[‡] | Agricultural management | Fisheries | Food manufacturers | Devolved Administrations (except Northern Ireland)



Data processors

Lab scientists | Data scientists | Business analysts



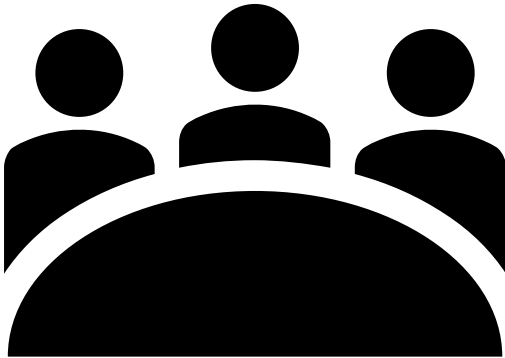
Data consumer

Government agencies* - Policy makers, Operational managers and Board members/executives

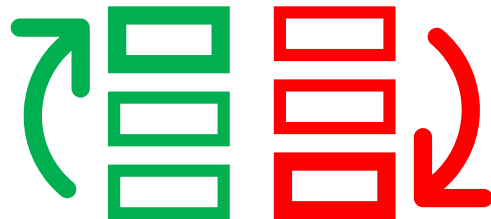
User Story Building Exercise

User Story:

What do I want to need or want from an OHSS?



User groups then ranked these user stories - high, medium or low priority.






Exercise 1

AMR One Health Surveillance System Exercise

13:35 – 14:15

The OHSS exercise requires you to place yourself in the shoes of the allocated users, think about what objectives this person would have for OHSS and the reasons for these objectives.

- Attendees have been **divided into groups** according to whether they **provide data, process data or receive data**. **Names of group members** are included in each frame. 
- Each group will be asked to **define user stories** for the users within their section, using the **templates** in the sticky notes. 
Note: user groups on there that aren't represented in the attendees, so we are asking you to think of what those users may require and we will engage them at a later date.
- Groups will then be asked to **prioritise the user stories**, by pasting the user stories into the **relevant category: low, medium or high priority**. 

11 OFFICIAL


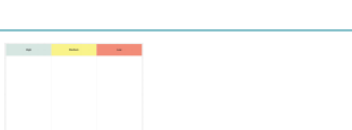
[Link](#)

Exercise 2

AMR Environmental Surveillance System Exercise

14:30 – 14:55

The ESS exercise is similar to the OHSS exercise just completed but requires you to place yourself in the shoes of the allocated users specifically concerned with the ESS.

- Attendees will be asked to **define user stories** for a variety of users using the **templates** in the sticky notes. 
- Attendees will then be asked to **prioritise the user stories**, by pasting the user stories into the **relevant category: low, medium or high priority**. 
Note: user groups on there that aren't represented in the attendees, so we are asking you to think of what those users may require and we will engage them at a later date.

13 OFFICIAL

[Link](#)

Number of user stories identified

| User Group | OHSS | ESS |
|-------------------------------------|-----------|-----------|
| Public Health Outbreak Specialists | 17 | 12 |
| Sewage/ Wastewater Treatment Plants | 11 | 7 |
| Policy Maker | 11 | 8 |
| Data Scientist | 10 | 4 |
| Lab Scientist | 7 | 5 |
| Clinicians | 7 | 4 |
| Academia | 5 | 3 |
| Board Members / Executives | 4 | 3 |
| Food Manufacturers | 3 | 1 |
| Fisheries | 3 | 2 |
| Pharmaceutical Companies | 2 | 1 |
| Frontline Workers | 2 | - |
| Environmental Scientist | 2 | 5 |
| Data / Business Analyst | 2 | - |
| Agricultural Management | 2 | 2 |
| Lab Scientist | 1 | 5 |
| Operational Managers | - | 1 |
| Total | 89 | 63 |

User Story Prioritisation





| | For each source, what resistance is present and in what organisms? | What is the level of resistance? | What is the context of resistance? | How is resistance distributed? | What is the risk? | Has the resistance been investigated and acted upon? | System set up, integrity and governance |
|------|--|----------------------------------|------------------------------------|--------------------------------|-------------------|--|---|
| OHSS | 3 | 6 | 0 | 7 | 8 | 10 | 19 |
| | 3 | 4 | 0 | 4 | 2 | 3 | 7 |
| | 1 | 2 | 0 | 0 | 0 | 2 | 10 |
| ESS | 0 | 2 | 0 | 2 | 1 | 3 | 8 |
| | 0 | 0 | 0 | 1 | 0 | 1 | 2 |
| | 0 | 0 | 0 | 0 | 0 | 0 | 2 |

NB: No user stories were aligned to Epic 3, “what is the context of resistance?”. A new category, “system set up, integrity, and governance” was created for user stories that described process requirements and governance features.

Key:
 High priority ■
 Medium priority ■
 Low priority ■

Data Maturity Assessment

- User stories broken down and assessed against the following pillars: completeness, accuracy, accessibility
- The initial rank of the user stories was an output from the workshop and is an assessment of the relative value the story has to One Health AMR surveillance.
 - *Note that this ranking may have been subject to change based on further stakeholder input and evaluation throughout discovery.*

| Completeness | Accuracy | Accessibility | Automation* |
|--|--|--|---|
| <p>Are there existing and suitable system? Are new systems required</p> | <p>Is data capture subject to error due to human involvement and complexity level?</p> | <p>How easy is it to access and manipulate data?</p> | <p>How feasible is it to have data captured automatically e.g. through API calls to LIMS system?</p> |
|  <p>No data → Fully complete</p> |  <p>Inaccurate → Fully accurate</p> |  <p>Not available → Fully accessible</p> |  <p>Completely manual → Fully automated</p> |

*Note: Automation may be populated at a later date as deemed appropriate during wider OHSS development.

Summary of Engagements: User Needs and Requirements

- ✓ Monitoring Trends, thresholds/ Benchmarks
- ✓ Source and flow of AMR through the Ecosystem
 - ✓ Sequencing Data
 - ✓ Metadata and Provenance
 - ✓ Increase in Testing
- ✓ Governance, data access and sharing
 - ✓ Communication
 - ✓ Incomplete/ Inconsistent Data
 - ✓ Timeliness of Data
- ✓ Policy Not Practice
 - ✓ Pragmatic Approach
- ✓ System capacity
 - ✓ Technology Agnosticism
 - ✓ Future Proofing
 - ✓ Front-end & Flexibility of Information
 - ✓ Linkage to Authoritative Databases/ Infrastructure
 - ✓ Method Alignment
 - ✓ Data dictionary
- ✓ Sample Matrices and Analysis Pipelines

Summary of Engagements: Considerations from Devolved Administrations

- ✓ Interoperability
 - ✓ Different testing methods for susceptibility
 - ✓ Unstandardized LIMS systems
 - ✓ Different sampling regimes and lab processing techniques
 - ✓ Agile processes
- ✓ Data quality and presentation
 - ✓ Lack of comparative dashboards/functions
 - ✓ Data quality and representativeness
 - ✓ Exploration of data
 - ✓ Lack of constant metadata collected
- ✓ Lack of coherence between sources of AMR
- ✓ Inferential frameworks and understanding of causation
- ✓ Identification of shared commitments
- ✓ Governance and commercially sensitive considerations
- ✓ Loss of control over data
 - ✓ Misinterpretation of data
 - ✓ Accessibility and practicality of insights

