



Use of genomic sequencing for AMR surveillance an introduction

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University of Oxford

Regional Antimicrobial Resistance Data Sharing and Analysis (RADSA) Virtual Workshop
Southeast Asia

July 14th 2021



Centre for Genomic Pathogen Surveillance



Machine Learning | CS & AI



Sequencing / lab / bioinformatics

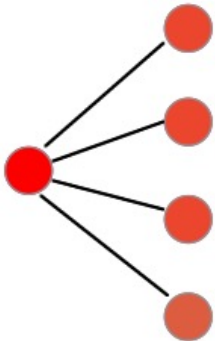
Analysis of large, complex heterogeneous datasets for research into the causes and consequences, prevention and treatment of disease

Translational big data and genomics for public health

Genomic Pathogen Surveillance



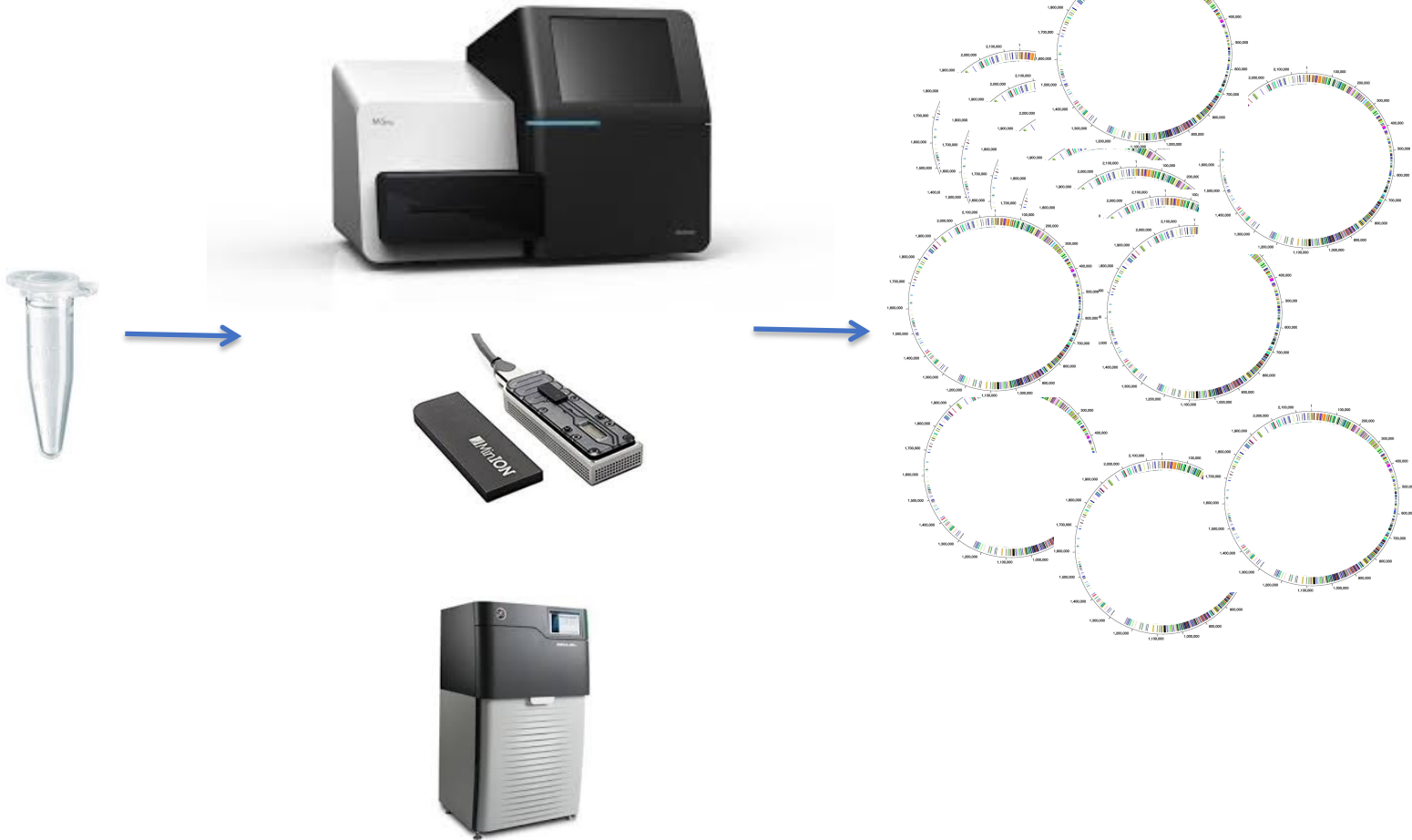
Where, what, when, who



Related Cases / clone

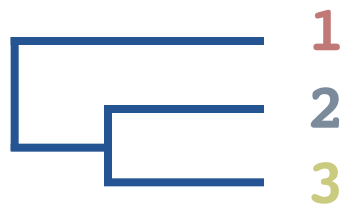


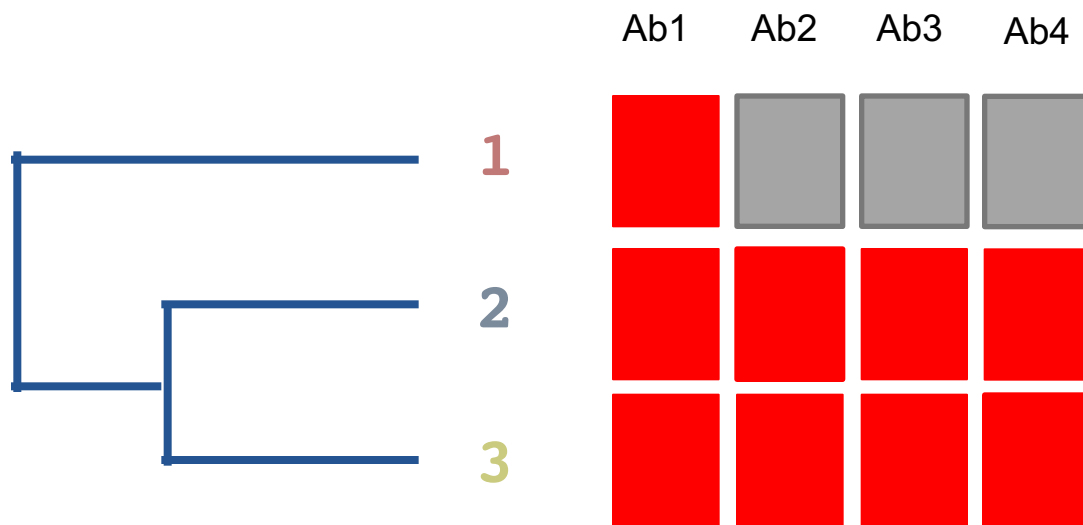
Unrelated Isolates

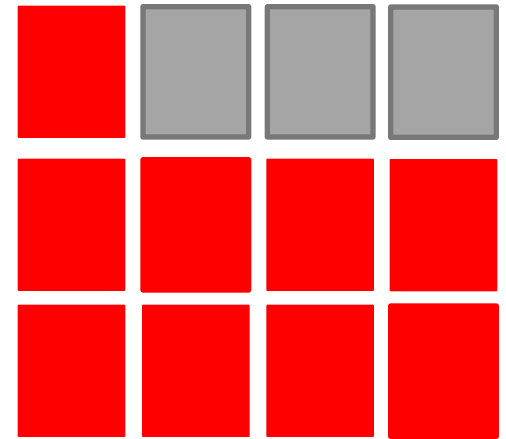
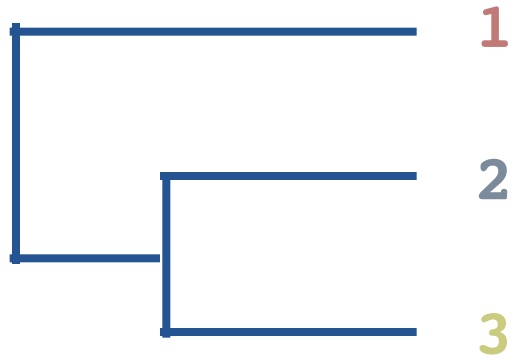


