Big data starts small: refocused global AMR surveillance

Paul Turner

Clinical Microbiologist
Cambodia Oxford Medical Research Unit
University of Oxford

Hosted by Jane Barnett
jane@webbertraining.com

COMRU.

My environment… not big or high tech

2

AMR surveillance takes all sorts…

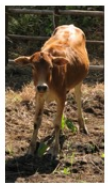


Image credit:
https://www.sanger.ac.uk/news_item/2014-04-29-two-human-genomes-per-hour/

3

Why do **human** AMR surveillance?

- To estimate burden of disease
- To characterise trends in space and time
- To serve as benchmark to measure the impact of interventions
- To provide local evidence for empiric treatment guidelines and clinical decision making

4

5

The Fleming Fund

A Summary of Phase One

Surveillance is the solution

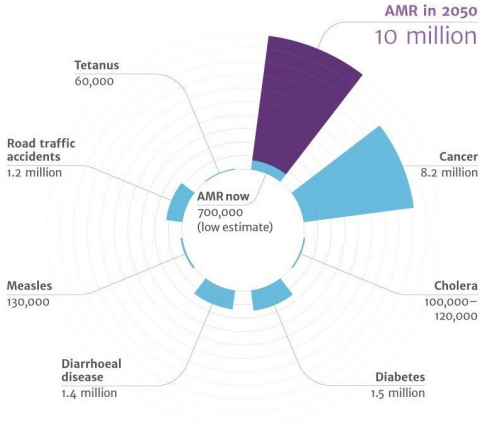
> *It is time for us all to step up and speak out against the 'silent pandemic' of AMR.*

Professor Dame Sally Davies, *UK Government Special Envoy on Antimicrobial Resistance*

https://www.flemingfund.org/

6

How much AMR is there and what impact does it have?



PLOS | MEDICINE

ESSAY

Will 10 Million People Die a Year due to Antimicrobial Resistance by 2050?

Marlieke E. A. de Kraker[1]*, Andrew J. Stewardson[2], Stephan Harbarth[1]

1 Infection Control Program, Geneva University Hospitals and Faculty of Medicine, Geneva, Switzerland,
2 Infectious Diseases Department, Austin Health, Heidelberg, Australia

- Current global estimates of the burden of AMR are not very informative; we need detailed, reliable data to be able to improve AMR control measures, preferably based on comprehensive, population-based surveillance data from low-, middle-, and high-income countries.

PLoS Med. 2016;13(11):e1002184

7

O'Neill report (2016)

Improving the estimation of the global burden of antimicrobial resistant infections

Direk Limmathurotsakul, Susanna Dunachie, Keiji Fukuda, Nicholas A Feasey, Iruka N Okeke, Alison H Holmes, Catrin E Moore, Christiane Dolecek, H Rogier van Doorn, Nandini Shetty, Alan D Lopez, Sharon J Peacock, Surveillance and Epidemiology of Drug Resistant Infections Consortium (SEDRIC)

***Panel*: Key actions to improve the estimation of the global burden of AMR infections**

Strengthen health systems

- Increase country capability and capacity to:
  - Reliably detect the global priority list of AMR bacteria reported by WHO
  - Document clinical outcomes and link to laboratory data

8

Lancet Infect Dis. 2019;19(11):e392-e8

Is there any good data?

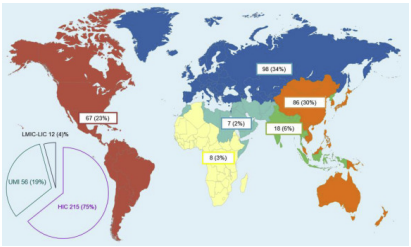
- Recent review of 286 studies
- Mostly:
  - High income countries
  - Retrospective
  - Single centre
  - Methodologically sub-optimal
- Conclusion:
  - Need better studies / data urgently
  - Policy makers are unable to act until burden is clear

Contents lists available at ScienceDirect
Clinical Microbiology and Infection
journal homepage: www.clinicalmicrobiologyandinfection.com
CMI CLINICAL MICROBIOLOGY AND INFECTION
ELSEVIER

Systematic review

Methodological quality of studies evaluating the burden of drug-resistant infections in humans due to the WHO Global Antimicrobial Resistance Surveillance System target bacteria

Maria Diletta Pezzani [1,*], Barbara Tornimbene [2], Carmem Pessoa-Silva [2], Marlieke de Kraker [3], Sebastiano Rizzardo [1], Nicola Duccio Salerno [1], Stephan Harbarth [3], Evelina Tacconelli [1,4]



Clin Microbiol Infect. 2021. 10.1016/j.cmi.2021.01.004

JAC Antimicrob Resist
doi:10.1093/jacamr/dlaa130
JAC-Antimicrobial Resistance

Mortality attributable to third-generation cephalosporin resistance in Gram-negative bloodstream infections in African hospitals: a multi-site retrospective study