Summary of Engagements: Challenges

- ✓ Linkage of differing AMR questions & interpretations
- ✓ Operationalisation of surveillance
- ✓ Communication
- ✓ Availability and management of data
 - ✓ Multiple large data systems
 - ✓ Limited data sharing systems
 - ✓ Variations in data collected
 - ✓ Frequency of data collection
 - ✓ Lack of robust data systems
 - ✓ Manual data system

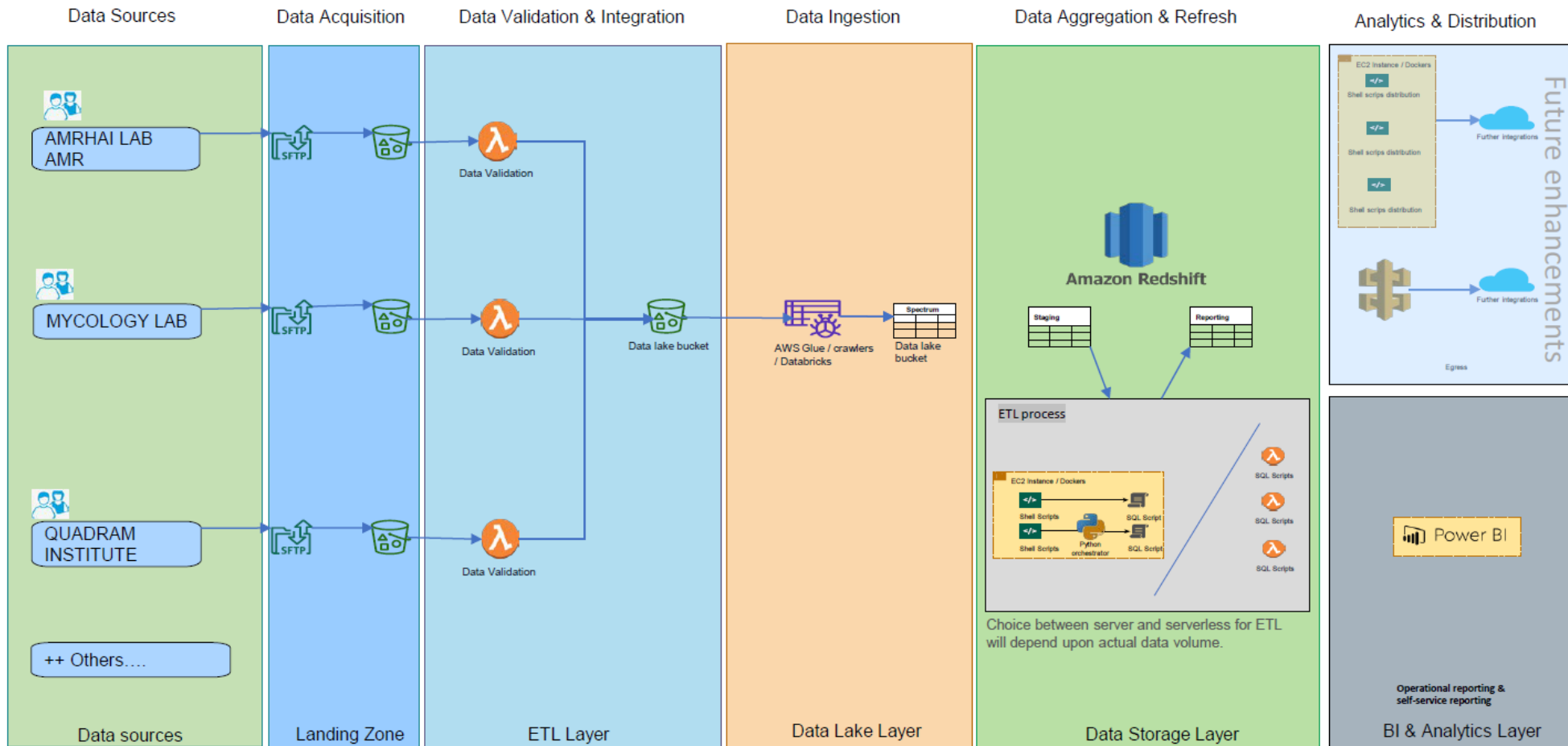


UK Health
Security
Agency

Exemplar Environmental Surveillance System

ESS – High Level Design Architecture

Target solution architect Environmental surveillance system - AMR



ESS Goals

- Exemplar for a UK wide One Health AMR surveillance data system (OHSS)
- Proof of concept for OHSS solution proposed at discovery

ESS – Low Level Design Architecture



ESS Goals

- Exemplar for a UK wide One Health AMR surveillance data system (OHSS)
- Proof of concept for OHSS solution proposed at discovery

User personas

JAMIE



ENVIRONMENTAL
LAB SCIENTIST

JOB CONTEXT

- Works in the FWE Lab
- Currently runs tests on two species of bacteria from river water samples
- Inserts test results into an Excel spreadsheet
- Currently regularly uses LIMS platform to monitor data and to produce regular reports
- Currently shares Excel data sheet and initial reports with other AMR stakeholders via email

ATTITUDE TOWARD TECHNOLOGY



SUSAN



DATA SCIENTIST

JOB CONTEXT

- Performs analysis on AMR data from FWE Lab
- Currently assists with test result recording in Excel spreadsheet
- Currently performs data analysis in Excel, R, SQL, and STATA
- Currently performs limited visualisations in RStudio
- Currently shares visualisations via PowerPoint with other AMR stakeholders via email

ATTITUDE TOWARD TECHNOLOGY



SAM



SUPPORT ENGINEER

JOB CONTEXT

- Provides operational and maintenance support, particularly around multiple data feeds and data processing once steady state of platform is achieved
- Owns platform following offboarding of development team
- Liaises with SMEs and data scientist/platform engineer(s) in the case of any issues with the system/ solution

ATTITUDE TOWARD TECHNOLOGY



NOLAN



PUBLIC HEALTH SPECIALIST

JOB CONTEXT

- Supports in sample collection from the field
- Currently supports test result data entry into Excel
- Currently supports data analysis in Excel and RStudio
- Currently performs basic visualisations in RStudio and presents via PowerPoint
- Currently presents basic AMR data visualisations from PowerPoint at stakeholder meetings

ATTITUDE TOWARD TECHNOLOGY



BROOKE



CLINICIAN

JOB CONTEXT

- Inputs AMR related test results into NHS Labs system which automatically syncs with SGSS (UKHSA clinical data platform)
- Currently uses basic AMR data visualisations from PowerPoint to inform policy decisions
- Patient results are currently sent to UKHSA and analysis is not shared with clinicians

ATTITUDE TOWARD TECHNOLOGY



TRUDY



POLICY MAKER

JOB CONTEXT

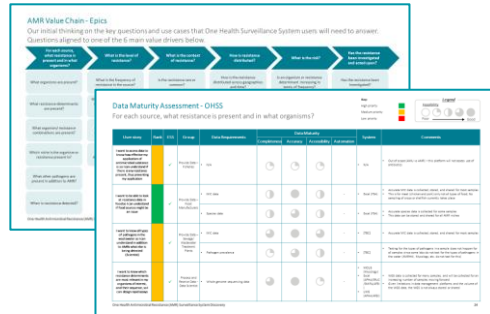
- Currently presents basic AMR data visualisations that were shared by colleagues via PowerPoint at stakeholder meetings
- Currently uses basic AMR data visualisations that were shared with them to inform policy decisions