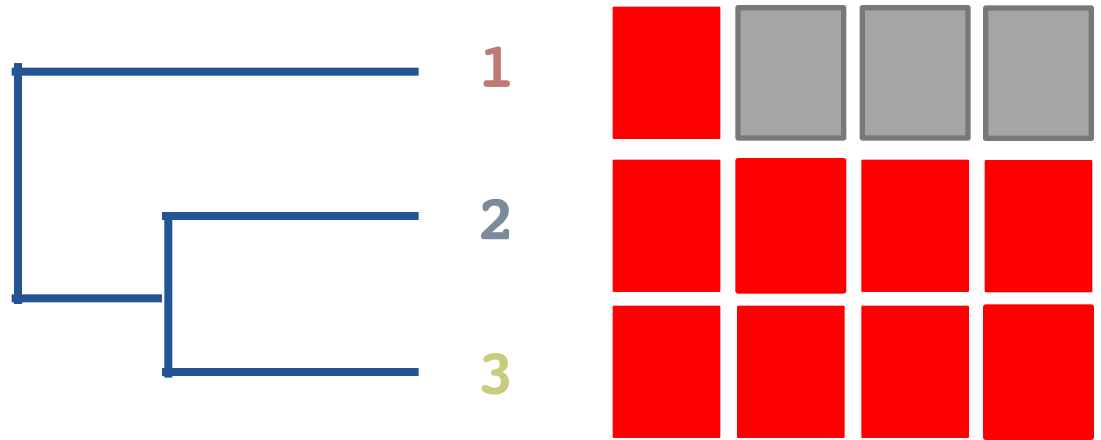
Sequence Comparison

1 AATCGCTTTACGACCAG...
2 AATGGCTTTATGACAAG...
3 AATCGCTTTATGACAAG...
 * * *



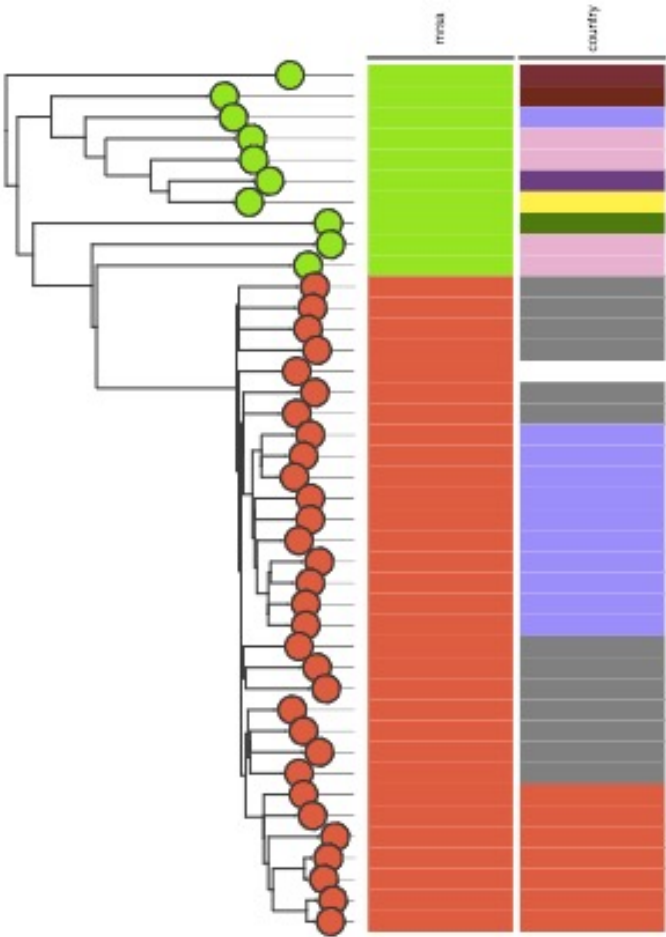




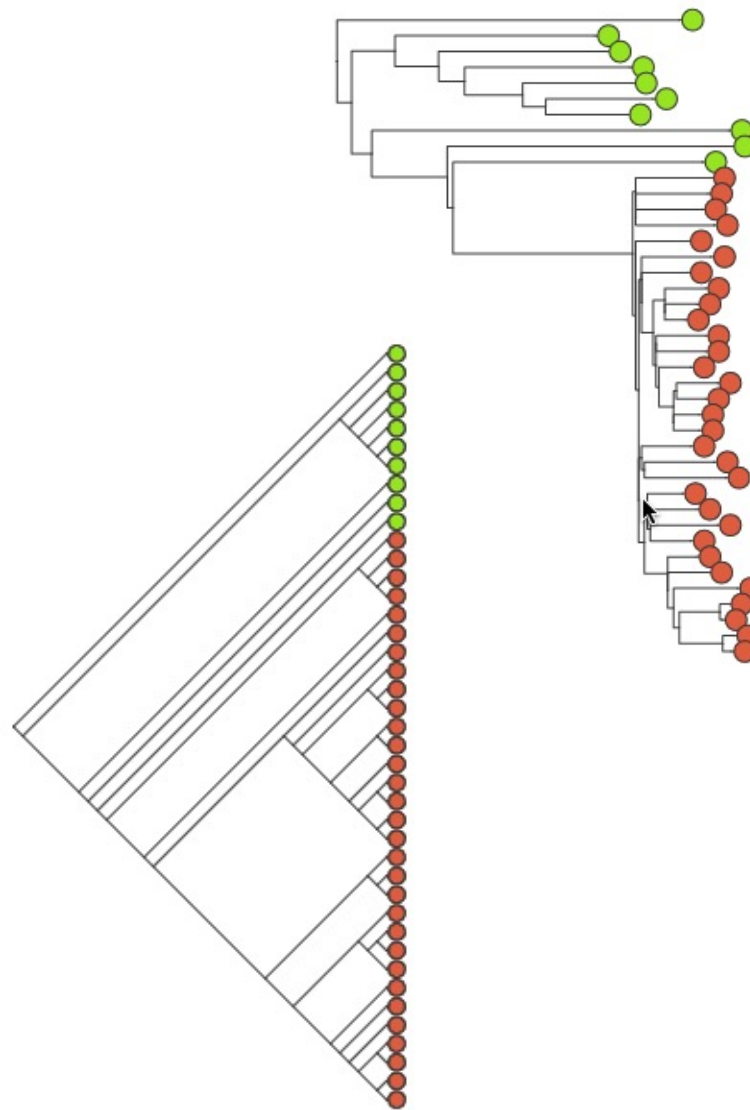
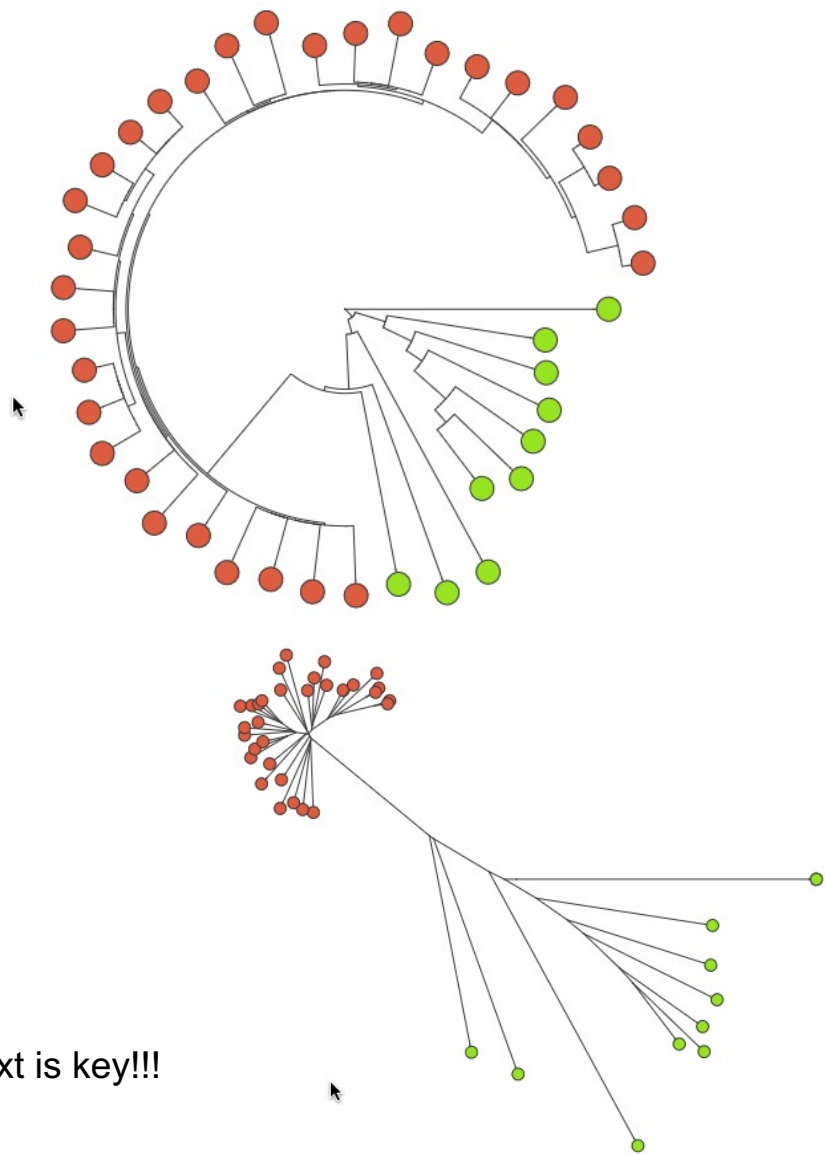


