

# Genomic Surveillance of antimicrobial resistance

## local and international value

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WHO Collaborating Centre  
on Genomic Surveillance  
of Antimicrobial Resistance

Thank you Pilar and Marcelo



WHO Collaborating Centre  
on Genomic Surveillance  
of Antimicrobial Resistance

Thank you Pilar and Marcelo **and Carmem!!**



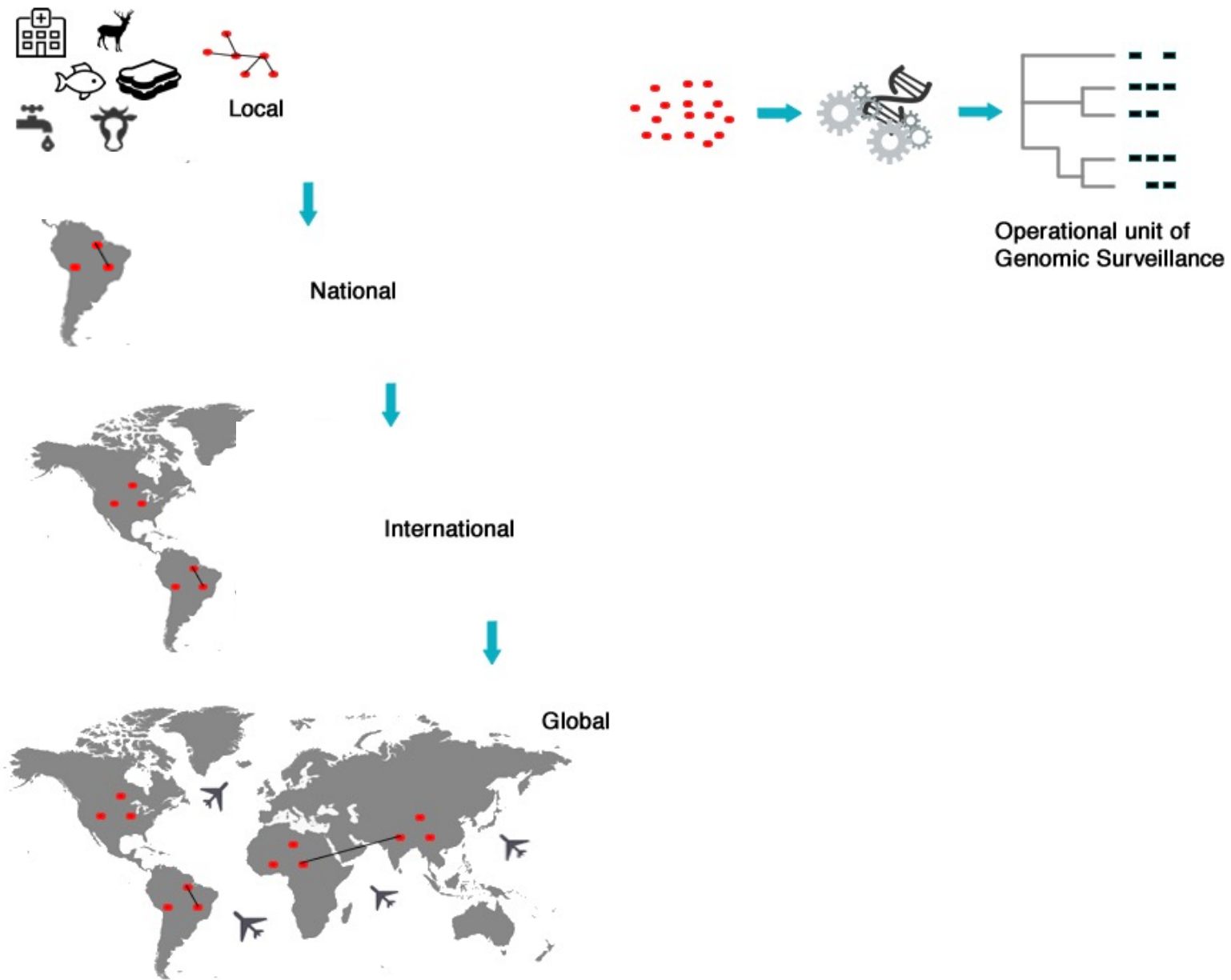
WHO Collaborating Centre  
on Genomic Surveillance  
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Thank you Pilar and Marcelo **and Carmem!!**  
**And John!!**

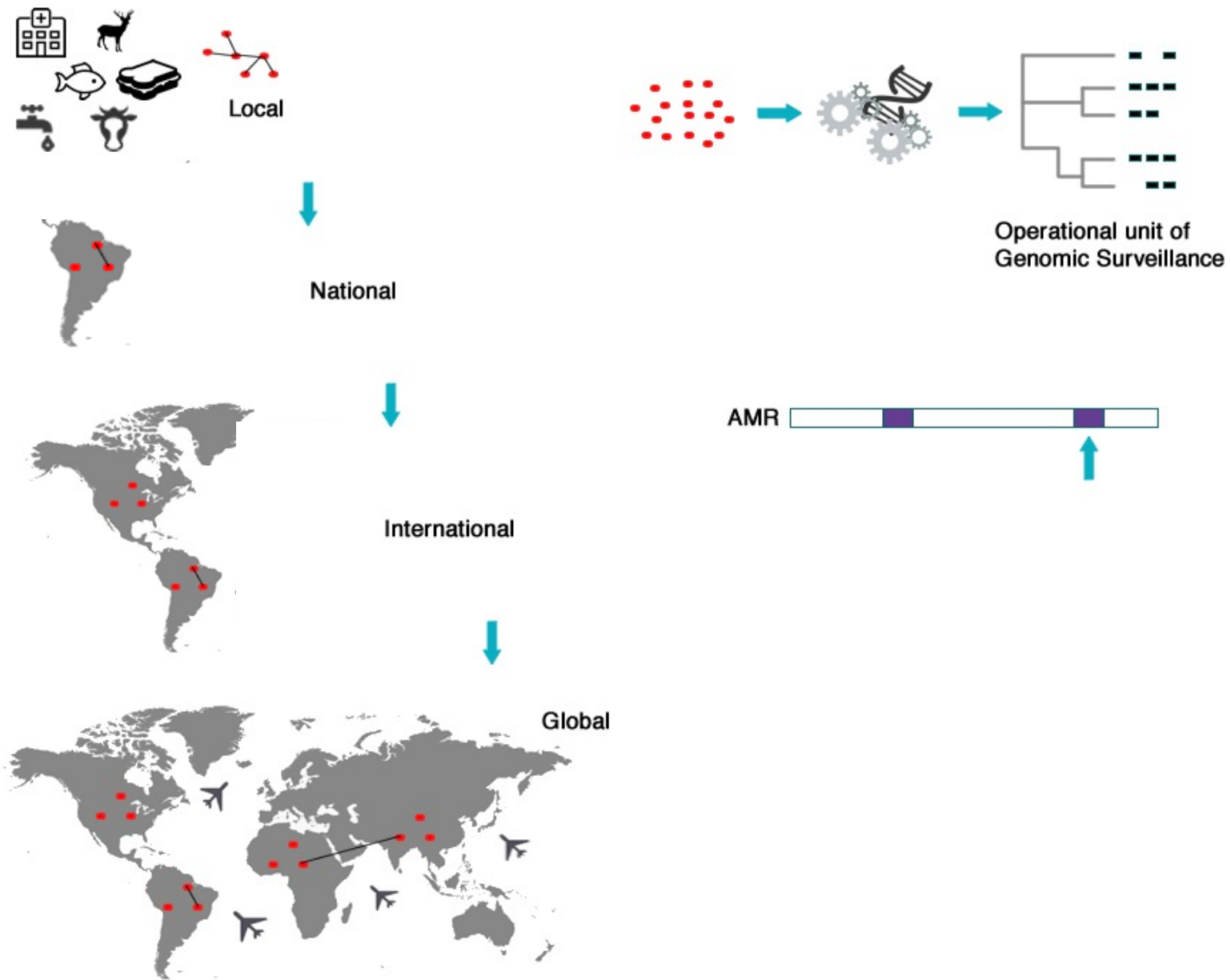
# Genomic Surveillance - Data Scales and challenges