ATTITUDE TOWARD TECHNOLOGY



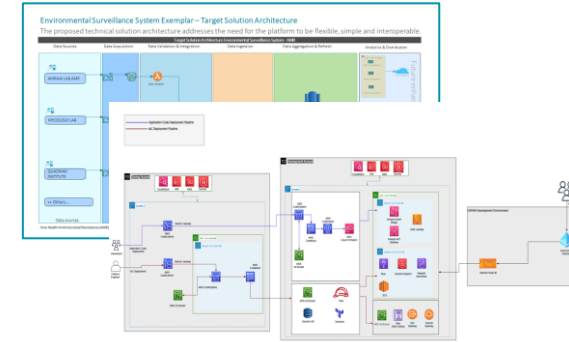
ESS: Development activities

Discovery



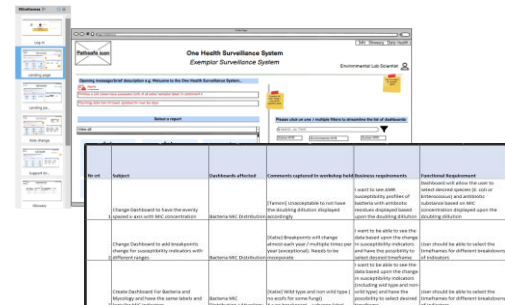
- Develop research plan
- Conduct stakeholder interviews to develop use cases and user personas

Alpha



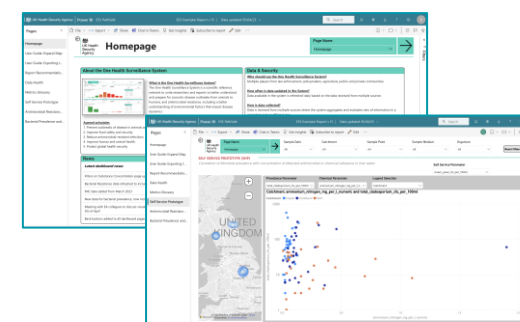
- Finalise user personas
- Build a basic cloud base data platform
- Develop wireframes and basic dashboard designs
- Develop low level design architecture

Beta



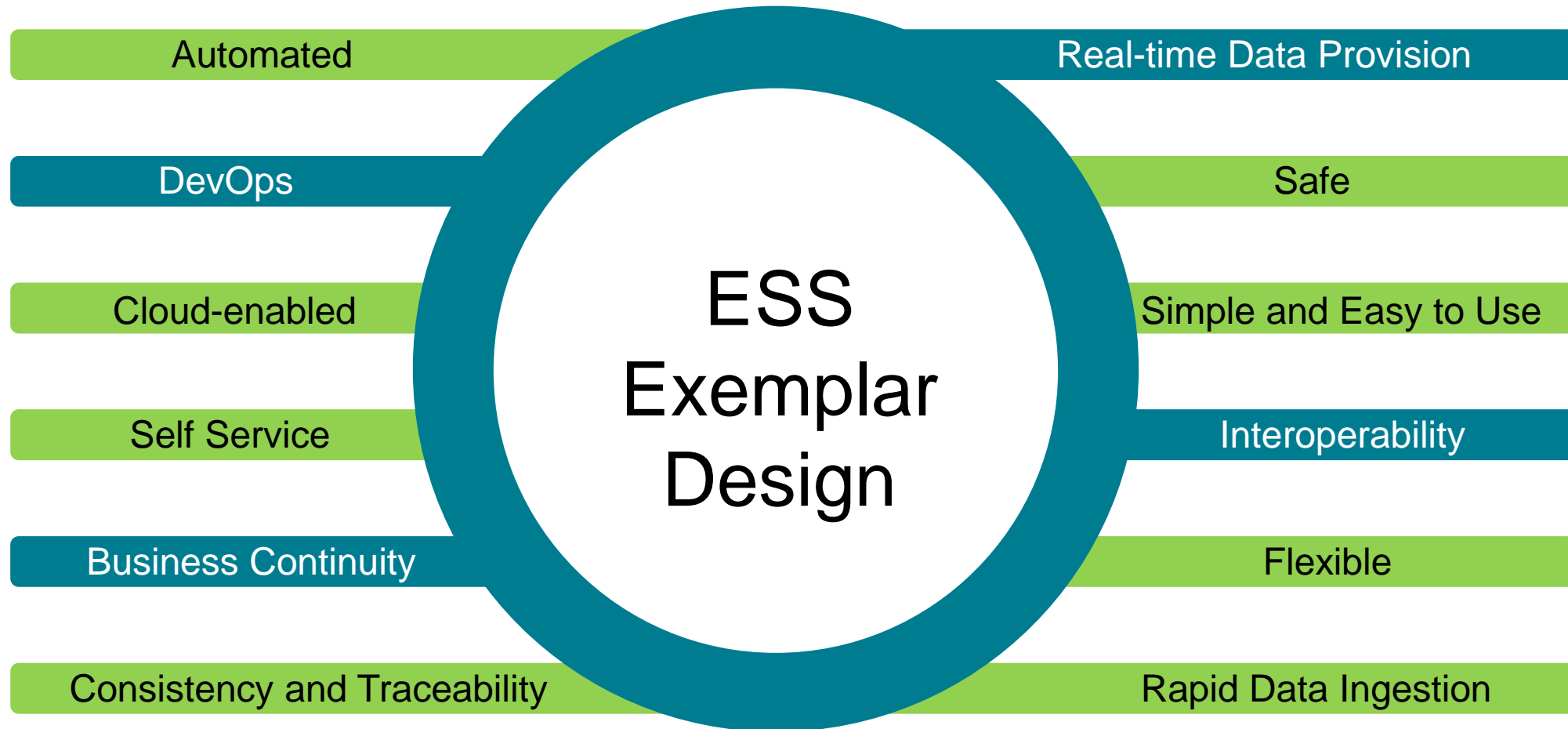
- Build dashboards using Power BI
- Conduct user testing of automated ingestion and validation of data source

Live



- Support and iterate the dashboards according to the user acceptance testing
- Knowledge transfer between Deloitte and UKHSA
- Prepare to decommission the system

Developed solution



About the ESS



What is the ESS?

The Environmental Surveillance System (ESS) is an exemplar IT platform for a one health surveillance system to report, analyse and visualise pathogen sequence and environmental antimicrobial resistance data.

Partners

1. Food Standards Agency (FSA)
2. Food Standards Scotland (FSS)
3. The Department of Environment
4. Food and Rural Affairs (Defra)
5. The Department of Health and Social Care (DHSC)
6. UK Health Security Agency (UKHSA)
7. The Environment Agency (EA)

Data & Security

Who should use the Environmental Surveillance System?

A wide range of stakeholders and policy makers across but not limited to public health, agricultural and environmental surveillance communities.

How often is data updated in the System?

Data available in the system is refreshed daily based on the data received from multiple sources

How is data collected?

Data is collected from multiple across different organisations.