Risk

Genomic Epidemiology. Delivering assessment of risk



Different views of same tree

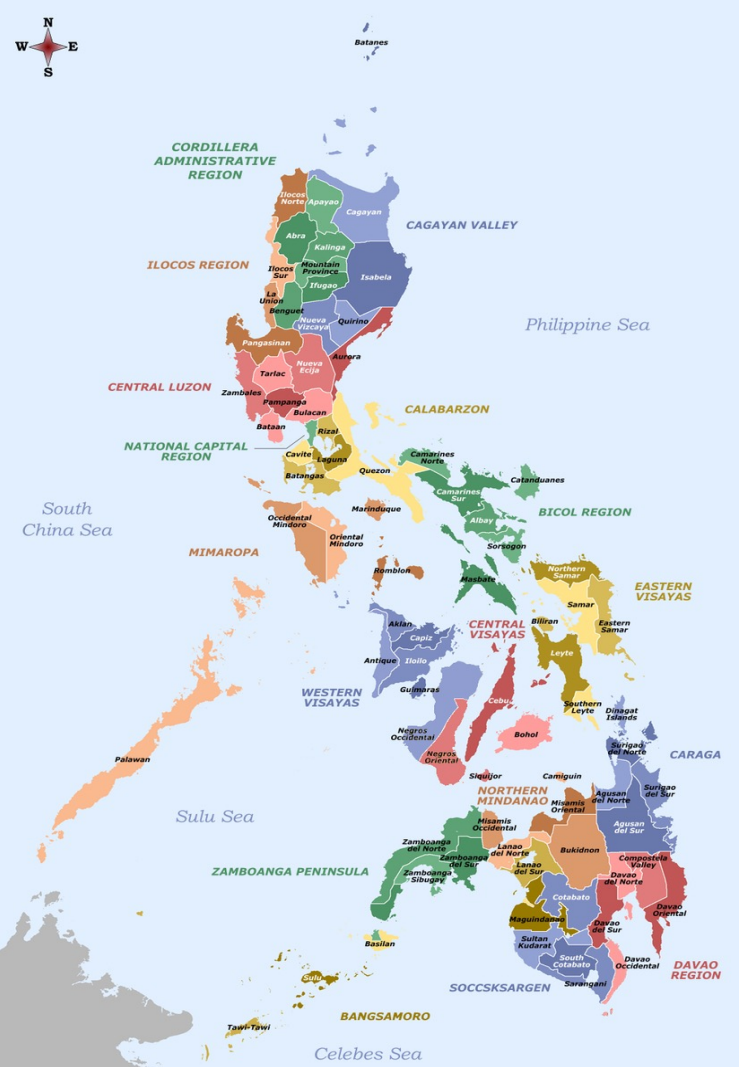


Context is key!!!

Two Applications:

- 1) Antimicrobial Resistance
- 2) COVID-19

Philippines AMR Surveillance Programme



Phillipines
Celia Carlos



30 year AMR surveillance

Phenotypic

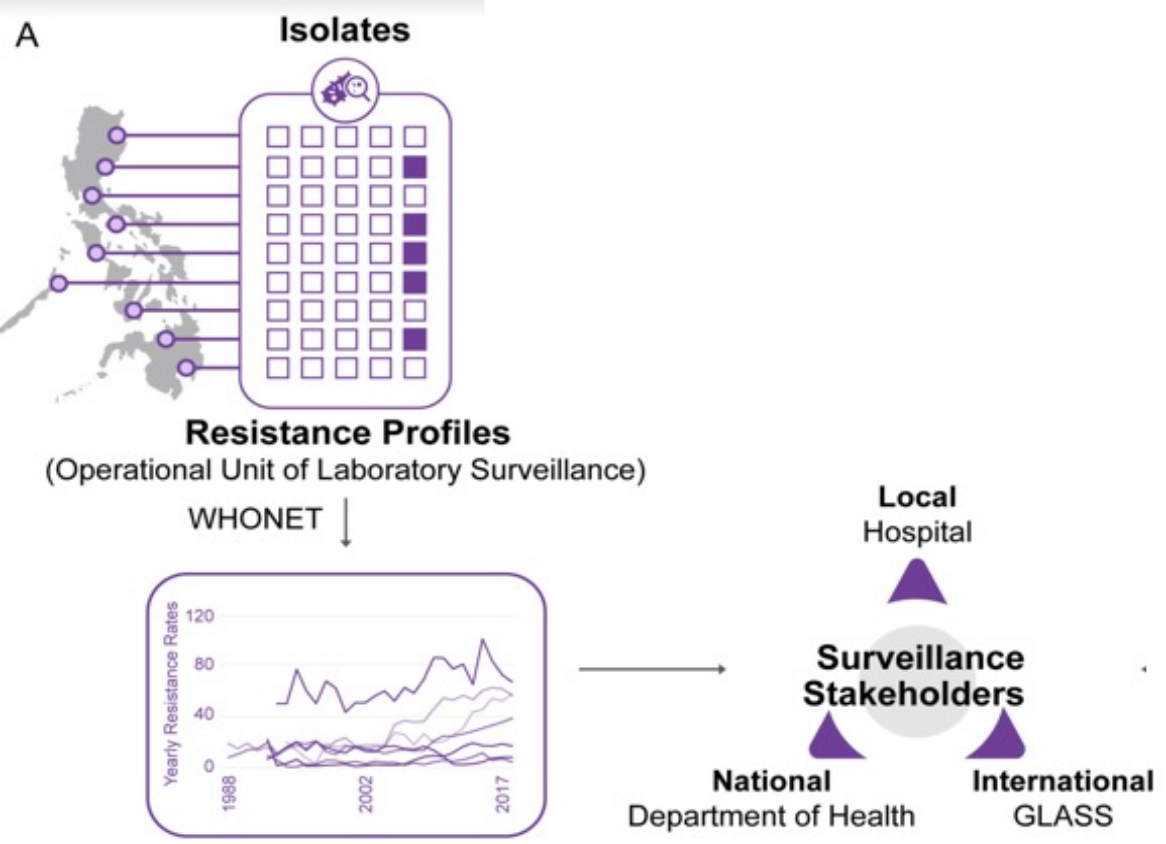
Sentinel hospitals

WHO Priority pathogens

Annual report for bug-drug combinations



Enhancing National AMR Programmes through Genomics : See and Sequence



Phillipines
Celia Carlos

Argimon S *et al* (2019) Biorxiv

Enhancing National AMR Programmes through Genomics : See and Sequence

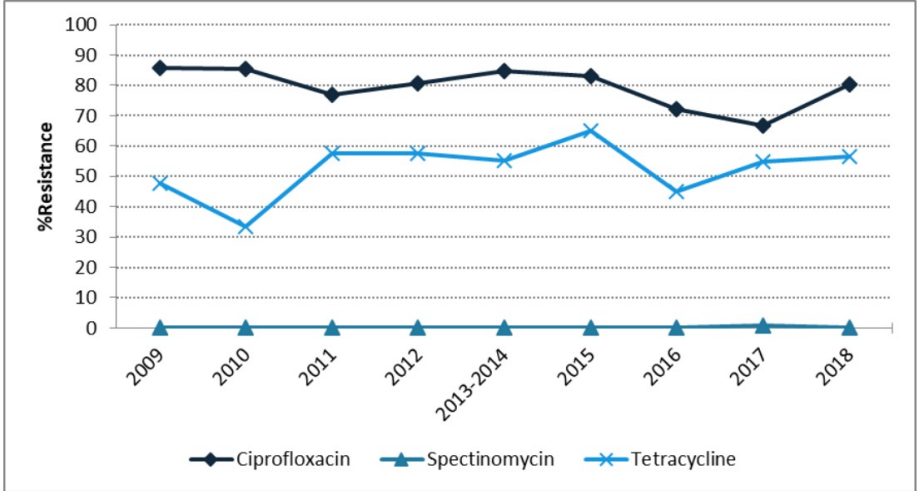
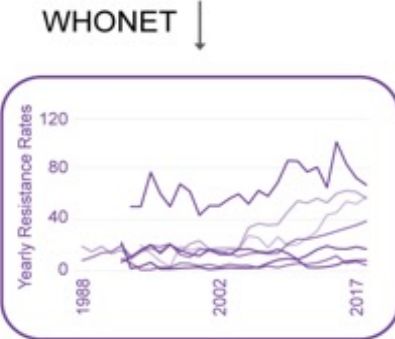
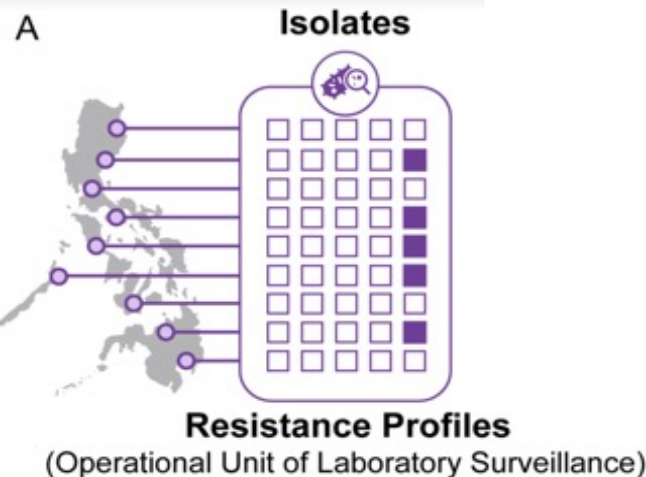


