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ACORN



NATIONAL INSTITUTE FOR  
COMMUNICABLE DISEASES

Division of the National Health Laboratory Service

# Genome Annotation for Antimicrobial Resistance

Lecture: Exploring Pathogenwatch

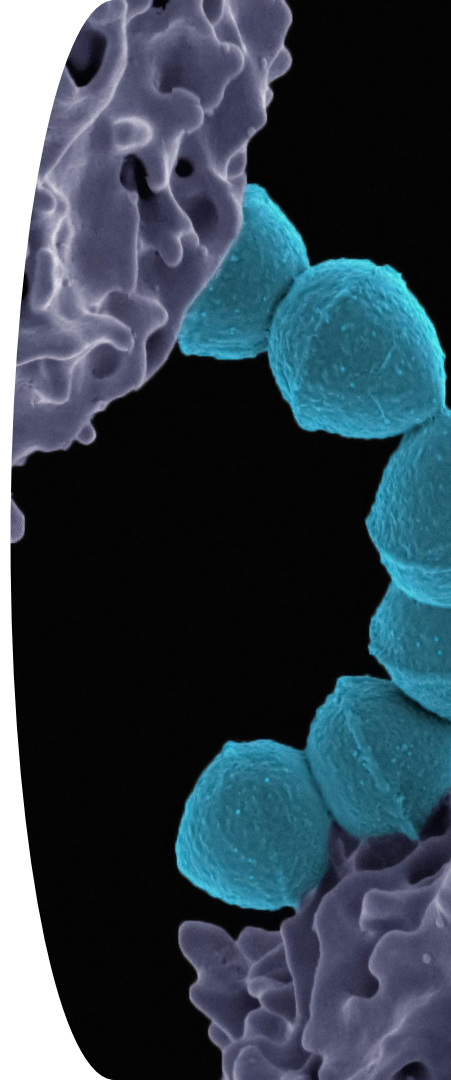
## Instructors:

Rito Mikhari

Julio Diaz Caballero

AMR Virtual course (Africa and Asia)

**04 June 2024**





<https://www.pathogensurveillance.net/>



<https://www.bdi.ox.ac.uk/>



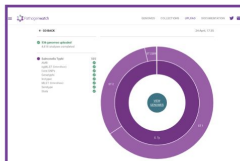
<https://wellcome.org/>

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## Learning outcome

Learn how to use **PathogenWatch** online application to characterize a bacterial genome

Upload  
View



Drag and drop input assemblies (fasta) or reads (fastq)

Outputs species ID and MLST while other analyses are running

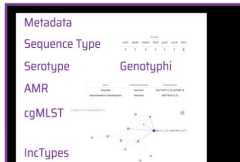
Genomes  
View

List of user-uploaded genomes (private) and public genomes with species identification and MLST information.

Map and assembly statistics

Select private/public genomes to create custom collections

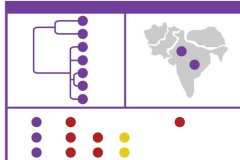
Genome  
Report



Single genome

- Species ID
- *in silico* serotyping
- Genotyping - MLST, Genotypyphi, IncTyper
- cgMLST clustering

Collection  
View



Collection Tree - clustering of user genomes

Map

Timeline

Metadata Table

Typing Table - MLST, Genotypyphi, IncTyper

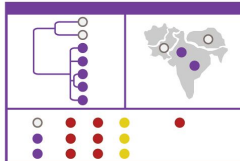
AMR Tables - Antibiotics, Genes, SNPs

Population  
View



Groups user genomes by their closest reference in the population tree

Population  
Subtree



Contextualises user genomes with the closest genomes in the public collection

# PathogenWatch application workflow



ARTICLE

<https://doi.org/10.1038/s41467-021-23091-2>

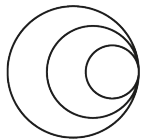
OPEN

Check for updates

## A global resource for genomic predictions of antimicrobial resistance and surveillance of *Salmonella* Typhi at pathogenwatch

Silvia Argimón<sup>1</sup>, Corin A. Yeats<sup>2</sup>, Richard J. Goater<sup>1,10</sup>, Khalil Abudahab<sup>1</sup>, Benjamin Taylor<sup>2</sup>, Anthony Underwood<sup>1</sup>, Leonor Sánchez-Bus6<sup>2,11</sup>, Vanessa K. Wong<sup>3</sup>, Zoe A. Dyson<sup>3,4,5</sup>, Satheesh Nair<sup>6</sup>, Se Eun Park<sup>7</sup>, Florian Marks<sup>7</sup>, Andrew J. Page<sup>8,12</sup>, Jacqueline A. Keane<sup>9</sup>, Stephen Baker<sup>9</sup>, Kathryn E. Holt<sup>4,5</sup>, Gordon Dougan<sup>3</sup> & David M. Aanensen<sup>1,2,8</sup>

file:///Users/user/Downloads/s41467-021-23091-2.pdf



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## Practical:

Upload a sample to Pathogen watch and explore outputs



A Global Platform for Genomic Surveillance.



- Assembly
- Serotyping
- MLST typing
- AMR profiles
- Population structure visualization
- Population comparative analysis