- Environmental sampling data - Sampling River catchments (Environmental Agency)
- Pathogen data - Bacteriology (AMRHAI reference unit) and Mycology (Mycology reference lab)
- Pathogen meta-genomic (QUADRUM Institute)

Security

Role Level Security security is implemented in Power BI and will allow the possibility to create a single set or a set of reports that targets a set of reports accessible to specified users

News

Latest dashboard news:

Filters on Substance Concentration page updated

Bacterial Resistance data refreshed to include columns containing fungal data

MIC data added from March 2023

New data for bacterial prevalence, now including VRE and ESBL percentages

Meeting with EA colleagues to discuss visualisation changes scheduled for 10am 5th of April

Back buttons added to all dashboard pages

User Guides

To **display an interactive user guide**, please click the **icon** shown **below**, found in the **top right corner** of data pages:



Click anywhere on the page to exit.

For **detailed user guide** documents, click the following **button**, found in the **top right corner** of data pages:



Using the expand map

Exporting the dataset

Useful Links

To view some report recommendations, data health page or the metrics glossary, please select one of the buttons below:

Report Recommendations

Data Health

Metrics Glossary

Help & Support

For queries and enquiries, you can contact us at:

UKHSA queries: enquiries@ukhsa.gov.uk

EA queries: enquiries@environment-agency.gov.uk

Quadram Institute queries: info@quadram.ac.uk

ESS: Report recommendation

UK Health Security Agency

Page Name
Homepage

REPORT RECOMMENDATIONS

Welcome to the Environmental Surveillance System (ESS) Exemplar

This system combines data from multiple UK environmental and health agencies to enable the analysis of AMR in the environment

Select a report using the Page Navigator/use the Keyword Selection to view the reports that are recommended for you, then select the relevant report using the Page Navigator.

What are you interested in?

Select Keyword(s)

- Select all
- AMR
- Antibiotic residues
- Antifungal residues
- Antimicrobial residues
- Bacteria
- Bacterial WGS
- Chemical residues
- Comparison
- Correlation
- Direct molecular testing
- Disinfectant residues
- E. coli
- Enterococcus
- Metagenome

Report Recommendations

Substance Concentration

Bacterial Prevalence

Mycology Prevalence

Antimicrobial Resistance

MIC Distribution

High-Throughput qPCR

Long-read metagenome sequencing data

AMR gene presence - short-read metagenome sequencing data

Microbial Taxa Composition – short-read metagenome sequencing data

Microbial Taxa Composition at Superkingdom Level – short-read metagenome sequencing data

Self Service

Antimicrobial Resistance and Substance Concentration

Bacterial Prevalence and Substance Concentration

Substance Concentration

Bacterial Prevalence

Mycology Prevalence

Antimicrobial Resistance

MIC Distribution

High-Throughput qPCR

Micro. Taxa Comp. Super.

Microbial Taxa Composition

AMR Gene Presence

Metagenome Sequencing

Self Service

Antimicrobial & Substance Conc.

Bacterial Prev & Substance Conc.

Homepage

User Guide: Expand Map

User Guide: Exporting the dataset

Report Recommendations

Data Health

Metrics Glossary



DATA HEALTH PAGE

Use this page to understand key information related to the health of each dataset. Filter the table using the slicers to narrow down your search.

File Name:
 Status:
 Source:
 Last Refresh Date:

| Project | File Name | Source | Sheet Name | Status | Description | Comments | Load |
|--------------|---|-------------------|-----------------|-----------|---|----------|----------|
| amr-pathsafe | AMRsampleChemDataTemplate_07032023_165200.xlsx | EA | qaqc | PROCESSED | EA qaqc | | 26/04/23 |
| amr-pathsafe | AMRsampleChemDataTemplate_07032023_165200.xlsx | EA | Catchment | PROCESSED | EA catchments | | 26/04/23 |
| amr-pathsafe | AMRsampleChemDataTemplate_07032023_165200.xlsx | EA | ChemicalAMRdata | PROCESSED | EA chemical data | | 26/04/23 |
| amr-pathsafe | Bacterial_ECOFF_and_Susceptibility_27032023_112112.xlsx | UKHSA | Sheet1 | PROCESSED | UKHSA MIC/ECOFF standards | | 26/04/23 |
| amr-pathsafe | Mycology_ECOFF_and_Susceptibility_29032023_142350.xlsx | MYCOLOGY | Sheet1 | PROCESSED | MYCOLOGY MIC/ECOFF standards | | 26/04/23 |
| amr-pathsafe | UKHSA_Ecoli_15032023_130920.xlsx | UKHSA | Sheet1 | PROCESSED | UKHSA Ecoli isolates | | 26/04/23 |
| amr-pathsafe | UKHSA_Ecoli_corrections_29032023_101500.xlsx | UKHSA | Sheet1 | PROCESSED | UKHSA Ecoli isolates | | 26/04/23 |
| amr-pathsafe | UKHSA_Enterococcus_27032023_162800.xlsx | UKHSA | Sheet1 | PROCESSED | UKHSA Enterococcus isolates | | 26/04/23 |
| amr-pathsafe | UKHSA_prevalence_data_river_water_15032023_155803.xlsx | UKHSA | Sheet1 | PROCESSED | UKHSA Prevalence | | 26/04/23 |
| amr-pathsafe | MIC-Results-PATH-SAFE-River-waters-indicators-2022_28032023_121212.xlsx | MYCOLOGY | Sheet1 | PROCESSED | Mycology MIC results | | 26/04/23 |
| amr-pathsafe | Results-of-PATH-SAFE-river-water-study-totals-2022_12122022_121212.xlsx | MYCOLOGY | Sheet1 | PROCESSED | Mycology Prevalence | | 26/04/23 |
| amr-pathsafe | AMR-class-summary_04012023_190000.xlsx | Quadram Institute | Sheet1 | PROCESSED | Quadram Institute Antimicrobial class | | 26/04/23 |
| amr-pathsafe | AMR-origin_table_20042023_150001.xlsx | Quadram Institute | Sheet1 | PROCESSED | Quadram Institute genes origin | | 24/05/23 |
| amr-pathsafe | AMR-origin_table_21042023_150000.xlsx | Quadram Institute | Sheet1 | PROCESSED | Quadram Institute genes origin | | 26/04/23 |
| amr-pathsafe | AMR-presence_table_04012023_190000.xlsx | Quadram Institute | Sheet1 | PROCESSED | Quadram Institute genes presence | | 26/04/23 |
| amr-pathsafe | Genera-read-proportion_table_21042023_150000.xlsx | Quadram Institute | Sheet1 | PROCESSED | Quadram Institute Taxa species level | | 26/04/23 |
| amr-pathsafe | Superkingdom-read-proportion_table_04012023_190000.xlsx | Quadram Institute | Sheet1 | PROCESSED | Quadram Institute Taxa superkingdom level | | 26/04/23 |
| amr-pathsafe | Resistomap_RelativeAbundances_01012023_182000.xlsx | Resistomap | Sheet1 | PROCESSED | Resistomap Relative abundance | | 26/04/23 |
| amr-pathsafe | Resistomap_RelativeAbundances_09052023_121212.xlsx | Resistomap | Sheet1 | PROCESSED | Resistomap Relative abundance | | 24/05/23 |