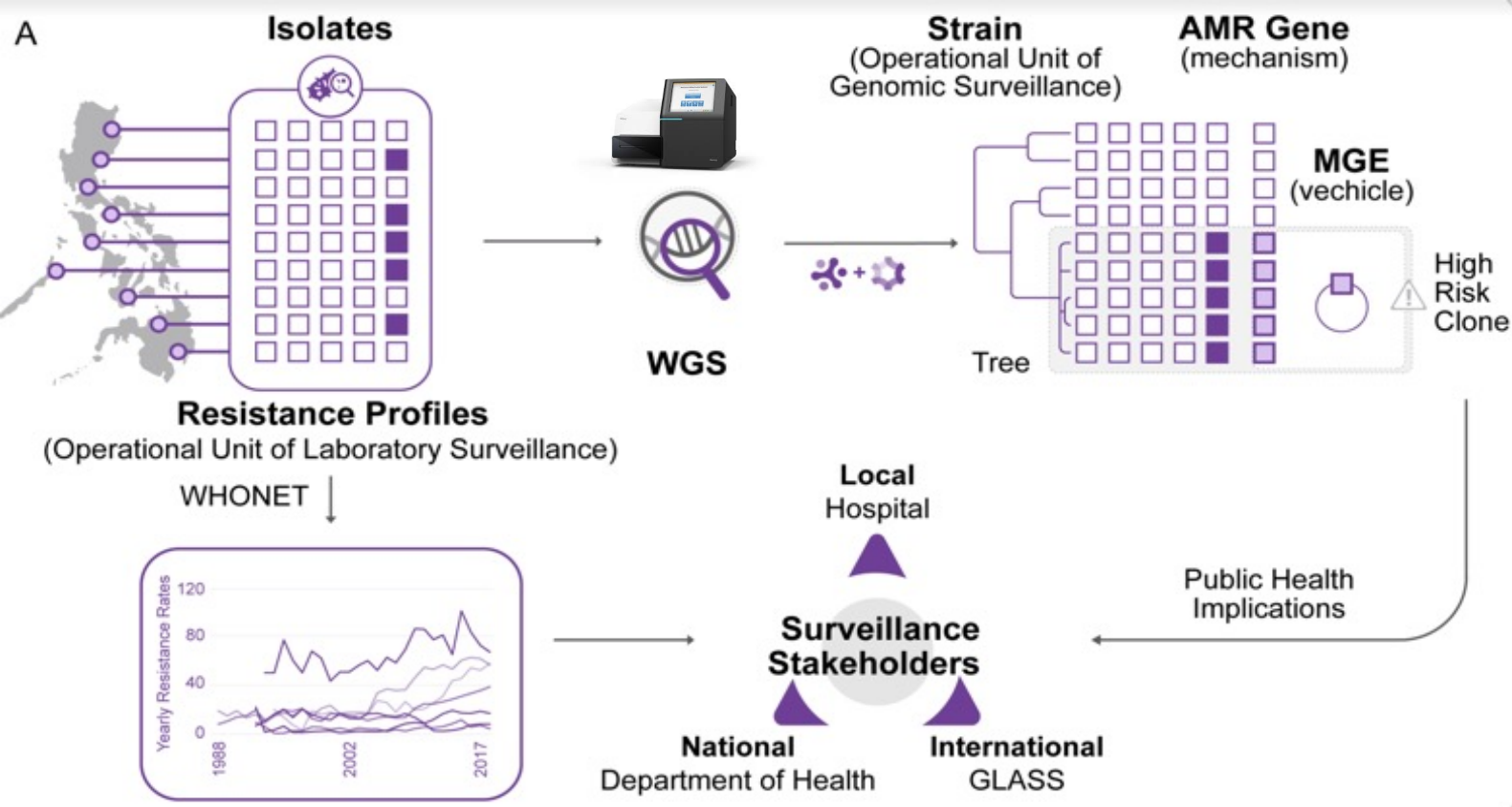
Figure 26. Yearly resistance rates of *Neisseria gonorrhoeae*, DOH ARSP, 2009-2018



Philippines
Celia Carlos

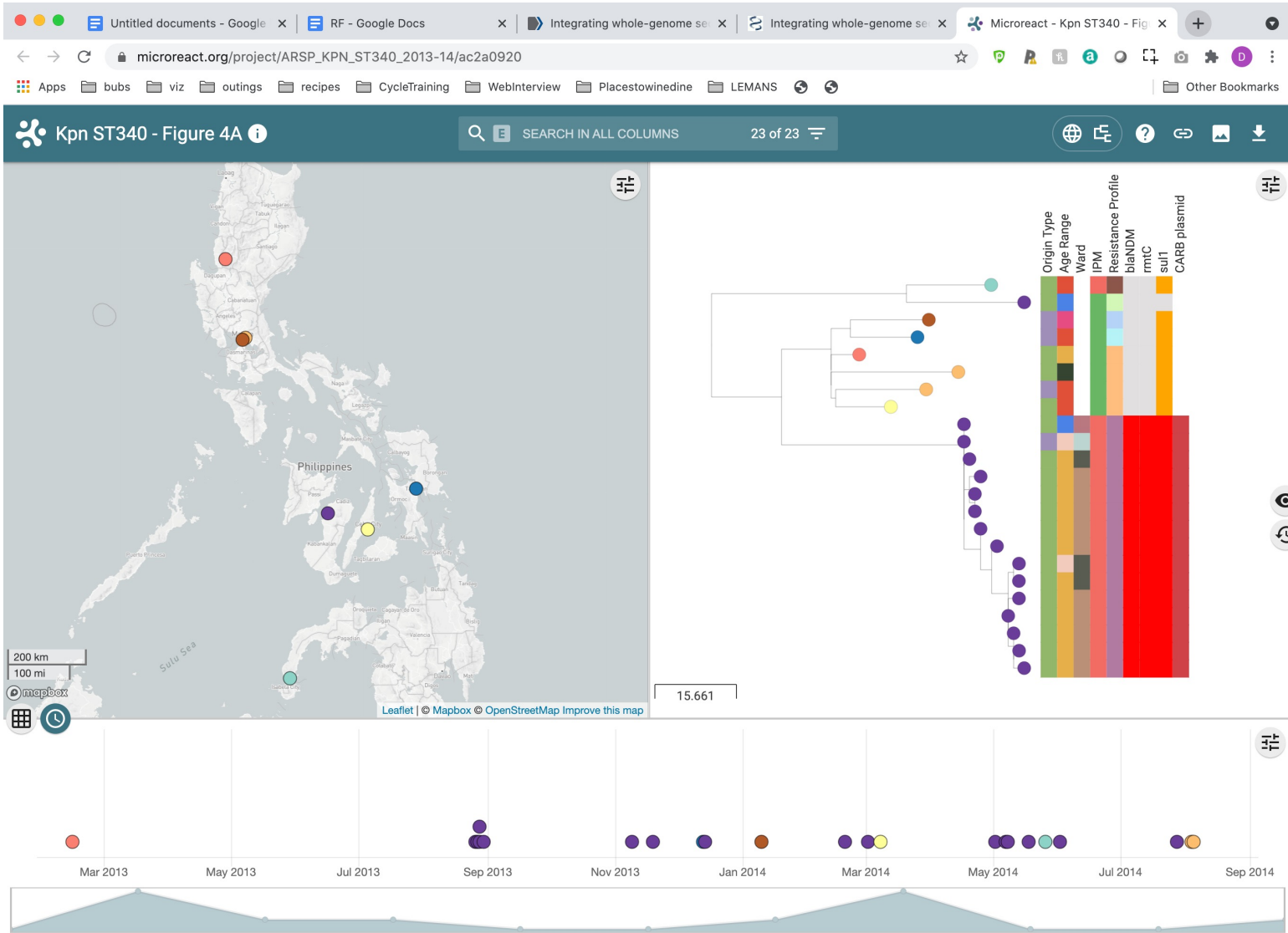
Argimon S *et al* (2020) Nature comms

Enhancing National AMR Programmes through Genomics : See and Sequence



Phillipines
Celia Carlos

Argimon S *et al* (2020) Nature comms



Argimon S *et al* (2020) Nature comms

Scaling to network of networks



Leaders of National Research Units



Colombia
Pilar Godoy



Nigeria
Iruka Okeke



India
Ravi Kumar



Philippines
Celia Carlos



SUPPORTED BY

NIHR | National Institute
for Health Research

Scalable technical support packages for capacity building

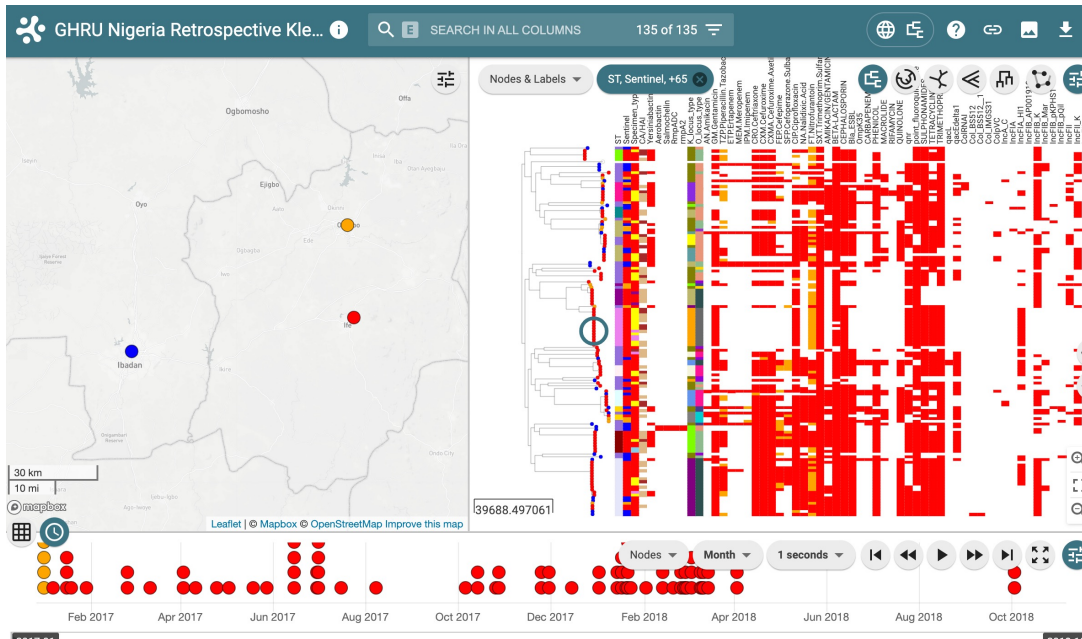
- Laboratory set up, EQA/IQA
- Data analysis and interpretation
- Training for operational excellence
- South-South capacity building

(Details here: <https://ghru.pathogensurveillance.net/>)

BMJ Glob Health. 2020 Nov;5(11):e002244.