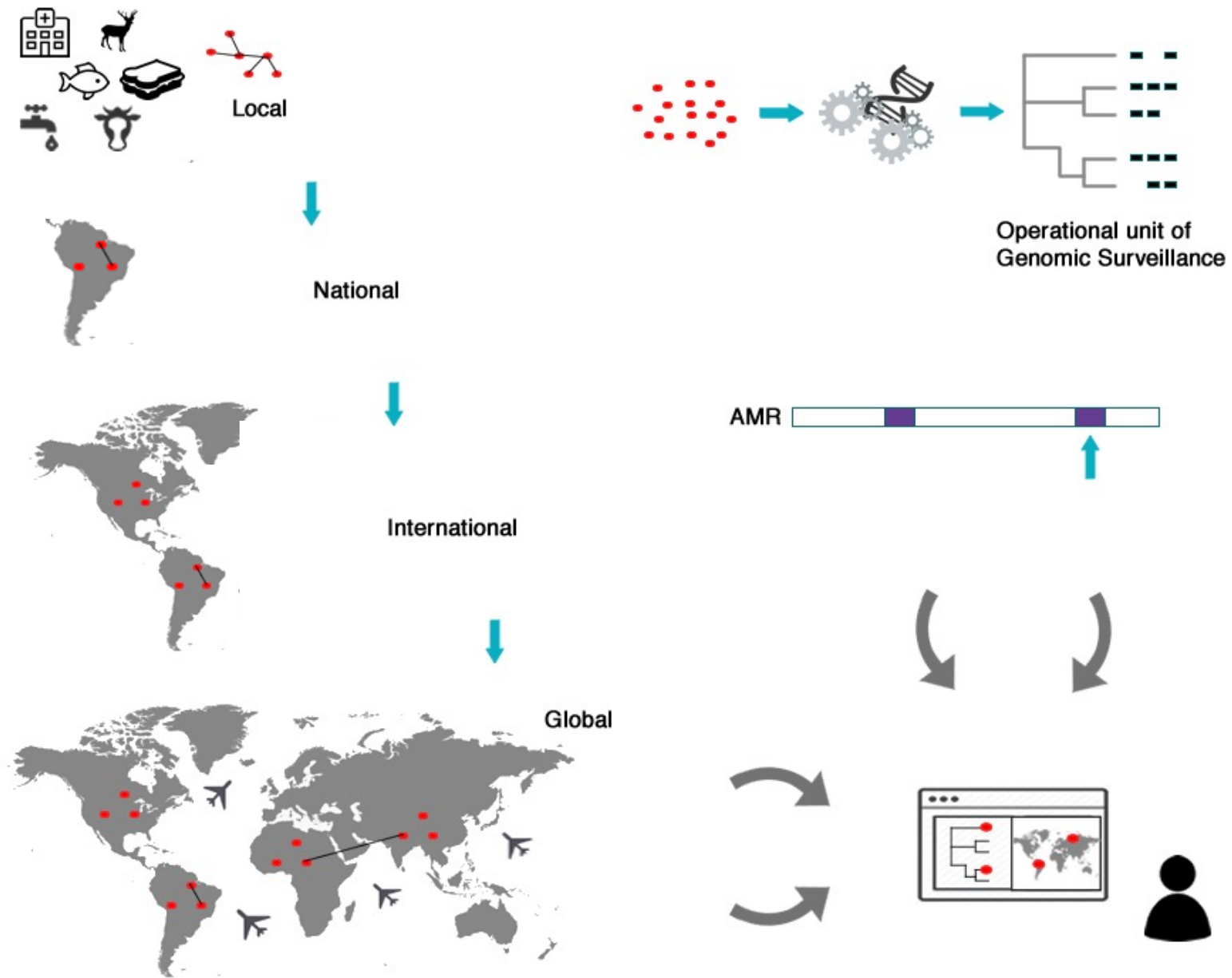
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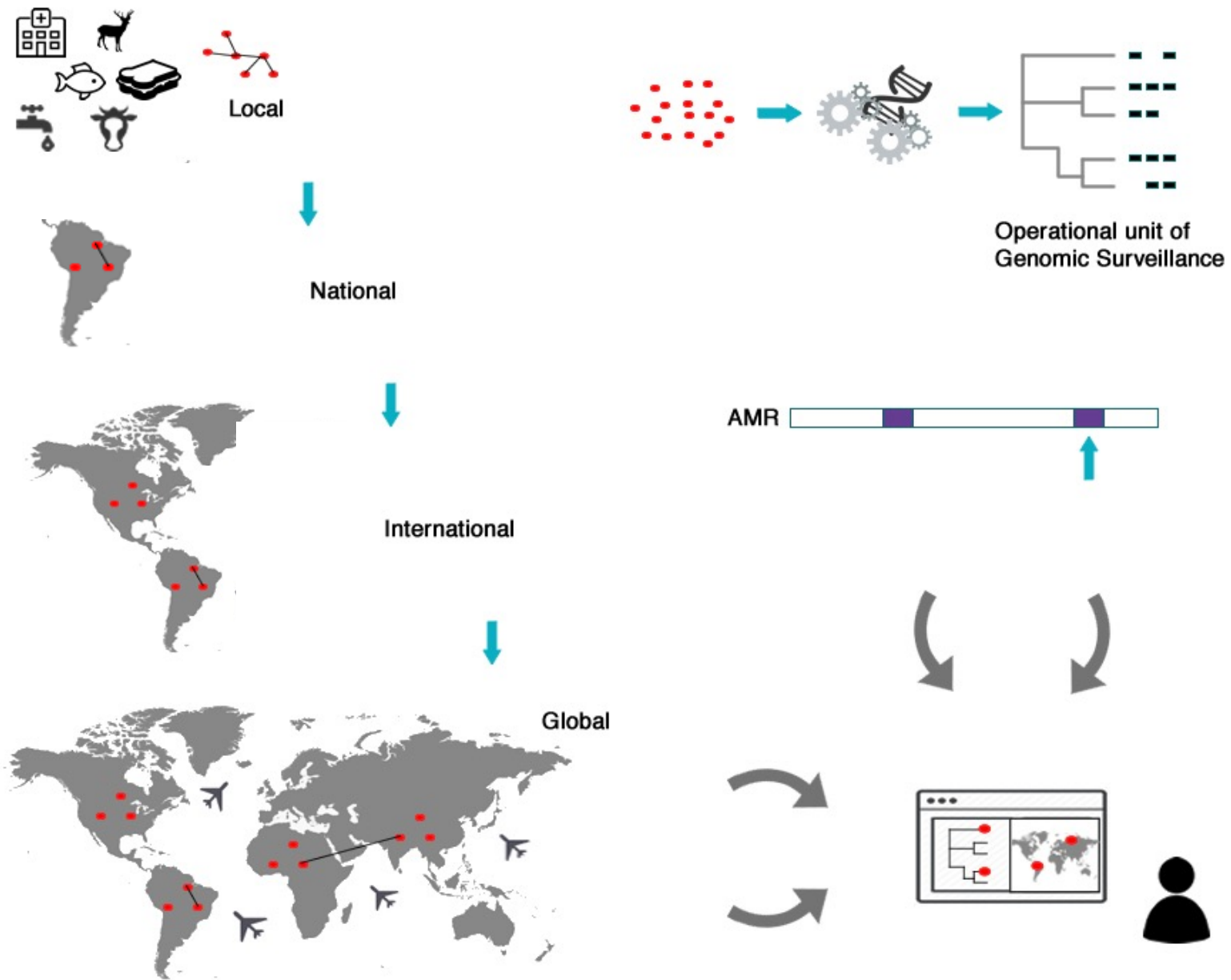