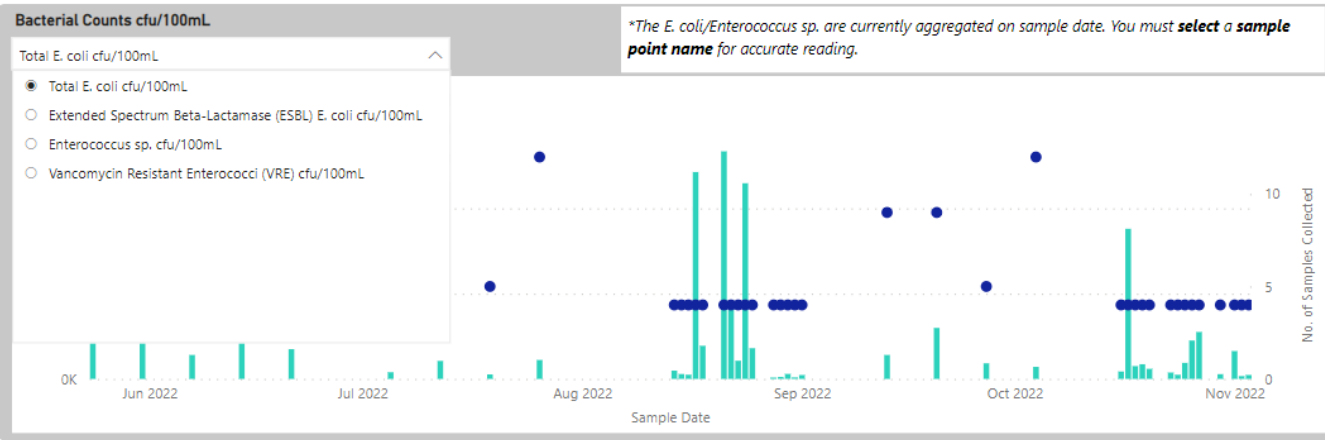
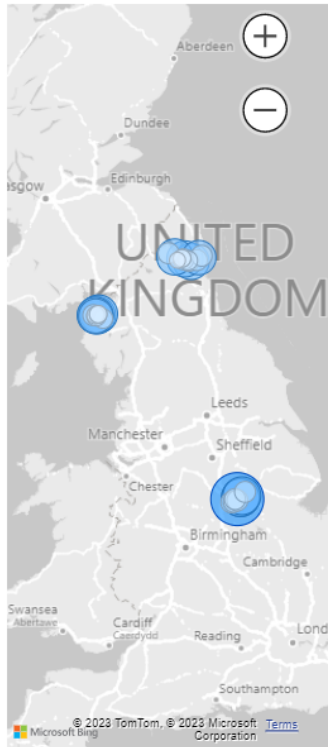
ESS: Bacterial prevalence


Page Name **Bacterial Prevalence** 
Sample Date All Catchment All Sample Medium All Anonymised Sample Point All

BACTERIAL PREVALENCE

Total counts of viable bacteria isolated from various sample types.

| | | |
|---------------|--------------|-----------------|
| Total Samples | Sample Dates | Catchment Areas |
| 233 | 42 | 32 |



| Lims ID | Catchment | Sample medium | Anonymised sample point name | Sample date | Sample time | Analysed date | Analysed time | Total E. coli c |
|--------------|-----------|---------------|------------------------------|-------------|-------------|---------------|---------------|-----------------|
| PO2207364-01 | Trent | Surface Water | Trent 1 | 24 May 2022 | 10:00 | 25 May 2022 | 10:00 | |
| PO2207364-02 | Trent | Surface Water | Trent 4 | 24 May 2022 | 13:50 | 25 May 2022 | 10:00 | |
| PO2207364-03 | Trent | Surface Water | Trent 7 | 24 May 2022 | 12:50 | 25 May 2022 | 10:00 | |
| PO2207364-04 | Trent | Surface Water | Trent 2 | 24 May 2022 | 10:40 | 25 May 2022 | 10:00 | |
| PO2207364-05 | Trent | Surface Water | Trent 5 | 24 May 2022 | 13:30 | 25 May 2022 | 10:00 | |
| PO2207364-06 | Trent | Surface Water | Trent 8 | 24 May 2022 | 12:00 | 25 May 2022 | 10:00 | |
| PO2207364-07 | Trent | Surface Water | Trent 3 | 24 May 2022 | 13:10 | 25 May 2022 | 10:00 | |
| PO2207364-08 | Trent | Surface Water | Trent 6 | 24 May 2022 | 14:50 | 25 May 2022 | 10:00 | |
| PO2207364-09 | Trent | Surface Water | Trent 9 | 24 May 2022 | 14:25 | 25 May 2022 | 10:00 | |

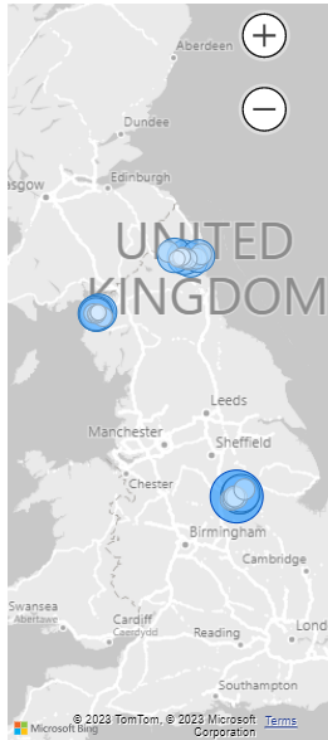
ESS: Mycology prevalence


Page Name Mycology Prevalence →
Sample Date All Catchment All Sample Medium All Anonymised Sample Point All

MYCOLOGY PREVALENCE

Counts of viable fungal isolates isolated from various sample types.

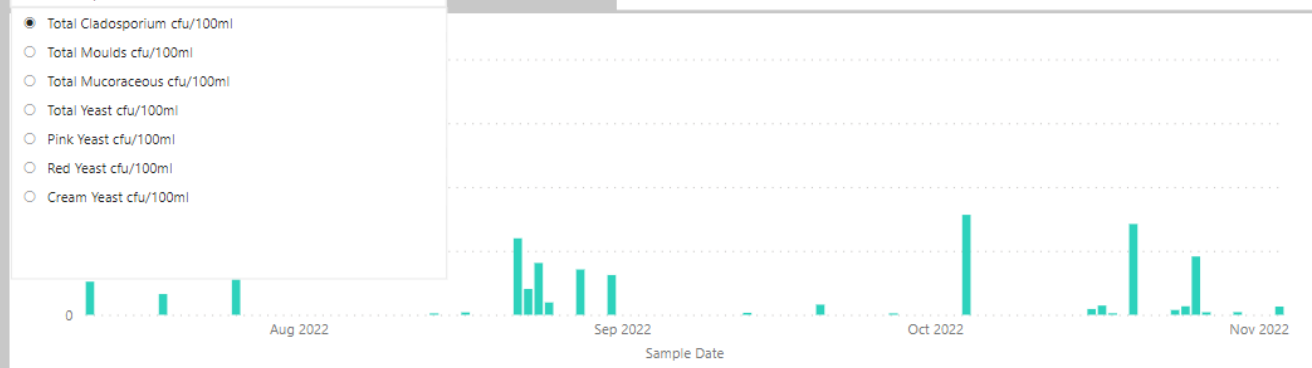
Total Samples **220** Catchment Areas **32**



Mycology Counts cfu/100mL

- Total Cladosporium cfu/100ml
- Total Moulds cfu/100ml
- Total Mucoraceous cfu/100ml
- Total Yeast cfu/100ml
- Pink Yeast cfu/100ml
- Red Yeast cfu/100ml
- Cream Yeast cfu/100ml

*The Cladosporium/Moulds/Mucoraceous/Yeast are currently aggregated on sample date. You must **select a sample point name** for accurate reading.