Clones and Clusters of Antimicrobial-Resistant Klebsiella from Southwestern Nigeria

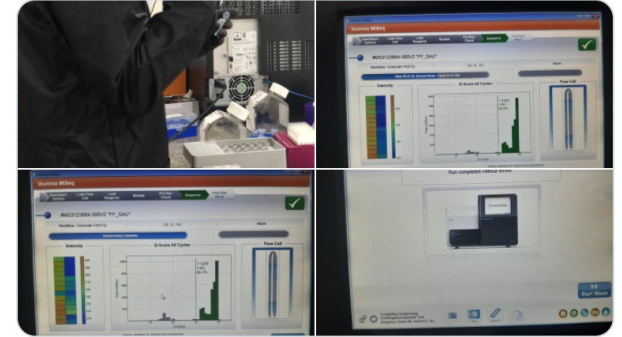
Afolayan et al Biorxiv



Ayorinde Afolayan Retweeted



Anderson Oaikhena @anderson_ose · May 28
Excited to see the output of my first @illumina #miseq run, after initial training by @cake_ray & colleagues @TheCGPS @ACSCEvents in #2018 amidst countless procurement and set-up delays. Took ~3 yrs to achieve this key deliverable of our @NIHR funded @GHRUamr grant. @iruka_okeke



6

13

37



Nigeria
Iruka Okeke



<https://microreact.org/project/GHRUNigeriaKpneumoniae>

Bottlenecks

Data and data tools

Linking genomics to epidemiology

Rapid Interpretation

As well as political / supply chains expense etc..

COVID-19

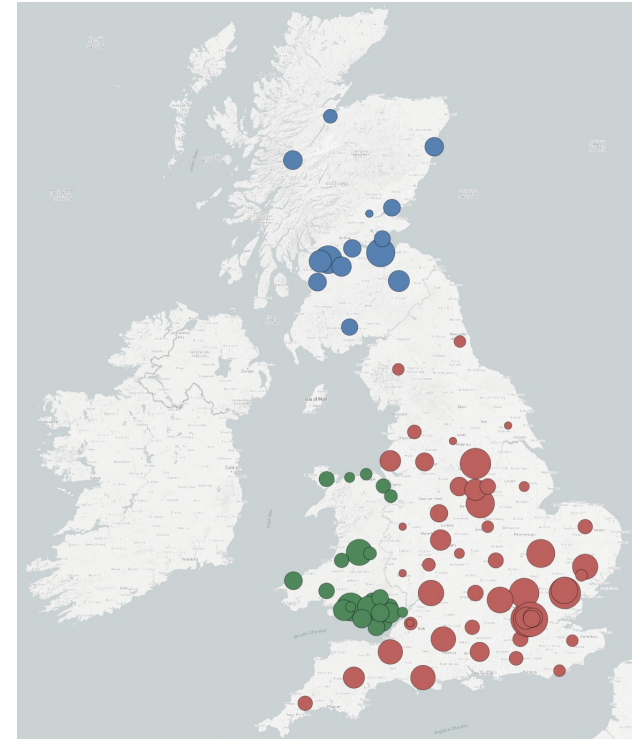
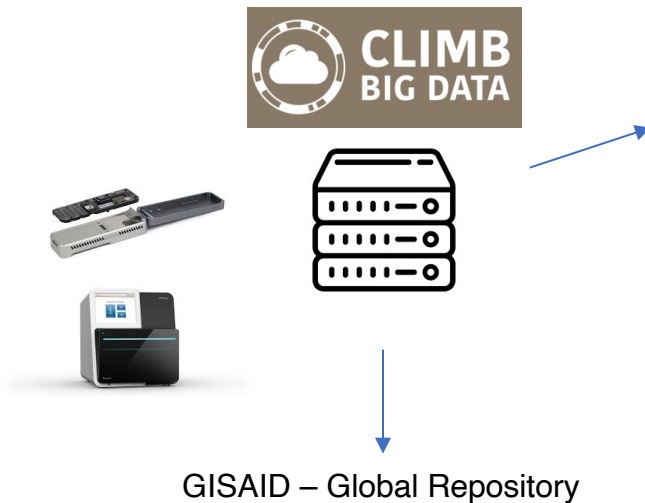
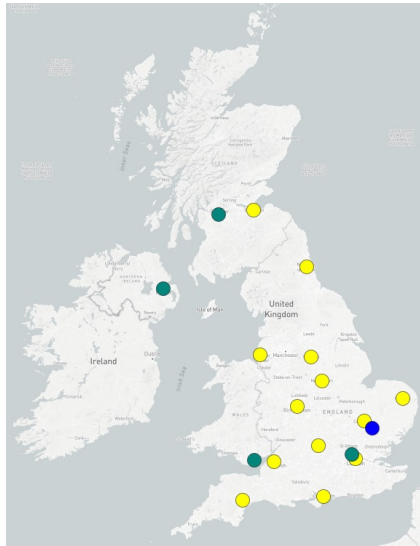


COVID-19 GENOMICS UK CONSORTIUM

The current COVID-19 pandemic, caused by the SARS-CoV-2 virus, represents a major threat to health.

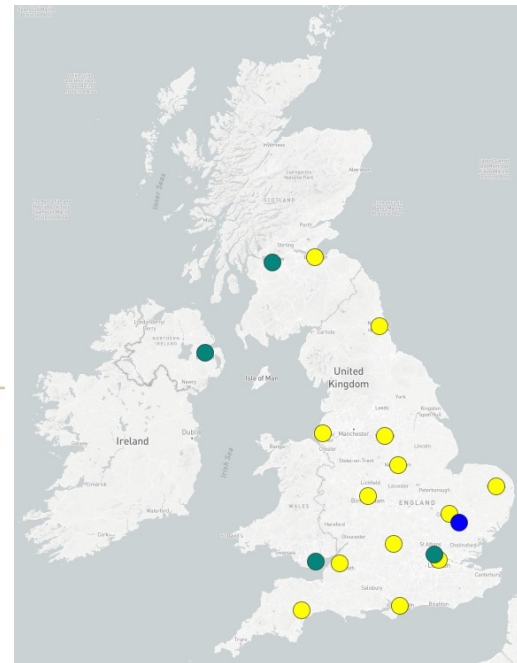
The COVID-19 Genomics UK (COG-UK) consortium was created to deliver large-scale and rapid whole-genome virus sequencing to local NHS centres and the UK government.

<https://www.cogconsortium.uk/>



UK Research
and Innovation

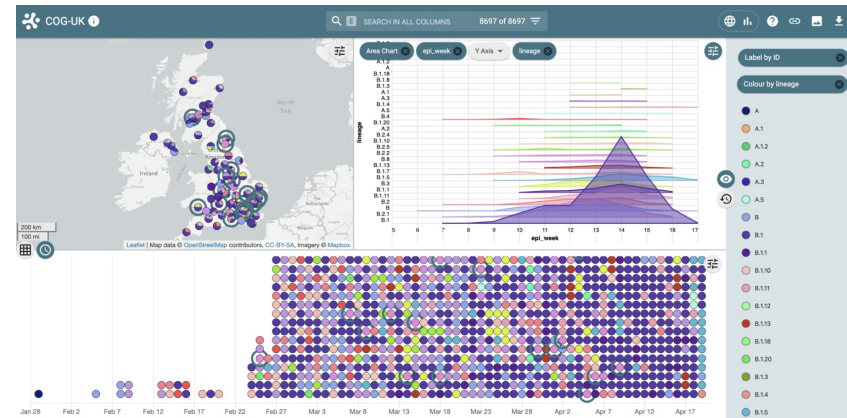
COVID Genomics Consortium UK



Huge Collaborative effort



COVID-19
GENOMICS
UK CONSORTIUM



Open access and data sharing

Data Linkage within NHS and PHX

Decentralised sequencing

Linkage to mobile data

Linkage to contact tracing etc.