# Genomic Surveillance - Data Scales and challenges

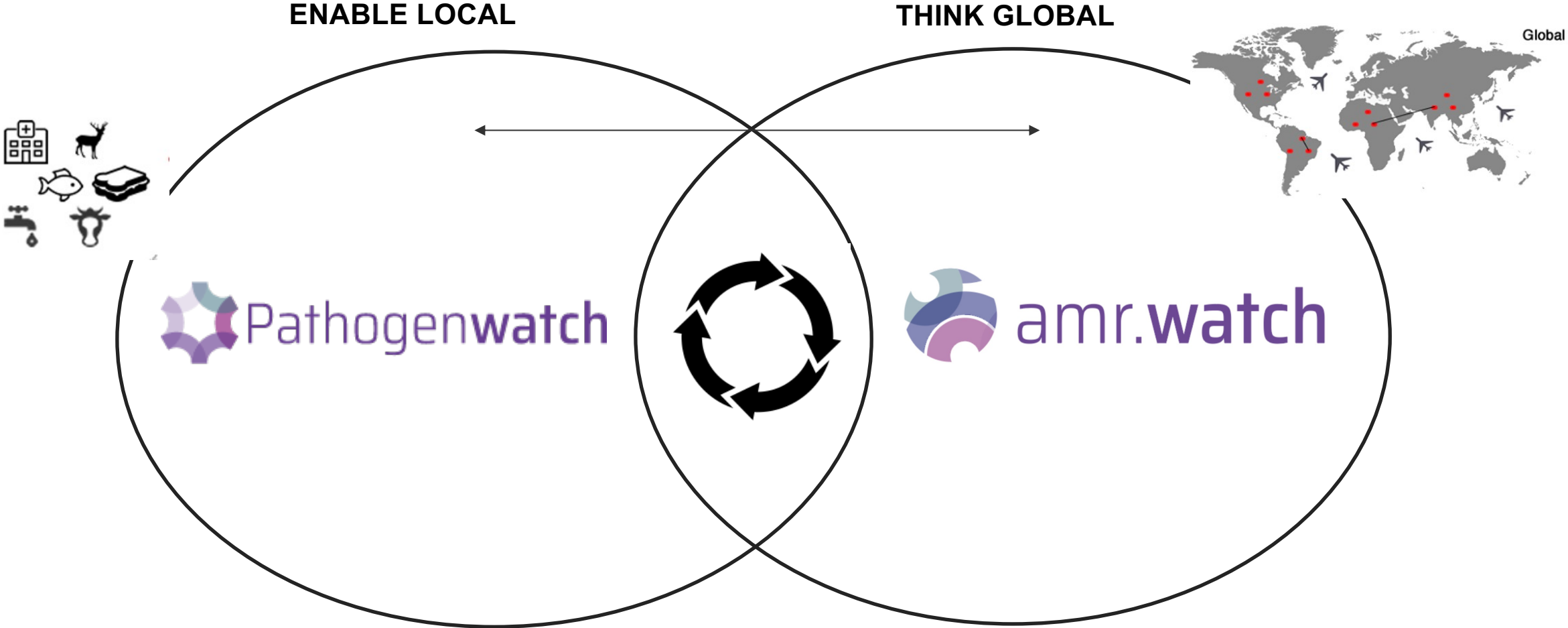




# Genomic Surveillance - Data Scales and challenges



# Genomic Surveillance of Antimicrobial resistance





# Pathogenwatch

# Genomic delivery for Public Health - what do we need?

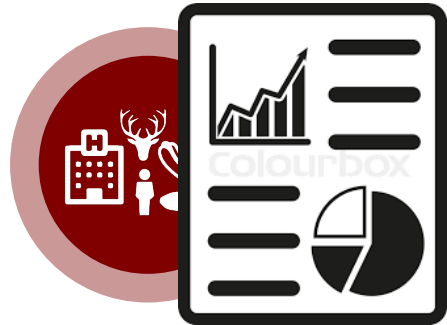
## Single Genome



Markers for local  
decision making

# Genomic delivery for Public Health - what do we need?

Single Genome



Markers for local  
decision making

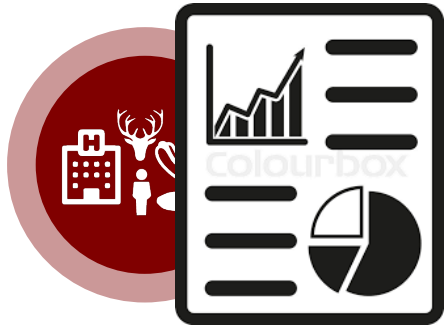
Multiple genomes



Outbreaks  
transmission  
cross-border

# Genomic delivery for Public Health - what do we need?

## Single Genome



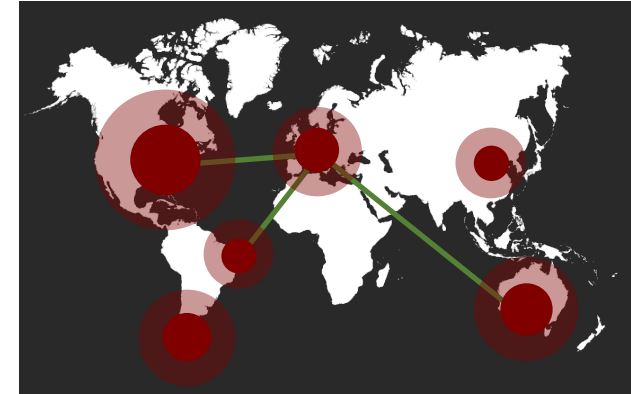
Markers for local  
decision making

## Multiple genomes



Outbreaks  
transmission  
cross-border

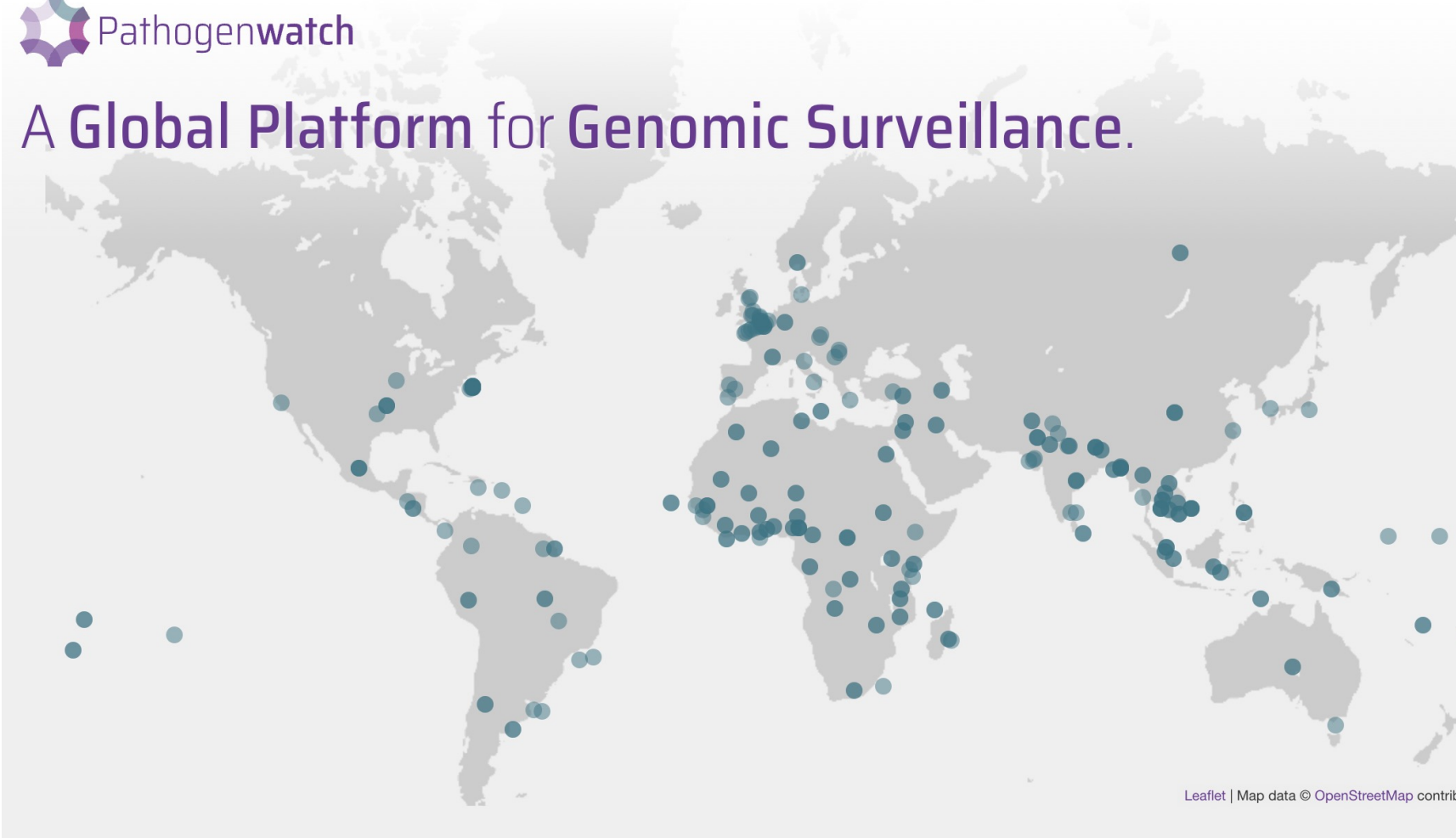
## Population level



Emergence and spread of  
lineages of risk



## A Global Platform for Genomic Surveillance.



No need for specialized bioinformatics

Community analytics


Open system | Data sharing

Delivering local value

# Jump out



## Relevant supported species – all include clustering

<i>Species</i>	<i>Variant / Typing</i>	<i>AMR</i>	<i>Other</i>