| External Ref | Sample Date | Catchment | Sample medium spec | Anonymised sample point name | Red yeast cfu per 100ml | Pink yeast cfu per 100ml |
|--------------|--------------|-----------|--------------------|------------------------------|-------------------------|--------------------------|
| PO2207941-01 | 07 June 2022 | Coquet | River | Coquet 1 | | |
| PO2207941-02 | 07 June 2022 | Coquet | River | Coquet 2 | | |
| PO2207941-03 | 07 June 2022 | Coquet | River | Coquet 3 | | |
| PO2207941-04 | 07 June 2022 | Coquet | River | Coquet 4 | | |
| PO2207941-05 | 07 June 2022 | Coquet | River | Coquet 5 | | |
| PO2207941-06 | 07 June 2022 | Coquet | River | Coquet 6 | | |
| PO2207941-07 | 07 June 2022 | Coquet | River | Coquet 7 | | |
| PO2207941-08 | 07 June 2022 | Coquet | River | Coquet 8 | | |
| PO2207941-09 | 07 June 2022 | Coquet | River | Coquet 9 | | |

ESS: Antimicrobial resistance

UK Health Security Agency

Page Name: Antimicrobial Resistance

Sample Date: All | Catchment: All | Anonymised Sample Point: All | Genus Name: All | Species Name: All | Substance Name: All

Antimicrobial Resistance

Antibiotic susceptibility testing data as determined by broth microdilution.

Up to 5 ESBL *E. coli* or up to 5 vancomycin resistant *Enterococcus sp.* colonies were selected per sample.

Total Samples: **449**
Catchment Areas: **28**



Switch to Fungal Data

| Ordpatname | Catchment | Sample medium spec | Anonymised sample point name | Sample date | Species name | SRA number |
|----------------------|-----------|--------------------|------------------------------|----------------|----------------------------|------------|
| PO2211701-02-VRE-01 | Trent | River | Trent 3 | 14 August 2022 | Enterococcus casseliflavus | |
| PO2211701-01-VRE-04 | Trent | River | Trent 2 | 14 August 2022 | Enterococcus gallinarum | |
| PO2211701-01-VRE-05 | Trent | River | Trent 2 | 14 August 2022 | Enterococcus gallinarum | |
| PO2211701-01-VRE-01 | Trent | River | Trent 2 | 14 August 2022 | Enterococcus gallinarum | |
| PO2211701-01-VRE-02 | Trent | River | Trent 2 | 14 August 2022 | Enterococcus gallinarum | |
| PO2211701-01-VRE-03 | Trent | River | Trent 2 | 14 August 2022 | Enterococcus gallinarum | |
| PO2211701-02-ESBL-05 | Trent | River | Trent 3 | 14 August 2022 | Escherichia coli | |
| PO2211701-02-ESBL-02 | Trent | River | Trent 3 | 14 August 2022 | Escherichia coli | |
| PO2211701-02-ESBL-01 | Trent | River | Trent 3 | 14 August 2022 | Escherichia coli | |
| PO2211701-02-ESBL-04 | Trent | River | Trent 3 | 14 August 2022 | Escherichia coli | |
| PO2211701-01-ESBL-01 | Trent | River | Trent 2 | 14 August 2022 | Escherichia coli | |
| PO2211701-02-ESBL-03 | Trent | River | Trent 3 | 14 August 2022 | Escherichia coli | |

Kingdom: Fungi | Standard Version: CLSI v1 - 2017-11-01

*Use filters on the left to change the interpretation source

MIC Distribution

| Genus | Species name | Order | Substances | S | I | R |
|---------|--------------|-------|---------------|---|---|---|
| Candida | jadinii | 1 | Isavuconazole | 5 | 3 | 2 |
| | | 2 | Itraconazole | 1 | 7 | 2 |
| | | 3 | Fluconazole | 2 | 6 | 1 |
| | | 4 | Posaconazole | 1 | 3 | 6 |
| | | 5 | Voriconazole | 5 | 5 | |
| Candida | lusitaniae | 1 | Isavuconazole | 2 | | |

Interpretations are based on Clinical Laboratory Standards Institute (CLSI), version M60 1st Edition published on 2017-11-01.

ESS: MIC distribution

UK Health Security Agency

Page Name: Antimicrobial Resistance

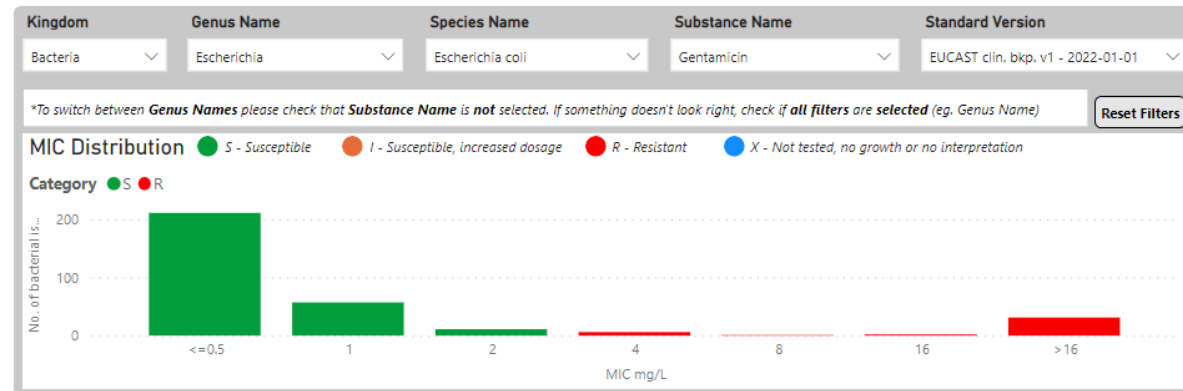
Sample Date: All

Catchment: All

Sample Medium: All

Anonymised Sample Point: All

MIC DISTRIBUTION

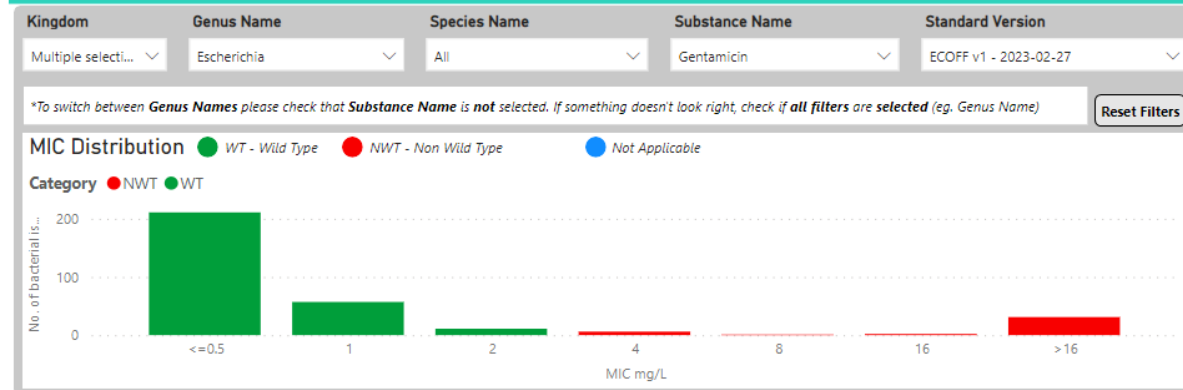


| Lower testing concentration limit mg/L | Upper testing concentration limit mg/L |
|--|--|
| 0.500 | 16.000 |

Change Table

| Substance Value | S | R |
|-----------------|-----|---|
| <=0.5 | 211 | |
| 1 | 57 | |
| 2 | 11 | |
| 4 | | 6 |
| 8 | | 1 |

Interpretations are based on European Committee on Antimicrobial Susceptibility Testing (EUCAST) clinical breakpoints, version v12.0 published on 2022-01-01 and EUCAST Expected Resistant Phenotypes, v...



| Lower testing concentration limit mg/L | Upper testing concentration limit mg/L |
|--|--|
| 0.500 | 16.000 |

Change Table

| Substance Value | NWT | WT |
|-----------------|-----|-----|
| <=0.5 | | 211 |
| 1 | | 57 |
| 2 | | 11 |
| 4 | 6 | |
| 8 | 1 | |

Interpretations are based on European Committee on Antimicrobial Susceptibility Testing Epidemiological cut-off values accessed on 2023-02-27.