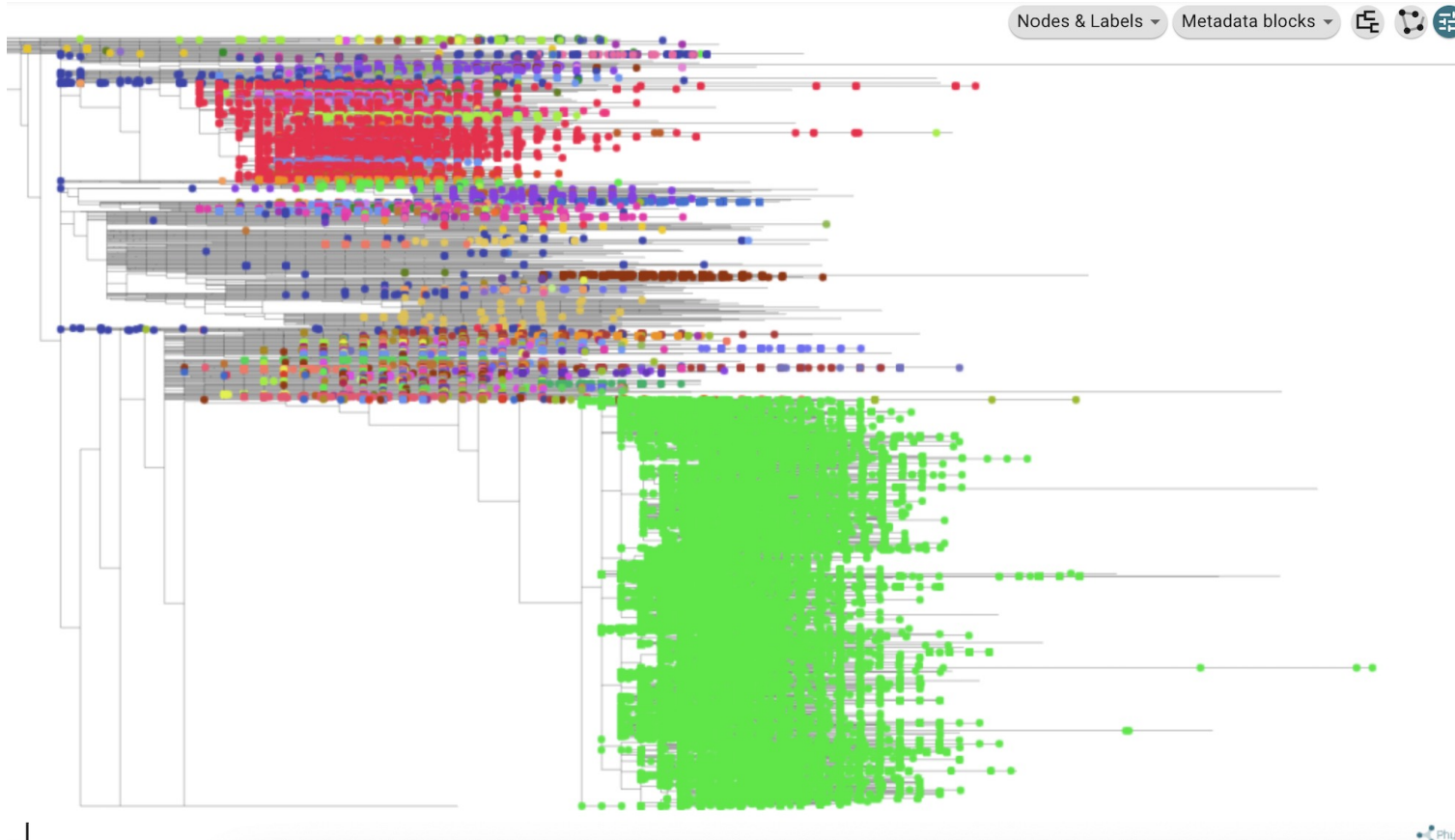
Identification and monitoring of lineages - Pangolin