<i>Acinetobacter baumannii</i>	<i>MLST /cgMLST</i>	<i>Yes</i>	<i>MGEs</i>
<i>Pseudomonas aeruginosa</i>	<i>MLST /cgMLST</i>	<i>Yes</i>	<i>MGEs</i>
<i>Enterobacteriaceae</i>	<i>MLST /cgMLST</i>	<i>Yes (kleborate)</i>	<i>K/O antigen / serotyping / virulence</i>
<i>Enterococcus faecium</i>	<i>MLST /cgMLST</i>	<i>Yes</i>	<i>MGEs</i>
<i>Staphylococcus aureus</i>	<i>MLST /cgMLST</i>	<i>Yes</i>	<i>MGEs SCCMec</i>
<i>Helicobacter pylori</i>	<i>MLST /cgMLST</i>	<i>Yes</i>	
<i>Campylobacter</i>	<i>MLST /cgMLST</i>	<i>Yes</i>	<i>Setotyping</i>
<i>Salmonella typhi</i>	<i>Genotypi</i>	<i>Yes</i>	<i>serotyping</i> 
<i>Neisseria gonorrhoeae</i>	<i>MLST /cgMLST</i>	<i>Yes</i>	
<i>Streptococcus pneumoniae</i>	<i>GPSC groups</i>	<i>Yes</i>	<i>serotyping</i>
<i>Haemophilus influenzae</i>	<i>MLST</i>	<i>Yes</i>	<i>serotyping</i>
<i>Shigella spp.</i>	<i>MLST /cgMLST</i>	<i>Yes</i>	<i>coming</i>

Also fungal  
/ viral  
Eg  
SARS-CoV2  
C.auris



WHO Priority for new Abx



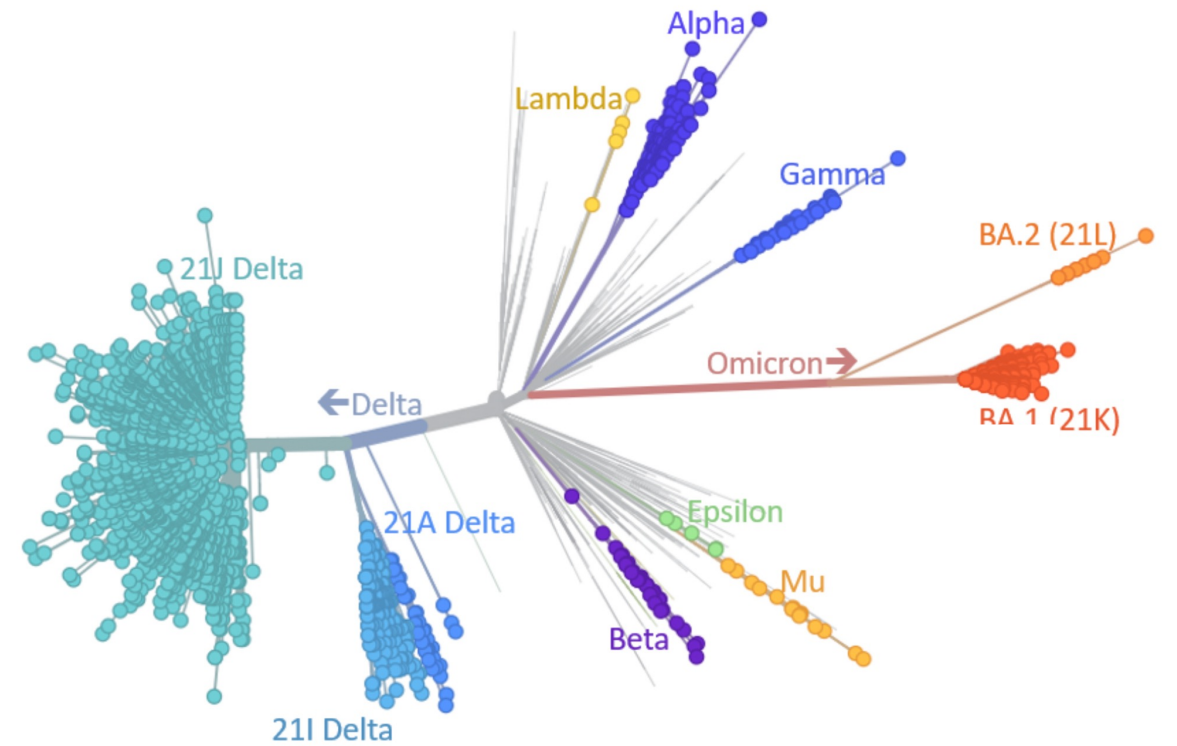
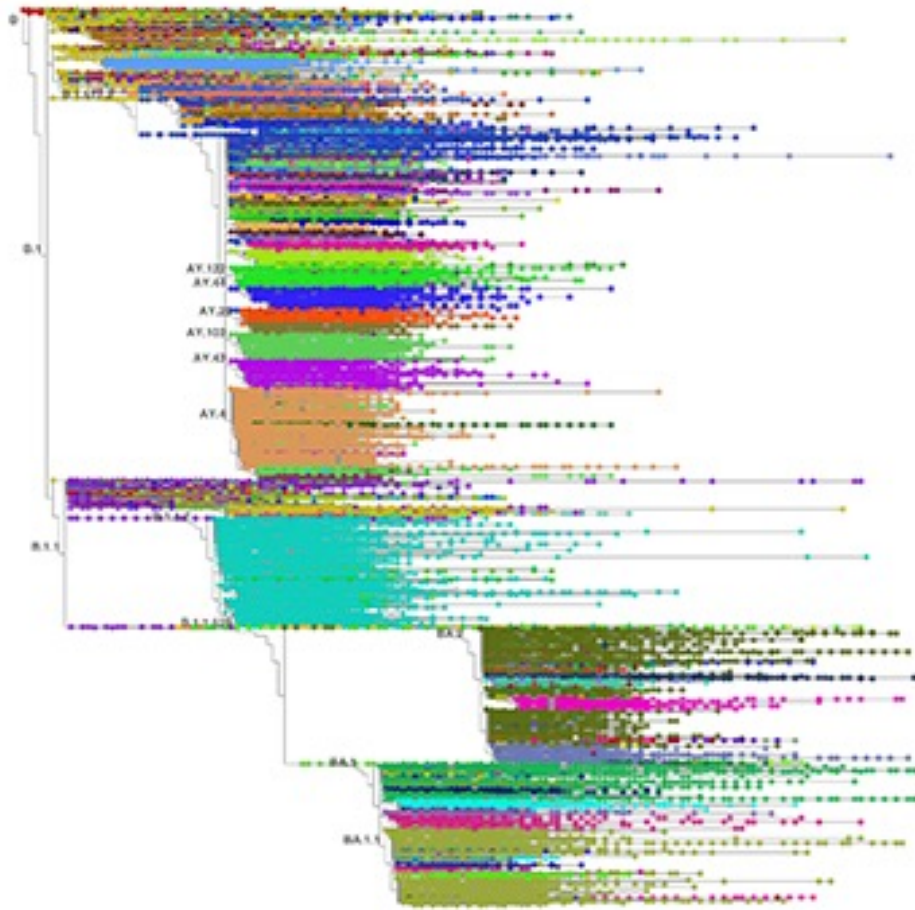
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# Call to organise our global genomic information for AMR

