



Genomic epidemiology:

visualization and practical applications with Pathogenwatch and Microreact

<Creation date of the training material>

Intended Learning Objectives

- **Specific objectives for this session:**

1. Work with a real-life scenario and data
2. Learn to work in an interdisciplinary team
3. Familiarize yourself with tools for genomic analysis (Pathogenwatch)
4. Familiarize yourself with visualization tools for genomic epidemiology (Pathogenwatch and Microreact)

- **Related to other course objectives:**

1. Assembly of Illumina data > Nabil Alikhan (Tue 28th)

Outline

This session consists of the following elements:

1. Scenario
 - Presentation of a real-life dataset for genomic analysis
2. What shall you do next?
 - Reflection on the main steps that can be performed for genomic analysis after genome assembly
3. Pathogenwatch
 - Brief introduction to the platform
 - Demo
4. Microreact demo

Scenario



You are a team of scientists working at Public Health England (now UKHSA).

You have **533 Salmonella enterica serovar Typhi** isolates from **2014-2017** available in your lab.

These were isolated all over the UK, but **92%** have a **patient travel** history.

You want to use this routine data for passive surveillance to inform **Public Health actions** in different geographical regions.

The **epidemiologist** in your team has taken care of gathering all the metadata (e.g., year of isolation, host age, travel history, clinical symptoms, ...).

Isolation and species identification were carried out by your **microbiologist**. They also performed DNA extraction and Illumina sequencing.

Your **bioinformatician** has assessed the quality of the sequenced reads and assembled the genomes. After genome QC, you're left with 524 high-quality genome assemblies.

What shall you do next?

What shall you do next?

Genomic typing:

- MLST
- cgMLST
- Species-specific genotype schemes, e.g., genotypi for *Salmonella* Typhi
- Species-specific schemes for surface antigens, e.g., K types and O types in *Klebsiella pneumoniae*
- AMR genes
- Virulence genes
- Plasmids

Phylogeny:

- Alignment
- Visualization

Visualization and interpretation

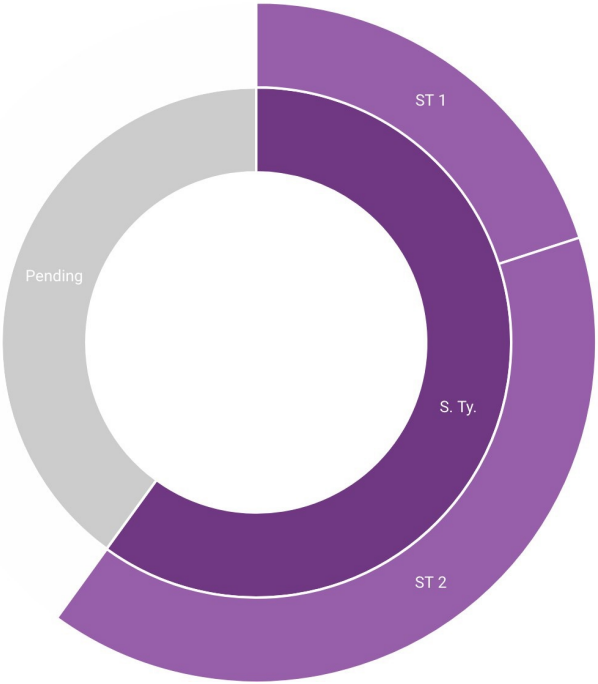
Pathogenwatch

← GO BACK

Today, 11:09

✓ 5 genomes uploaded

● Salmonella Typhi	3
AMR	3
cgMLST (Enterobase)	3
Core Summary	3
Genotypi	3
Inctyper	3
MLST (Enterobase)	3
Serotype	3
Stats	3
● Pending	2