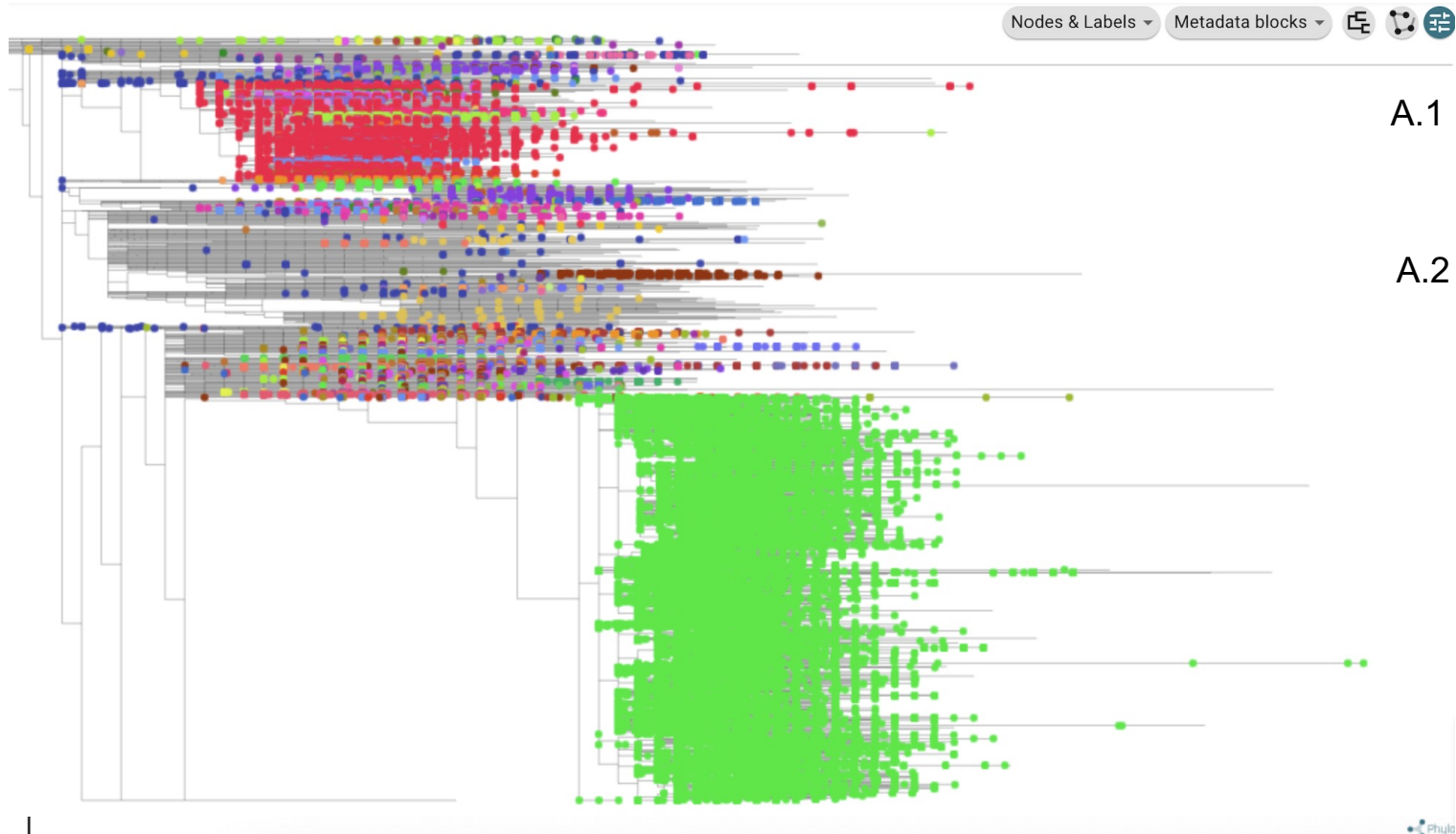
- monitor removal of interventions



COVID-19 GENOMICS UK CONSORTIUM

Tree of 532957 genomes





A.1

A.2.1

A.2

A.2.2

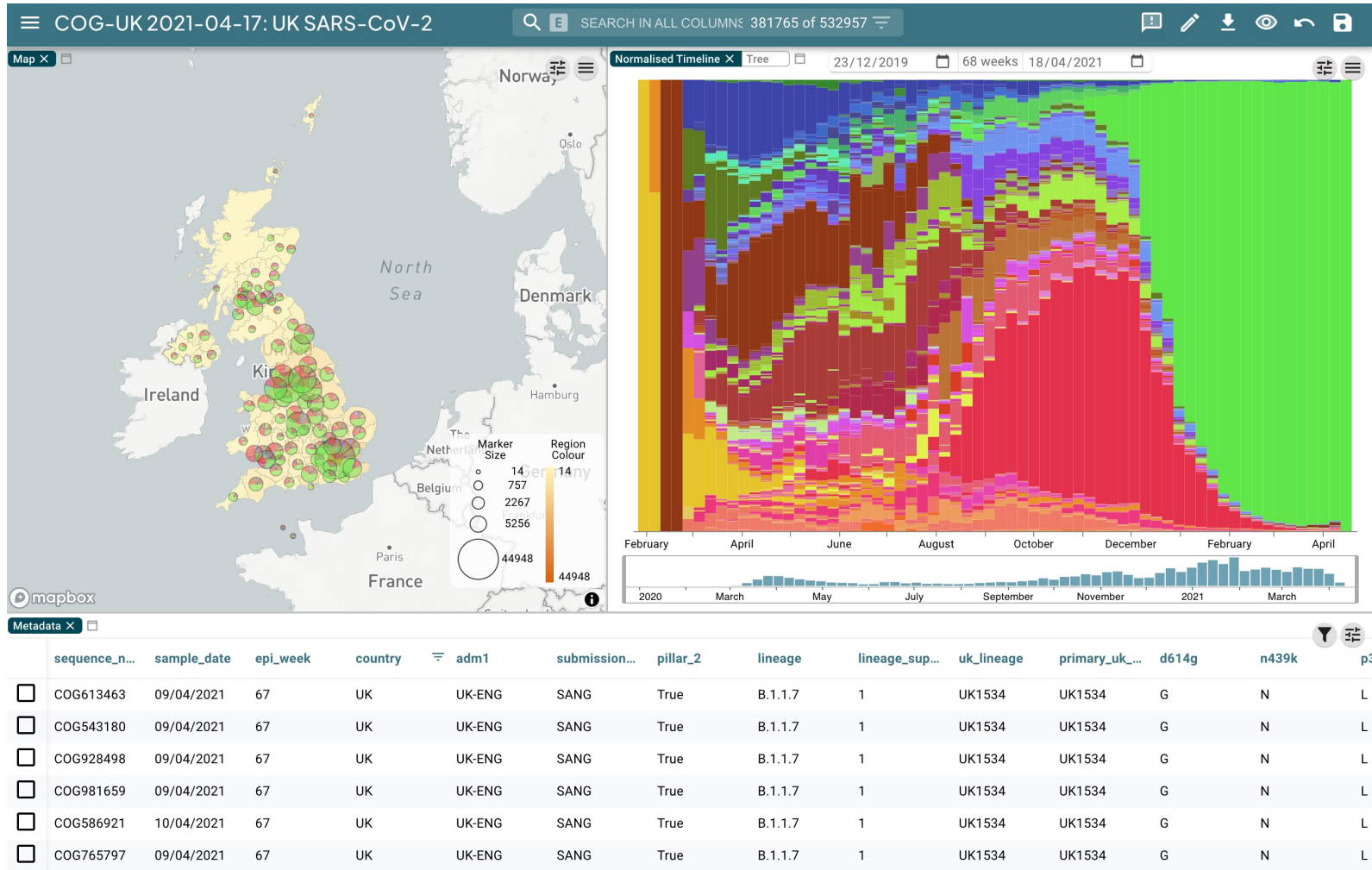
b.1.1.7

Alpha



COVID-19 GENOMICS UK CONSORTIUM

<https://microreact.org/project/cogconsortium>



Bottlenecks

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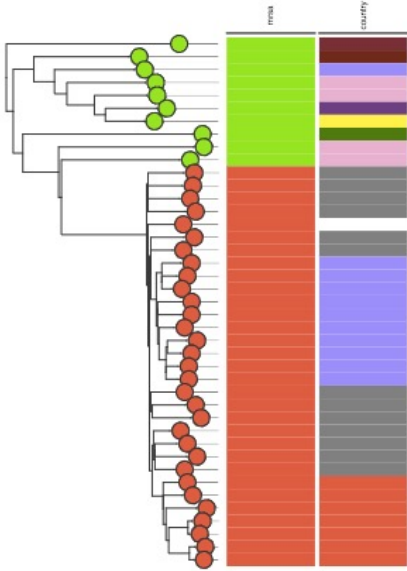
Pivoting Learnings

Horizontal data processes

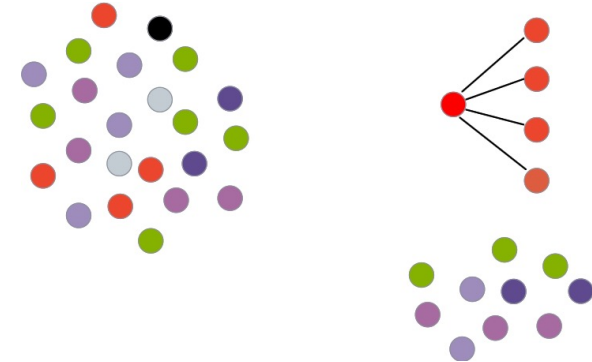
- Trees
- Maps
- Time
- Epi Variables

Vertical application

- SARS-CoV-2
- AMR



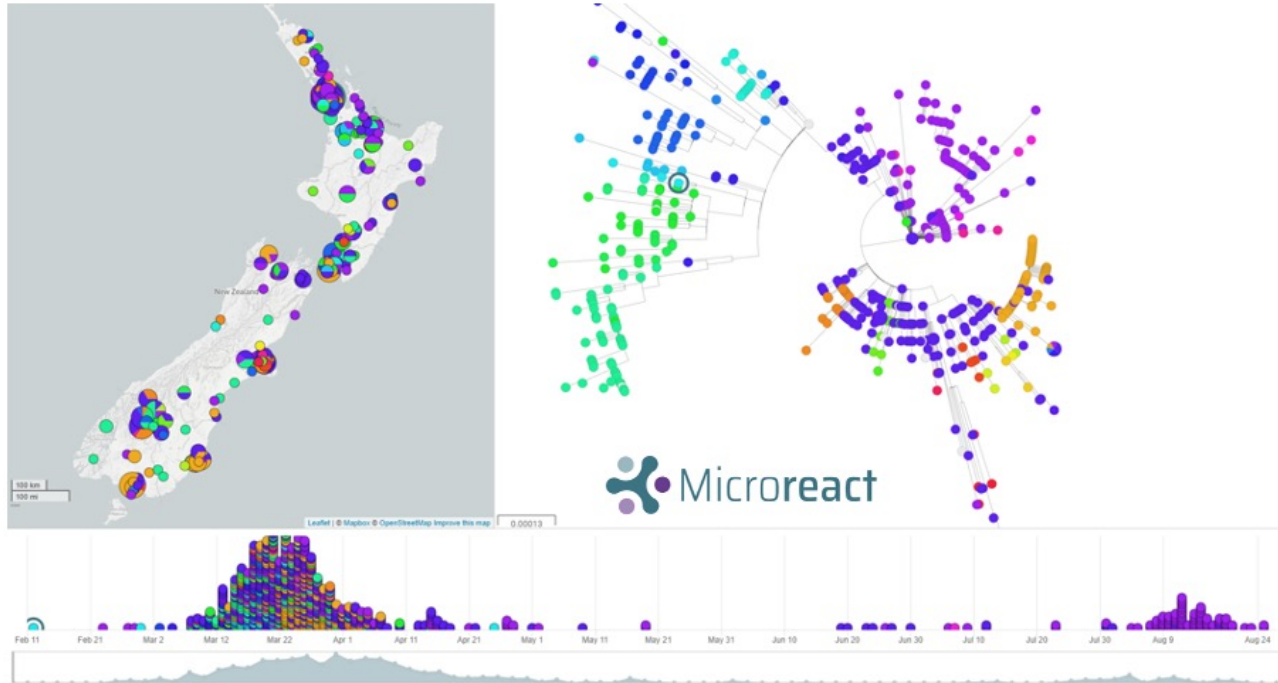
Genomic Data Landscape



	COVID	AMR
Type	Viral (SARS-CoV-2)	Bacterial / Fungal ...
Clone / lineage	Pangolin (b.1.1.7 etc)	MLST / cgMLST / Genotypi etc etc..
Risk markers	mutations of note	AMR determinants / genes / SNP. Many more – serotype etc..

Process is conceptually the same - horizontal data processes delivered for vertical organisms

Tools to transform Data into Actionable Insights

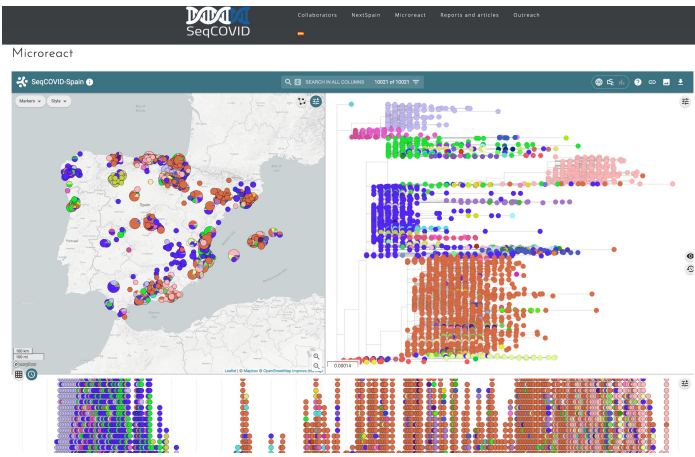
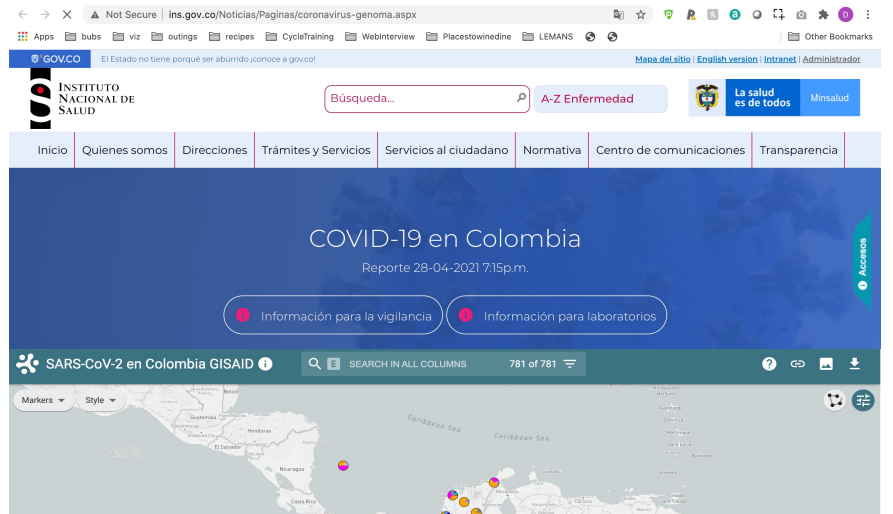
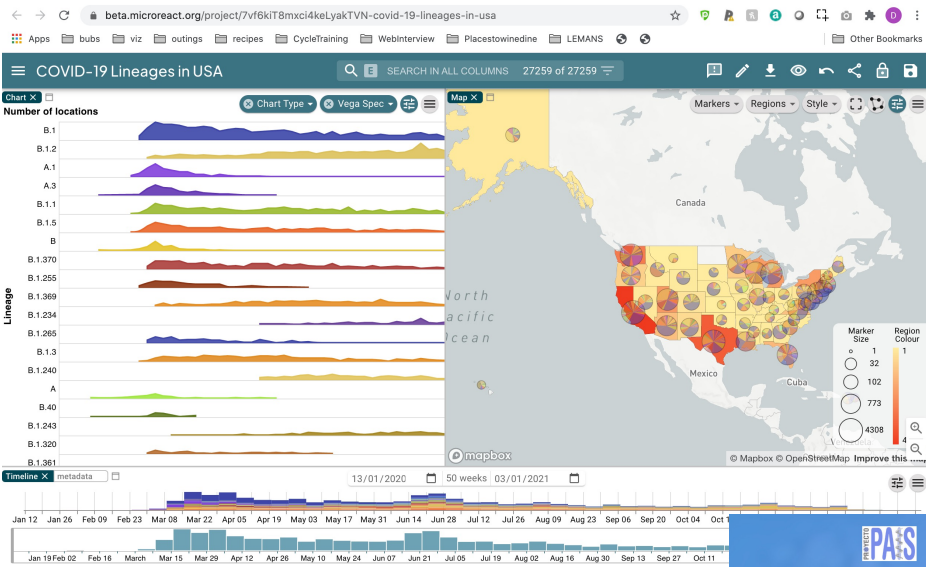