- Increasing volumes of global semi-unstructured archival data
- Organise for public health value and decision making
- Deliver situational risk awareness for policy makers at national, regional and global scale

# Learning from SARS-CoV-2

# ~20million sequences shared globally



# Situational Awareness: Greater Specificity Enables Precision Targeting

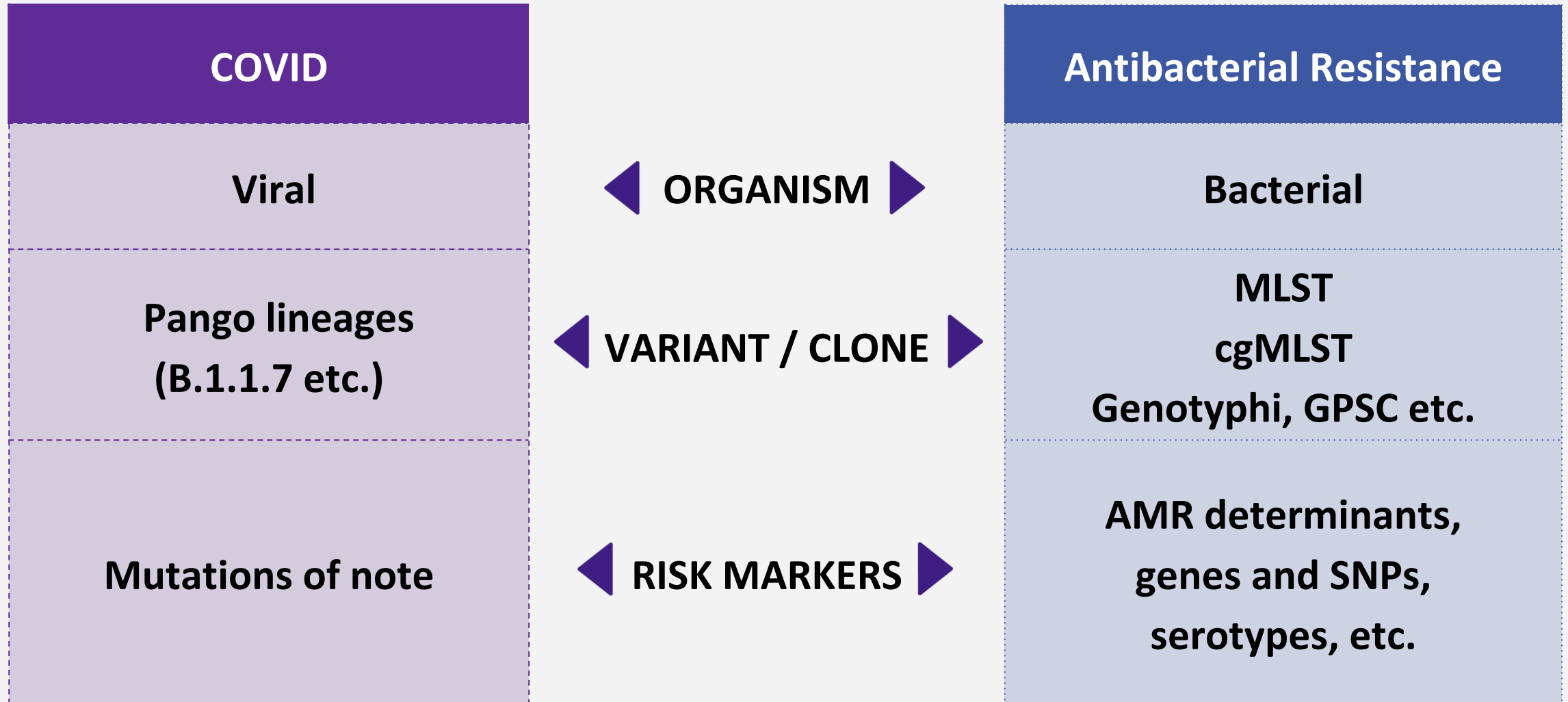
**Diagnostics**

**Therapeutics  
(+ monitoring)**

**Vaccines  
(+ monitoring)**

**Outbreaks /  
Transmission**

# Axes of information: Variant & Risk



# Axes of information: Geography & Time

Adding **geography** and **time** to data about **variants** and **risk** yields actionable intelligence

LOCAL



NATIONAL



INTERNATIONAL



GLOBAL



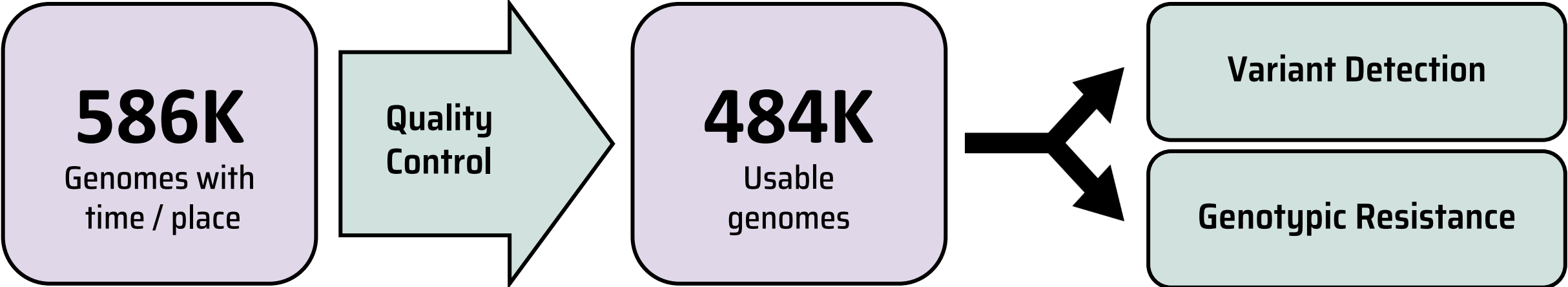


# **Establishing a Baseline: The Current Genomic AMR Landscape**

# Priority list for R&D of new antibiotics

Priority 1 CRITICAL	<i>Acinetobacter baumannii</i>	carbapenem-resistant
	<i>Pseudomonas aeruginosa</i>	carbapenem-resistant
	<i>Enterobacteriaceae</i>	carbapenem-resistant 3rd gen. cephalosporin-resistant
Priority 2 HIGH	<i>Enterococcus faecium</i>	vancomycin-resistant
	<i>Staphylococcus aureus</i>	methicillin-resistant vancomycin intermediate & resistant
	<i>Helicobacter pylori</i>	clarithromycin-resistant
	<i>Campylobacter</i>	fluoroquinolone-resistant
	<i>Salmonella spp.</i>	fluoroquinolone-resistant
	<i>Neisseria gonorrhoeae</i>	3rd gen. cephalosporin-resistant fluoroquinolone-resistant
	Priority 3 MEDIUM	<i>Streptococcus pneumoniae</i>
<i>Haemophilus influenzae</i>		ampicillin-resistant
<i>Shigella spp.</i>		fluoroquinolone-resistant