ESS: Substance concentration


Page Name: Substance Concentration
Sample Date: All
Catchment: All
Sample Medium: All
Anonymised Sample Point: All

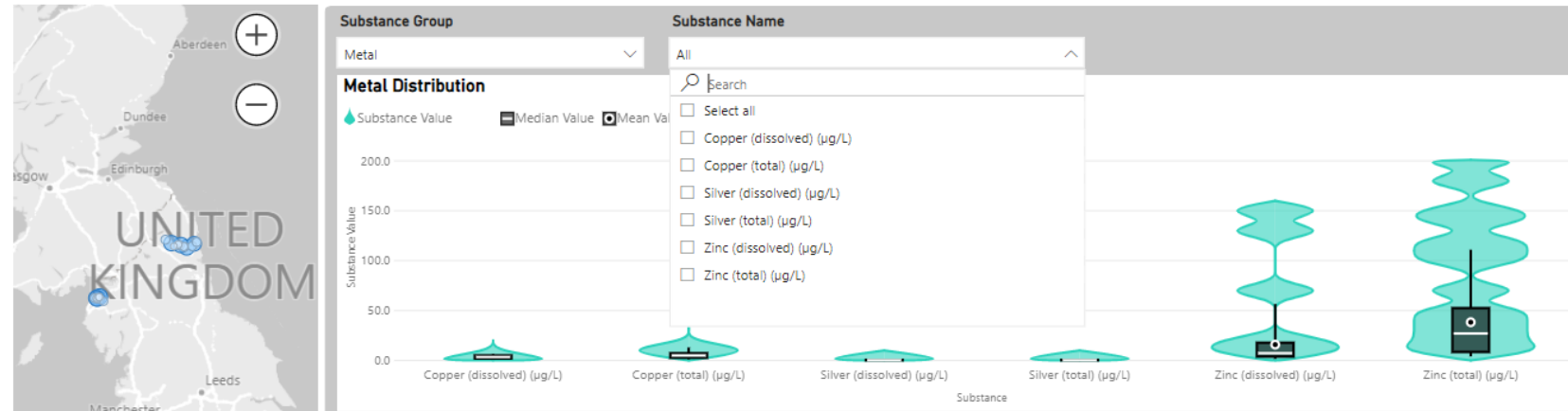
SUBSTANCE CONCENTRATION

Concentration of detected antimicrobial substances in river surface water samples.

Selected antimicrobials range across different antibiotic classes, clinical and agricultural antifungals, disinfectants and potential co-selecting heavy metals.


To aggregate data points that are <LoD the values have been divided by 2, for data points that are > the LoD 0.001 has been added to the value.

Total Samples: 233
Catchment Areas: 32



| Lims ID | Sample ID | Catchment | Sample medium | Anonymised sample point name | Sample medium spec | Sample date | Sample time | Nitrate m |
|--------------|-----------|-----------|---------------|------------------------------|--------------------|-------------|-------------|-----------|
| PO2207364-01 | 492157 | Trent | Surface Water | Trent 1 | River | 24 May 2022 | 10:00 | 23 |
| PO2207364-02 | 492160 | Trent | Surface Water | Trent 4 | River | 24 May 2022 | 13:50 | 38 |
| PO2207364-03 | 492163 | Trent | Surface Water | Trent 7 | River | 24 May 2022 | 12:50 | 38 |
| PO2207364-04 | 492158 | Trent | Surface Water | Trent 2 | River | 24 May 2022 | 10:40 | 41 |
| PO2207364-05 | 492161 | Trent | Surface Water | Trent 5 | River | 24 May 2022 | 13:30 | 36 |
| PO2207364-06 | 492164 | Trent | Surface Water | Trent 8 | River | 24 May 2022 | 12:00 | 34 |
| PO2207364-07 | 492159 | Trent | Surface Water | Trent 3 | River | 24 May 2022 | 13:10 | 37 |
| PO2207364-08 | 492162 | Trent | Surface Water | Trent 6 | River | 24 May 2022 | 14:50 | 39 |
| PO2207364-09 | 492165 | Trent | Surface Water | Trent 9 | River | 24 May 2022 | 14:25 | 33 |

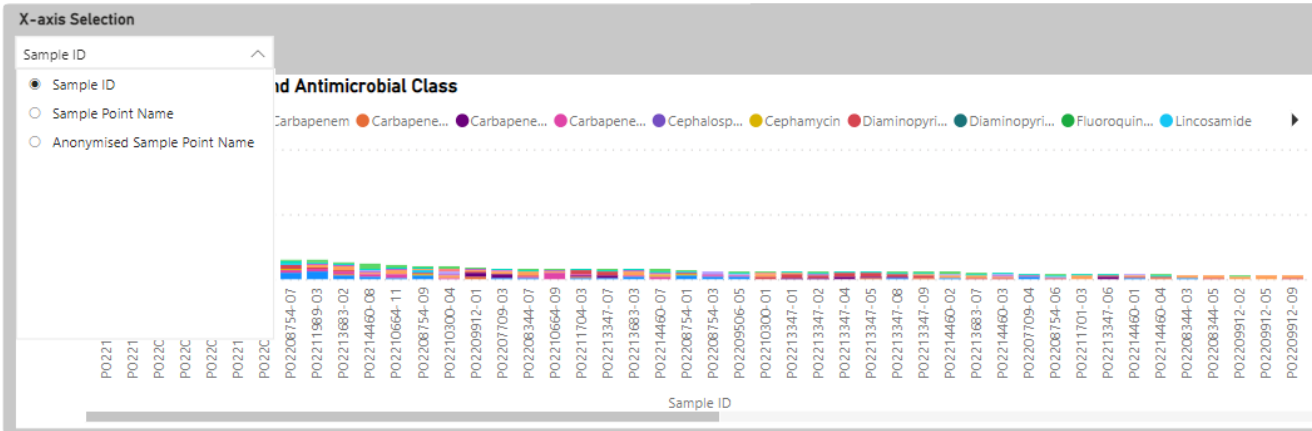
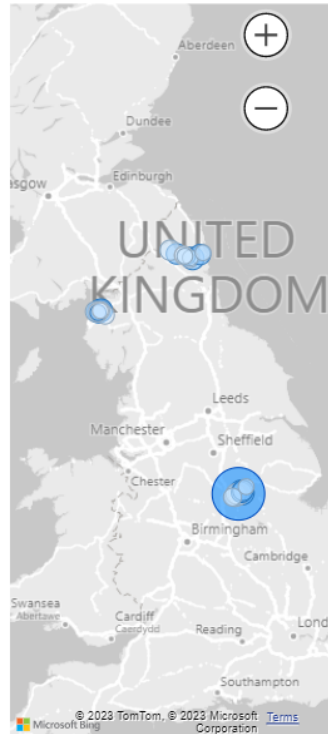
ESS: AMR gene presence


Page Name AMR gene presence - short-...
Sample Date All
Catchment All
Anonymised Sample Point All
AMR Class All
Gene All

AMR GENE PRESENCE - SHORT-READ METAGENOME SEQUENCING DATA

Metagenomic sequence data identifying antimicrobial resistance genes.