 Microreact

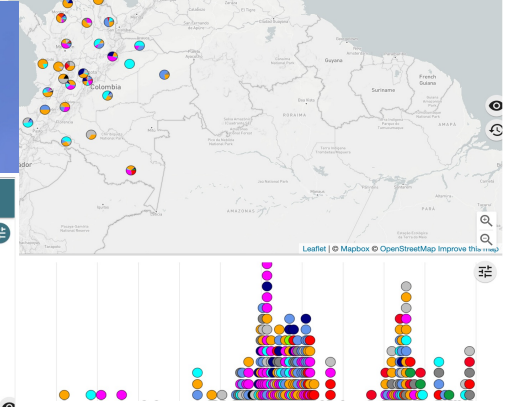
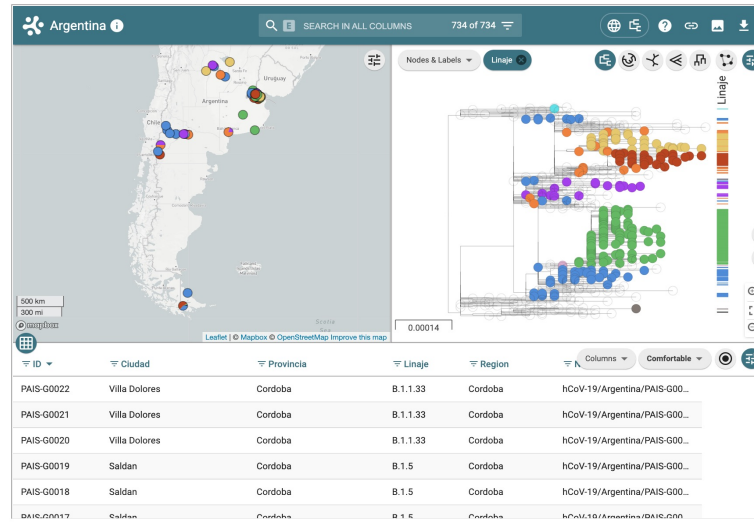
 Epicollect5

 Data-flo





Distribución de linajes en Argentina



Klebsiella pneumoniae

Salmonella Typhi

Priority 1: CRITICAL[#]

Acinetobacter baumannii, carbapenem-resistant

Pseudomonas aeruginosa, carbapenem-resistant

Enterobacteriaceae^{*}, carbapenem-resistant, 3rd generation cephalosporin-resistant

Priority 2: HIGH

Enterococcus faecium, vancomycin-resistant

Staphylococcus aureus, methicillin-resistant, vancomycin intermediate and resistant

Helicobacter pylori, clarithromycin-resistant

Campylobacter, fluoroquinolone-resistant

Salmonella spp., fluoroquinolone-resistant

Neisseria gonorrhoeae, 3rd generation cephalosporin-resistant, fluoroquinolone-resistant

Priority 3: MEDIUM

Streptococcus pneumoniae, penicillin-non-susceptible

Haemophilus influenzae, ampicillin-resistant

Shigella spp., fluoroquinolone-resistant

[#] *Mycobacteria* (including *Mycobacterium tuberculosis*, the cause of human tuberculosis), was not subjected to review for inclusion in this prioritization exercise as it is already a globally established priority for which innovative new treatments are urgently needed.

^{*} Enterobacteriaceae include: *Klebsiella pneumoniae*, *Escherichia coli*, *Enterobacter spp.*, *Serratia spp.*, *Proteus spp.*, and *Providencia spp.*, *Morganella spp.*

Pathways to Implementation



Global Action Plan
|
National Action Plans
|
Local delivery of value



Pathways to Implementation



Global Action Plan
|
National Action Plans
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Local delivery of value

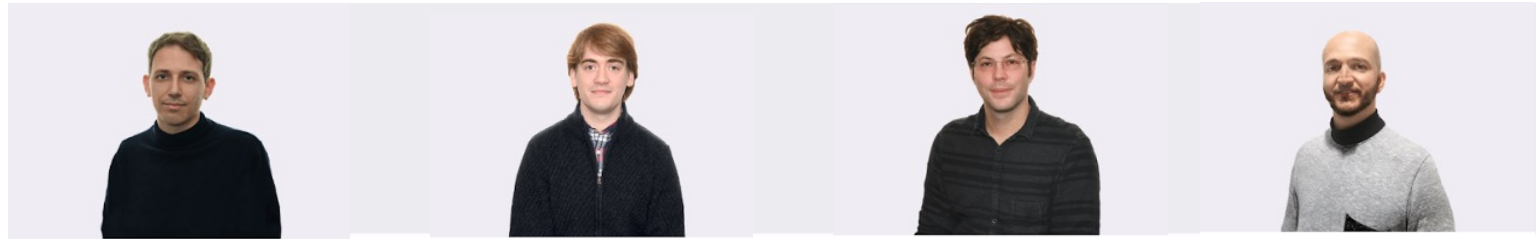


**Enhanced momentum
around COVID-19 MUST
be harnessed**

Team



Engineering



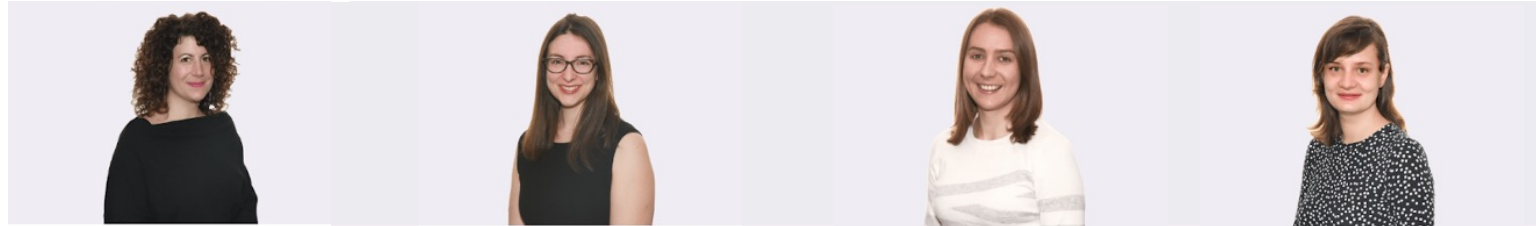
Dr. Khalil Abudahab
Principal Software Developer

Ben Taylor
Principal Software Developer

Dr. Corin Yeats
Computational Biologist

Mirko Menegazzo
Epicollect Lead

Science



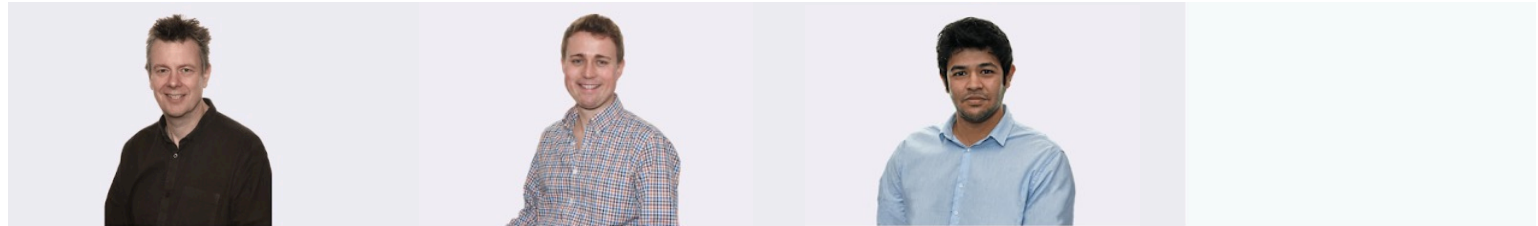
Dr. Silvia Argimón
Genomic Epidemiologist

Dr. Nicole Wheeler
Postdoctoral Fellow - Machine Learning

Dr. Sophia David
Postdoctoral Fellow - Epidemiology

Dr. Monica Abrudan
Postdoctoral Fellow - Data Modelling

Implementation



Dr. Anthony Underwood
Bioinformatics Implementation Manager

Harry Harste
Finance Implementation Manager

Mihir Kekre
Operations Lead - Next Generation

<https://pathogensurveillance.net>