# Methods and workflow



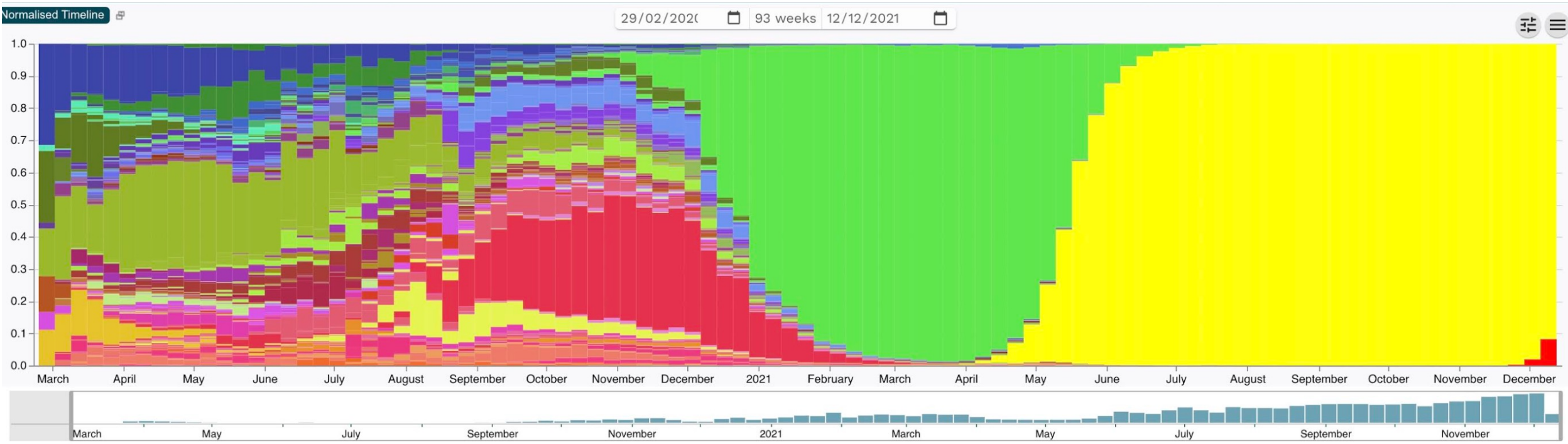
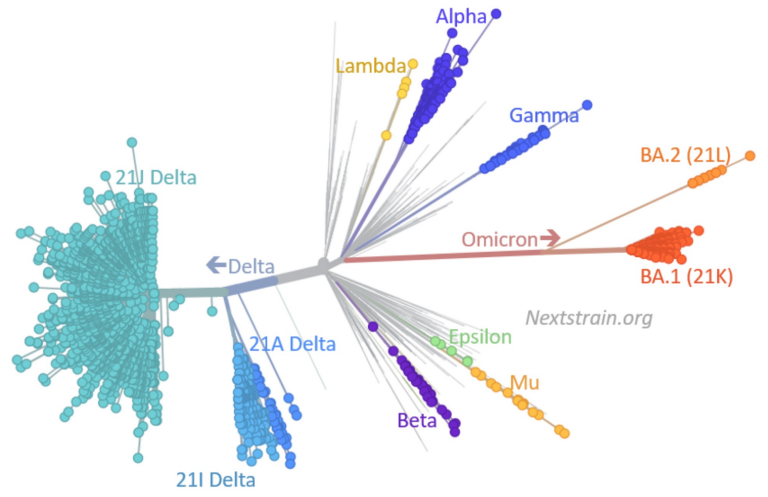
# Initial Baseline Data

# A Data Platform for local and Global Policy

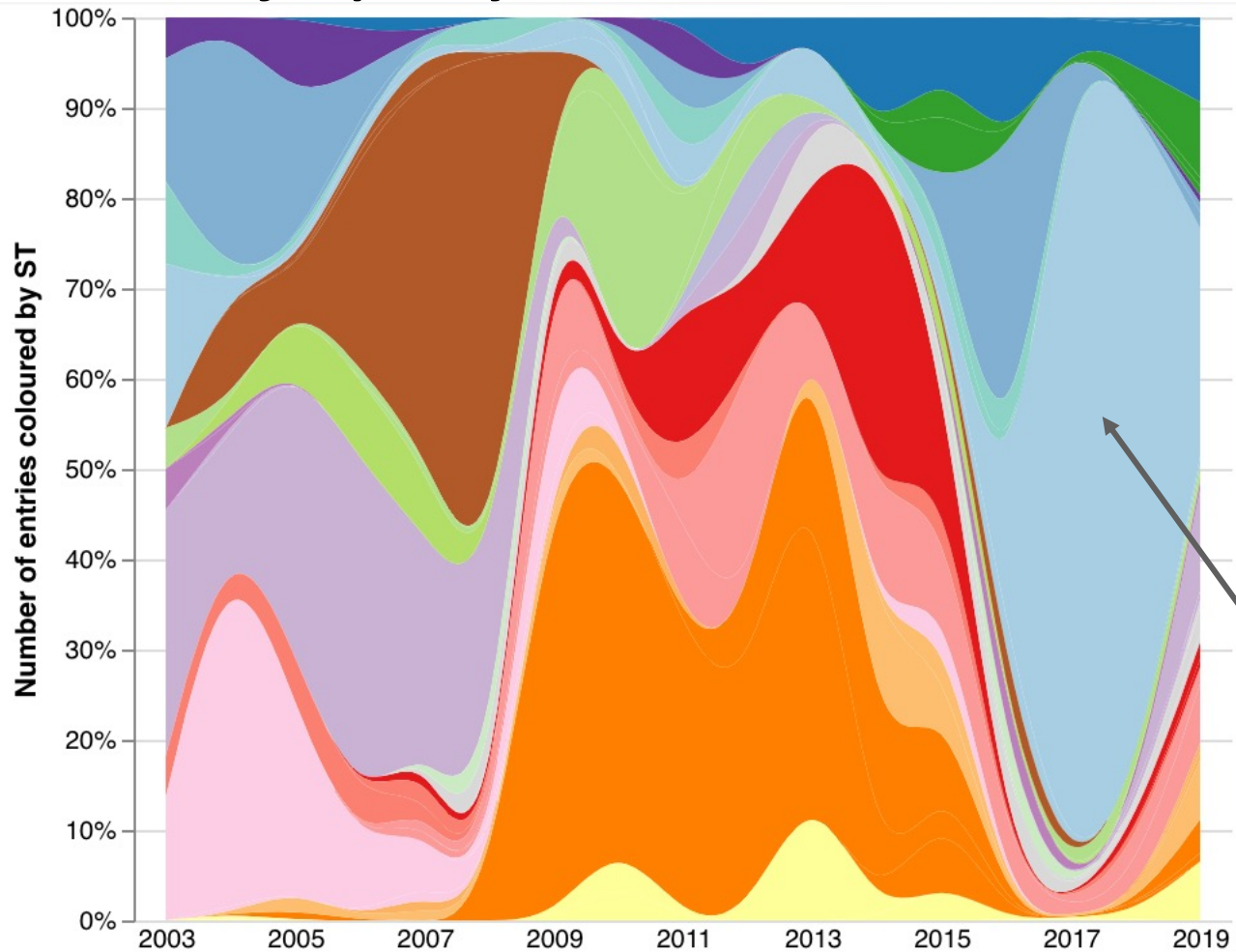


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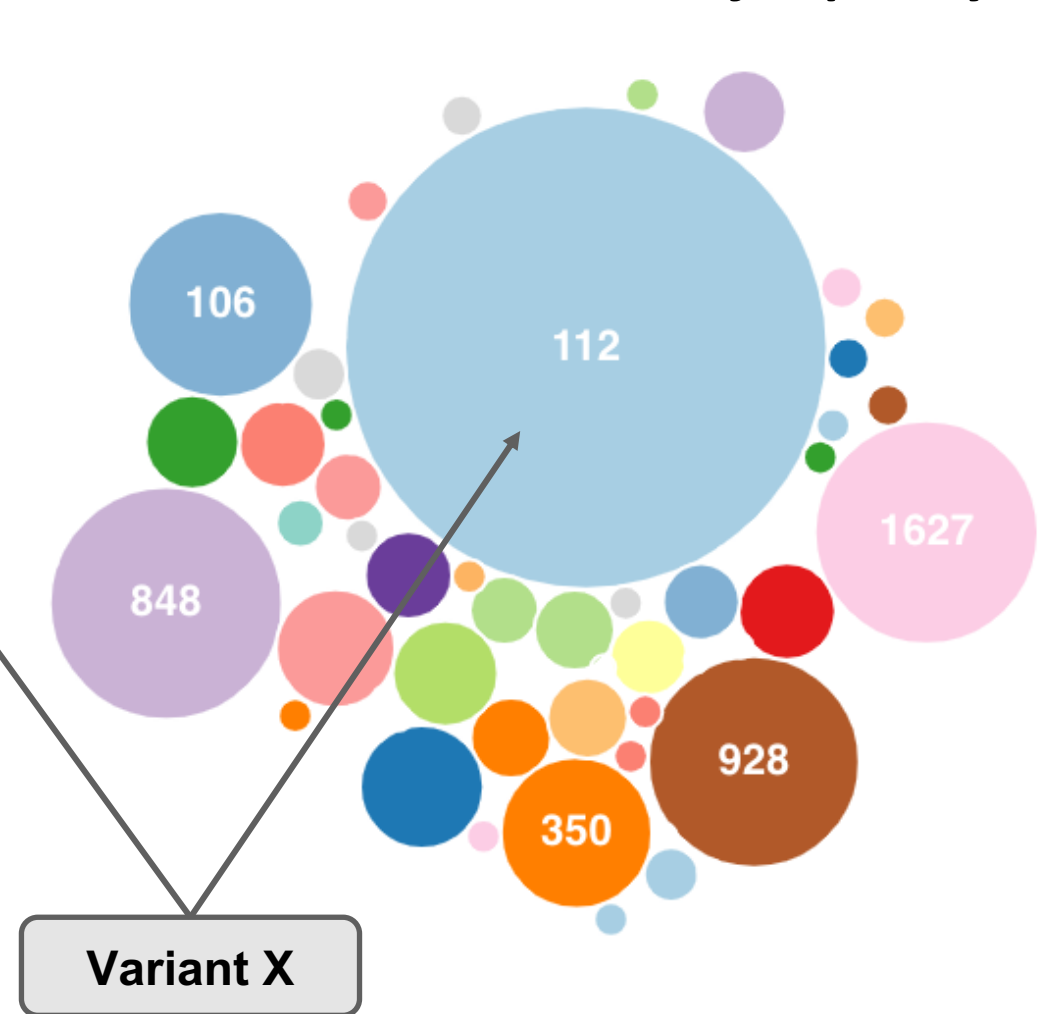
- interactive data visualization
- pathogen genomics integrated with other data
- situational risk awareness for policy makers at national, regional and global scale



