Pathogen watch

Dr Luria Founou

Learning outcomes

❑ Use Pathogen Watch for bacterial species, AMR and ST prediction

❑ Retrieve assemblies available from Pathogen Watch

❑ Assess a collection of genome in Pathogen Watch

Agenda

❑ Basic concepts

❑ Bacterial species

❑ Sequence typing methods

❑ AMR prediction

❑ Genome browser

Pathogen watch – basic concepts

❑ Free online based platform

❑ Oxford Big Data Institute

❑ Comparing pathogen genome assemblies from around the world

    ❑ Species assignment for 60,000 variants of bacteria, viruses & fungi – Speciator

    ❑ Sequence typing

    ❑ AMR prediction

    ❑ cgMLST clustering and SNP-tree

    ❑ Plasmid prediction

https://pathogen.watch/

Pathogen watch – Bacterial species

Acinetobacter baumannii

Enterococcus faecium

Klebsiella quasipneumoniae

Mycobacterium africanum

Mycobacterium tuberculosis

Salmonella enterica

Campylobacter coli

Escherichia

Klebsiella variicola

Mycobacterium bovis

Neisseria gonorrhoeae

Shigella

Vibrio cholerae

Campylobacter jejuni

Klebsiella pneumoniae

Listeria

Mycobacterium canettii

Neisseria meningitidis

Staphylococcus aureus

Pathogen watch – Sequence typing methods

- cgMLST

- Genotyphi – S. Typhi

- Kaptive - typing the surface polysaccharide loci of *Klebsiella* and *A. baumannii*

- Kleborate – in-depth species, ST, virulence genes, capsule typing and antimicrobial resistance prediction for Klebsiella

- MLST

- Vista – Virulence and genotype annotation tool for Vibio cholerae

- PopPunk – *S. pneumoniae* GPSC strain assignment

- Pangolin – Phylogenetic Assignment of Named Global Outbreak LINeages

- NG-MAST– *Neisseria gonorrhoeae* multi-antigen sequence typing

- Klebsiella LIN codes – Infers Klebsiella lineage codes

- SeroBA

- SISTR – *Salmonella In Silico* Typing Resource

Pathogen watch – AMR prediction

❑ Pathogen watch AMR

❑ Kleborate – antimicrobial resistance prediction for *Klebsiella* genus

❑ SPN-PBP-AMR : Analysis of the Streptococcus pneumoniae PBPs and inferred MICs.

Pathogen watch – Browse genomes/collections
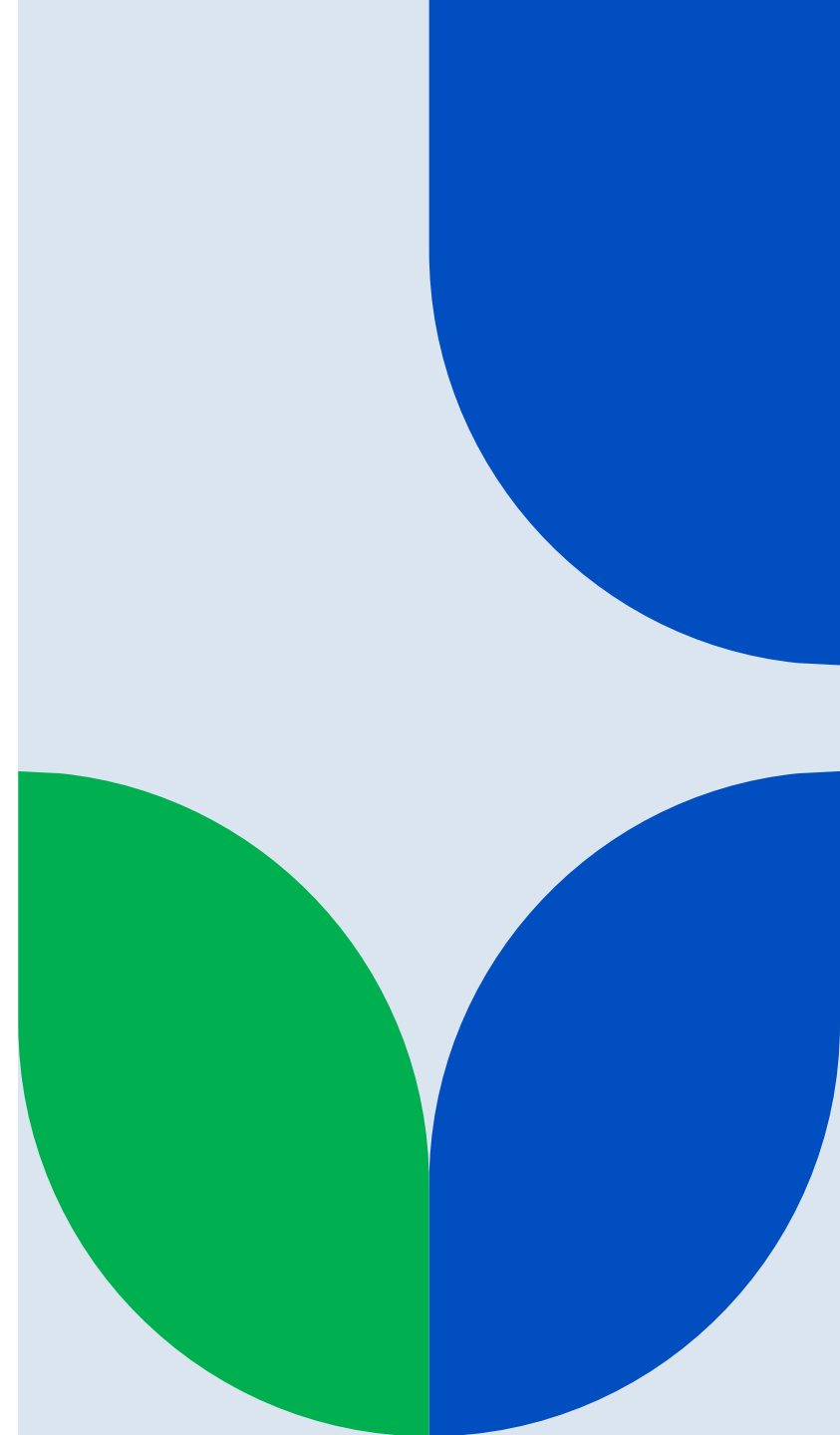
❑ All assemblies currently available from pathogenwatch can be accessed via the "Genomes"

❑ Pathogenwatch provides pre-generated collections of publicly available genomes from important papers, surveys and in-house collections.

Thank you

Dr Luria Leslie Founou

luriafounou@gmail.com

www.cedbcam.com

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