Total Samples **89** Catchment Areas **30**

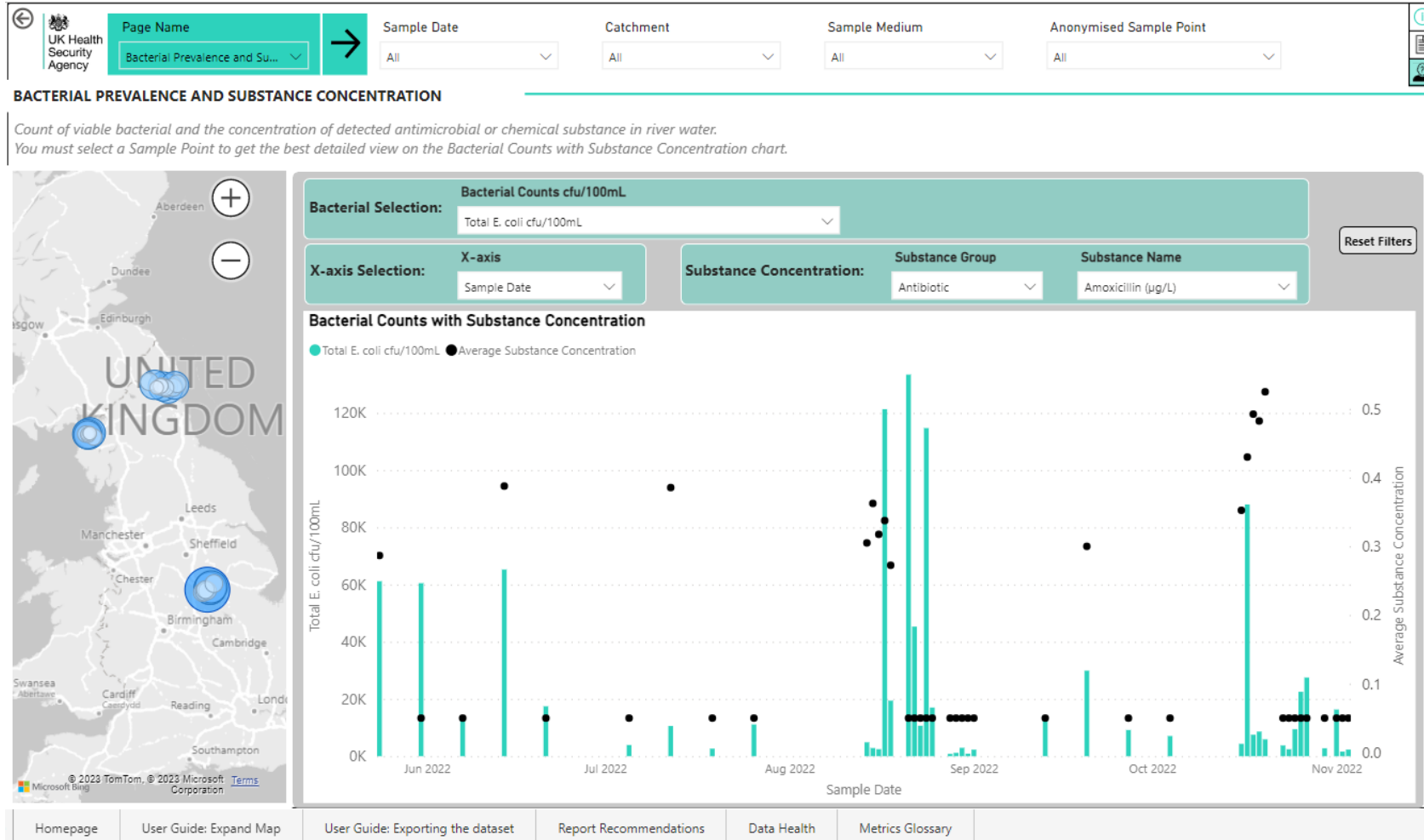


| Sample ID | Catchment | Sample medium spec | Anonymised sample point name | Mean read depth | Last modified timestamp | Summarised antimicrob |
|--------------|-----------|--------------------|------------------------------|-----------------|-------------------------|-----------------------|
| PO2207941-02 | Coquet | River | Coquet 2 | 1.18 | 26/04/2023 14:48 | Beta-lactam |
| PO2207941-04 | Coquet | River | Coquet 4 | 3.38 | 26/04/2023 14:48 | Diaminopyrimidine |
| PO2207941-05 | Coquet | River | Coquet 5 | 1.02 | 26/04/2023 14:48 | Diaminopyrimidine |
| PO2207941-07 | Coquet | River | Coquet 7 | 1.25 | 26/04/2023 14:48 | Beta-lactam |
| PO2209506-01 | Coquet | River | Coquet 1 | 1.91 | 26/04/2023 14:48 | Beta-lactam |
| PO2209506-01 | Coquet | River | Coquet 1 | 0.95 | 26/04/2023 14:48 | Beta-lactam |
| PO2209506-05 | Coquet | River | Coquet 10 | 1.90 | 26/04/2023 14:48 | Aminoglycoside |
| PO2209506-05 | Coquet | River | Coquet 10 | 0.92 | 26/04/2023 14:48 | Aminoglycoside |
| PO2209506-05 | Coquet | River | Coquet 10 | 1.23 | 26/04/2023 14:48 | Beta-lactam |

ESS: Self service



ESS: Bacterial prevalence and substance concentration



Summary

- We developed recommendations and strategic case for the development of a UK-wide one health surveillance system (OHSS)
- We developed an exemplar for this OHSS based on a proposed solution developed through discovery albeit, with limited scope
- Some learnings from this process are;
 - The choice of visualisation tool can limit desired functionalities
 - Timely availability of data
 - Uncertainty and time for approval process
- A key stakeholder feedback is one health being much more than generating and processing AMR data.
- Future work should focus on what we do with signals identified from the
 - More work and research is needed on how to decide appropriate action

Acknowledgement

- Nicola Rupawala and Russell Hope - UKHSA project team
- Ranjit Puri, Arun Singh, Nicole Advani and Nicholas Dellasanta - Deloitte
- Collet Allen, Katie Hopkins - AMRHAI reference unit
- Elizabeth Johnson - Mycology reference lab
- Caroline Willis - Food, Water and Environmental Laboratory Network
- Wiebke Schmidt, Jono Warren and Alwyn Hart - Environment Agency
- Greg Haden, Stephen Povey, Joana Blankson-Wilson – DEFRA
- Alison Mather and Samuel Bloomfield - Quadram Institute



UK Health
Security
Agency



Quadram
Institute



Department
for Environment
Food & Rural Affairs

Deloitte.



Environment
Agency