### Variant frequency over time



### Total variant frequency





SELECT AN ORGANISM



CRITICAL

- Acinetobacter baumannii
- Escherichia coli
- Enterobacter cloacae complex
- Klebsiella pneumoniae
- Pseudomonas aeruginosa

HIGH

- Campylobacter
- Enterococcus faecium

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# Priority list for R&D of new antibiotics

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SELECT AN ORGANISM



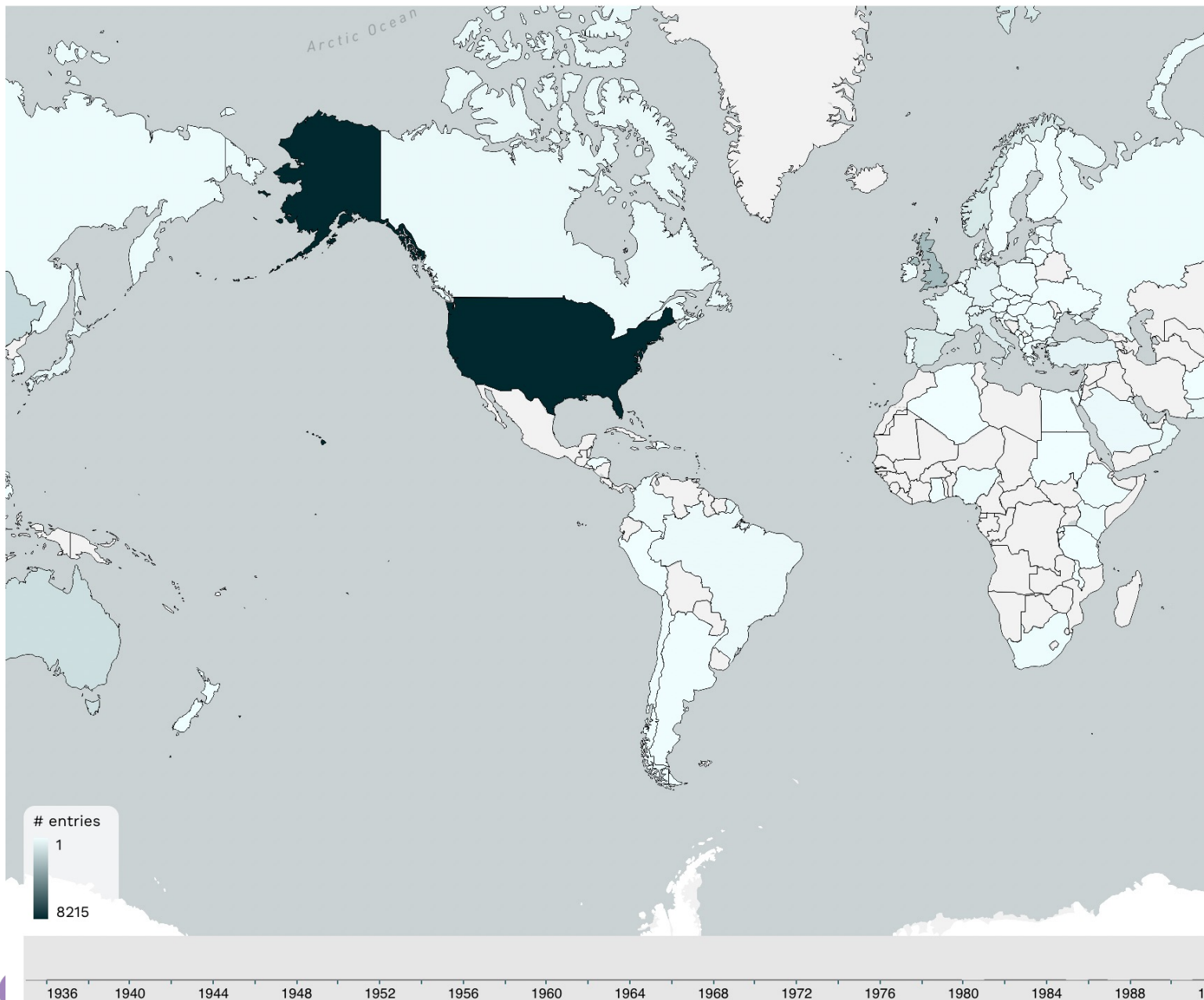
CRITICAL

- Acinetobacter baumannii
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- Enterobacter cloacae complex
- Klebsiella pneumoniae
- Pseudomonas aeruginosa

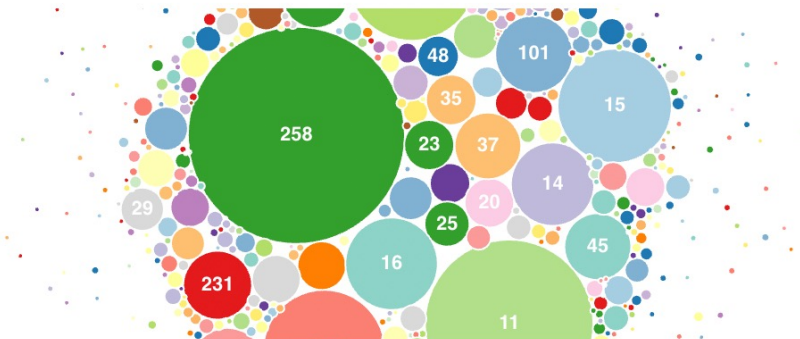
HIGH

- Campylobacter
- Enterococcus faecium

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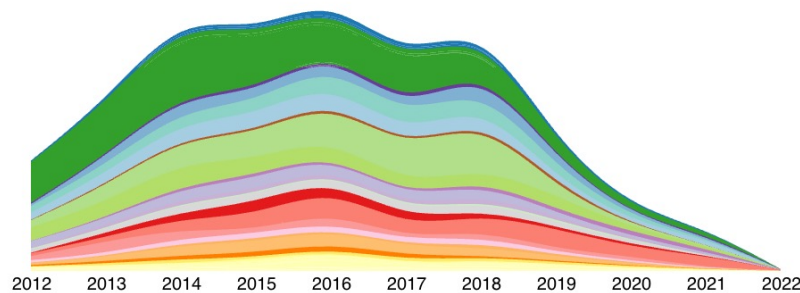