Pathogenwatch

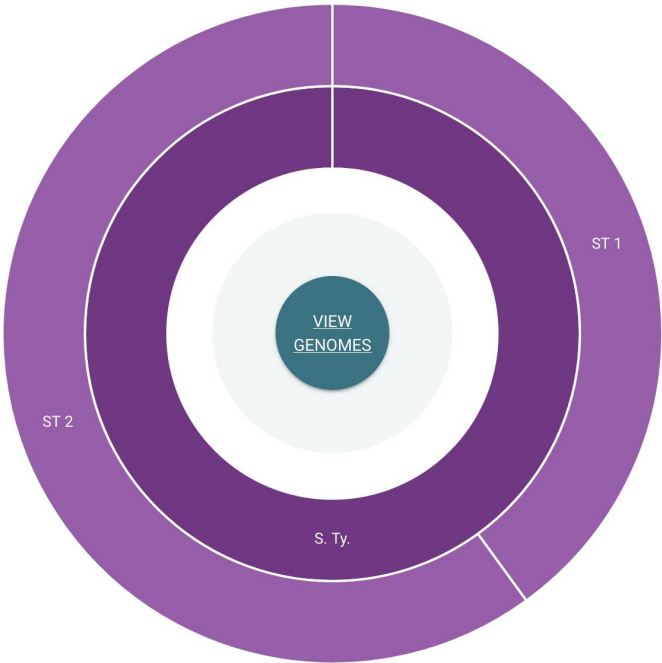
← GO BACK

Today, 11:09

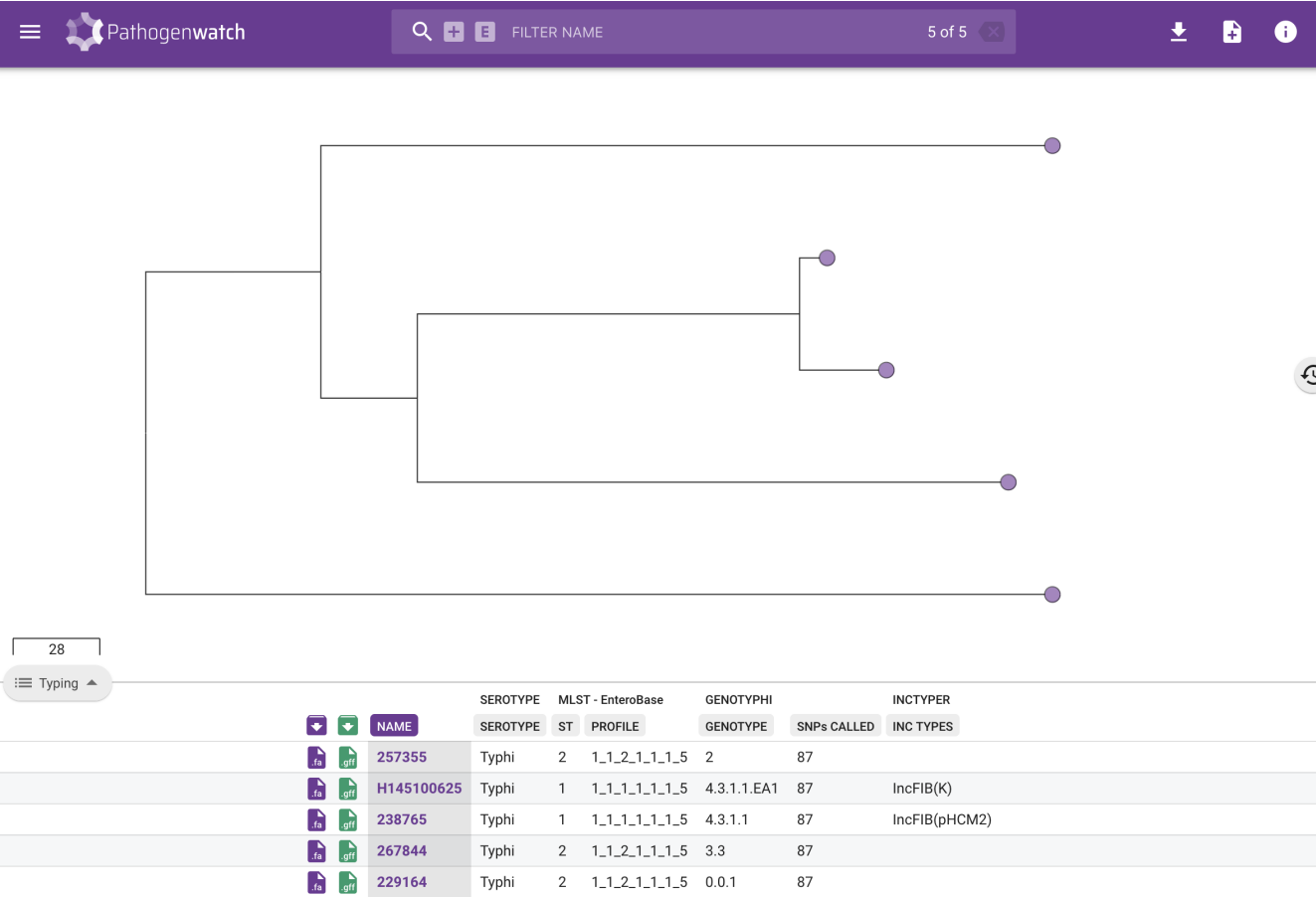
- ✓ 5 genomes uploaded
- ✓ 45 analyses completed

- **Salmonella Typhi**
 - AMR
 - cgMLST (Enterobase)
 - Core Summary
 - Genotypi
 - Inctyper
 - MLST (Enterobase)
 - Serotype
 - Stats

5
✓
✓
✓
✓
✓
✓
✓
✓



Pathogenwatch



Microreact



Microreact

Public Health Surveillance #1



Data used



PLOS NEGLECTED TROPICAL DISEASES

OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

Informal genomic surveillance of regional distribution of *Salmonella* Typhi genotypes and antimicrobial resistance via returning travellers

Danielle J. Ingle , Satheesh Nair, Hassan Hartman, Philip M. Ashton, Zoe A. Dyson, Martin Day, Joanne Freedman, Marie A. Chattaway, Kathryn E. Holt , Timothy J. Dallman

Paper: <https://journals.plos.org/plosntds/article?id=10.1371/journal.pntd.0007620>

Pathogenwatch collection: <https://pathogen.watch/collection/wcu2dojnu7ns-ingle2019>

Microreact project for GenEpi-BioTrain: <https://microreact.org/project/sHYMekifNfNvNqsuGPtwrM-genepi-biotrain-salmonella-uk-travellers-2014-2017>

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