### Variant (ST) overview

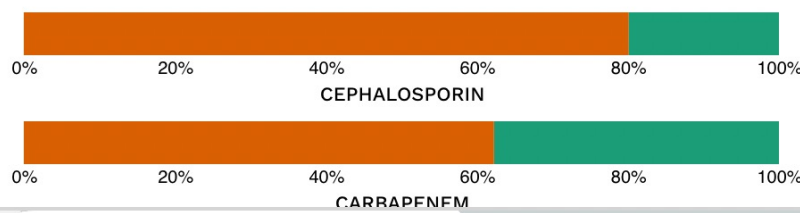


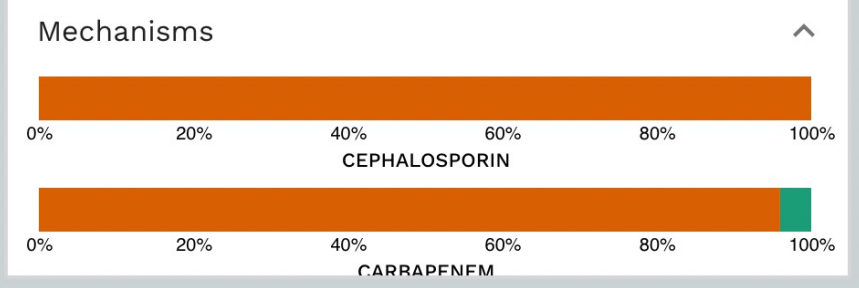
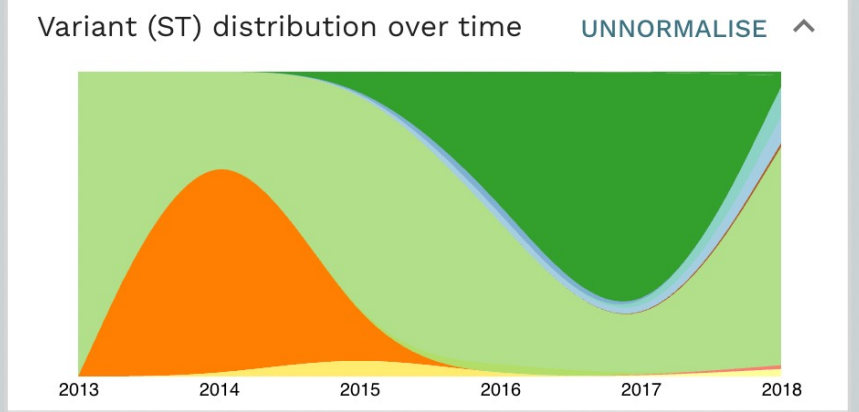
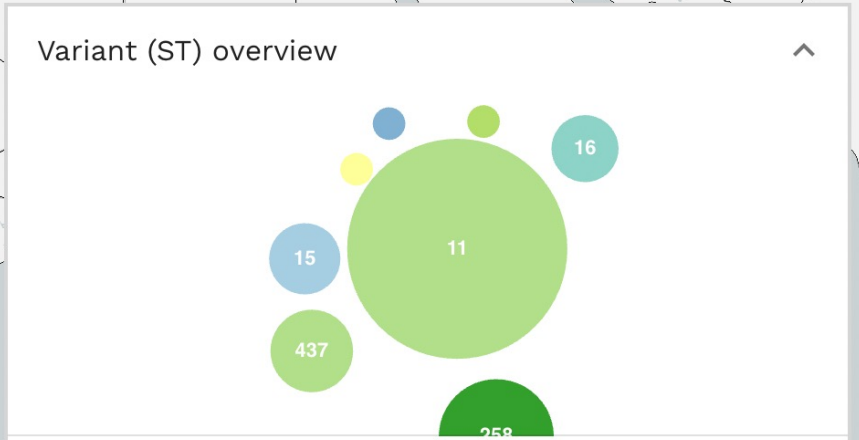
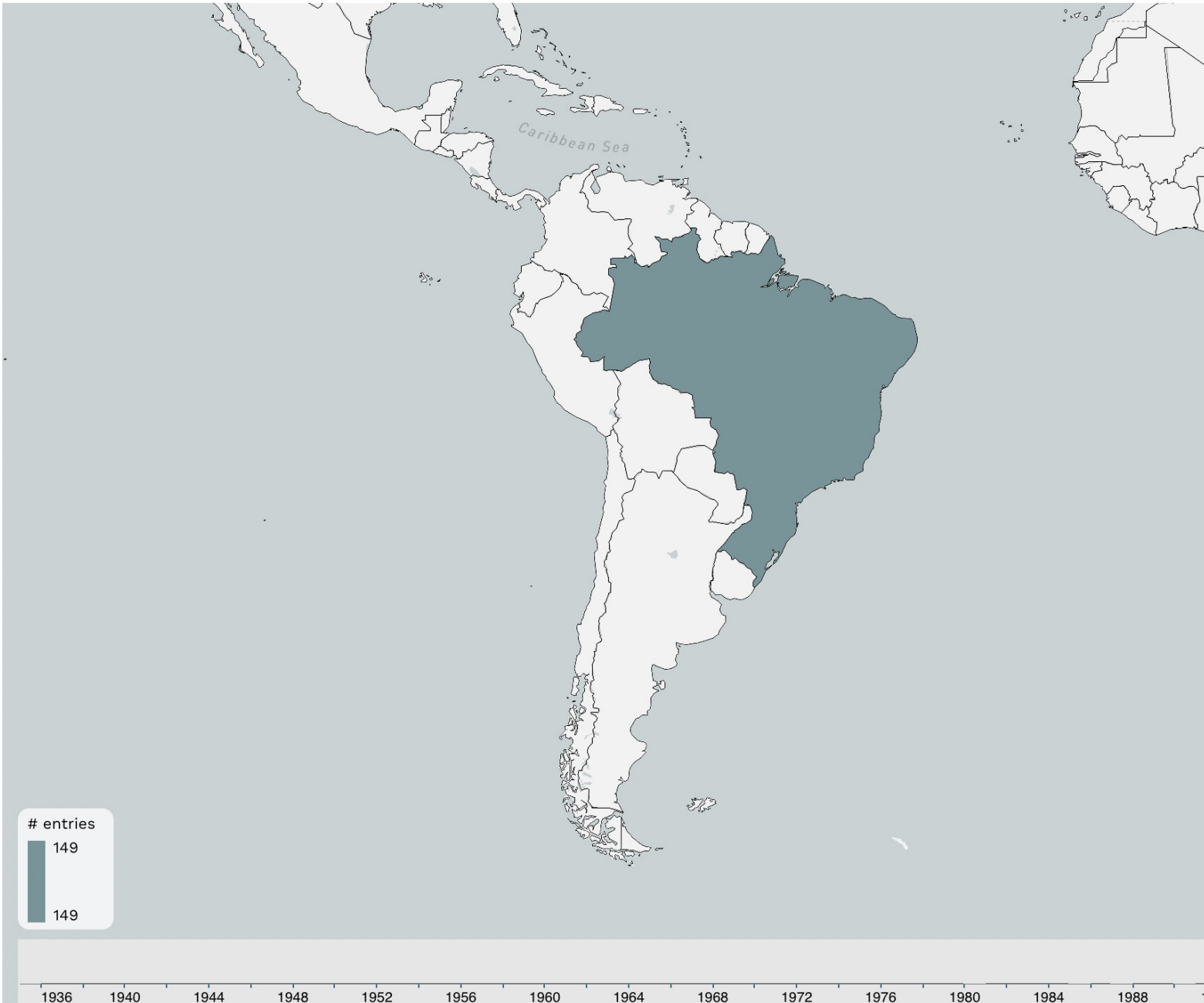
### Variant (ST) distribution over time

NORMALISE ^



### Mechanisms





# Situational Awareness: Greater Specificity Enables Precision Targeting

**Diagnostics**

**Vaccines  
(+ monitoring)**

**Therapeutics  
(+ monitoring)**

**Outbreaks /  
cross border**



# amr.watch

AMR burden  
estimates

Phenotypic  
data

Antibiotic  
usage

Climate data

# Thank you

## Scientific Advisors

Ed Feil  
Hajo Gründmann  
Matt Holden

## Scientists & Developers

Khalil Abudahab  
Silvia Argimón  
Julio Diaz Caballero  
Natacha Couto  
Corin Yeats

## Program Management

Diana Connor

## Strategy & Alliances

Heather Shane\*