Angela Dramowski[1], Gerald Ong'ayo[2], Andrea M. Rehman [3], Andrew Whitelaw[4], Appiah-Korang Labi[5], Noah Obeng-Nkrumah[6], Awa Ndir[7], Marcelyn T. Magwenzi[8], Kenneth Onyedibe[9], Martin Wolkewitz[10], Marlieke E. A. de Kraker [11], J. Anthony G. Scott[2,3] and Alexander M. Aiken [3]* on behalf of the MBIRA study collaborators†

Table 3. Impact of third-generation cephalosporin resistance on in-hospital mortality, discharge and length of stay in *E. coli* and *K. pneumoniae* BSI

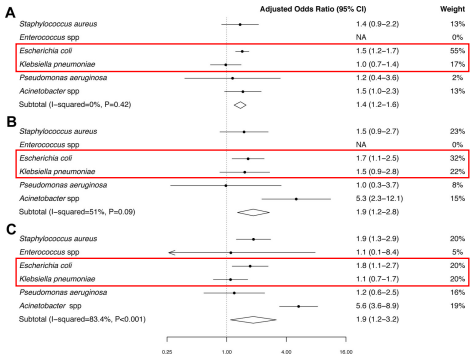
Comparison	HR (95% CI) Cox model (death)	Cox model (discharge alive)	Fine + Gray model (death)	Excess LOS, days (95% CI)
R-*E. coli* versus matched controls	2.82 (2.10–3.79)	0.51 (0.44–0.59)	4.10 (3.06–5.48)	1.9 (−1.4 to 5.1)
S-*E. coli* versus matched controls	2.73 (2.29–3.24)	0.54 (0.50–0.58)	3.81 (3.21–4.51)	4.5 (3.1–5.8)
R-*E. coli* versus S-*E. coli*[a]	1.03 (0.73–1.46)	0.94 (0.79–1.11)	1.08 (0.77–1.51)	0.80 (0.59–1.09)
R-*K. pneumoniae* versus matched controls	2.89 (2.38–3.50)	0.47 (0.43–0.51)	4.55 (3.77–5.49)	6.2 (4.5–7.8)
S-*K. pneumoniae* versus matched controls	2.61 (2.03–3.37)	0.51 (0.46–0.57)	3.99 (3.11–5.12)	6.0 (3.9–8.2)
R-*K. pneumoniae* versus S-*K. pneumoniae*[a]	1.10 (0.80–1.52)	0.92 (0.80–1.06)	1.14 (0.83–1.55)	1.01 (0.84–1.21)

"…there did not appear to be an impact of 3GC-resistance on mortality in *E. coli* or *K. pneumoniae* BSI in African hospitals, as compared with susceptible BSI with equivalent species"

Epidemiology and burden of multidrug-resistant bacterial infection in a developing country

Cherry Lim[1†], Emi Takahashi[1†], Maliwan Hongsuwan[1], Vanaporn Wuthiekanun[1], Visanu Thamlikitkul[2], Soawapak Hinjoy[3], Nicholas PJ Day[1,4], Sharon J Peacock[1,5,6], Direk Limmathurotsakul[1,4,7*]

Elife. 2016;5



"We estimate that 43% deaths in patients with hospital-acquired infection due to MDR bacteria in Thailand in 2010 represented excess mortality caused by MDR"

11

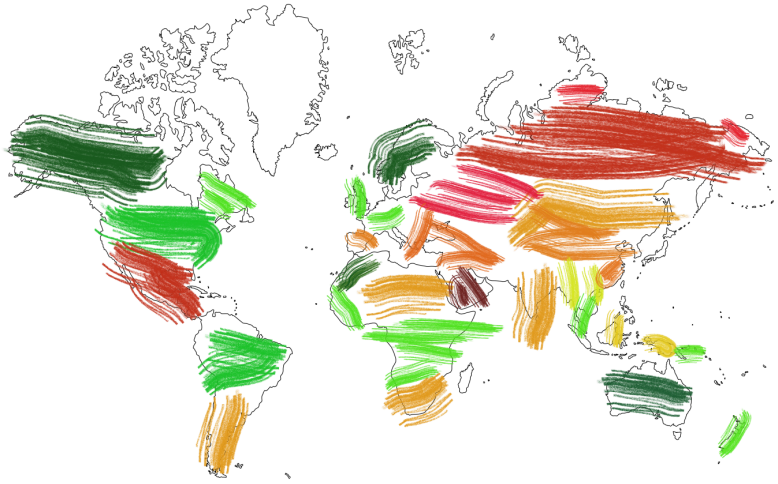
This is a step in the right direction

12

Can big data save the day?

13

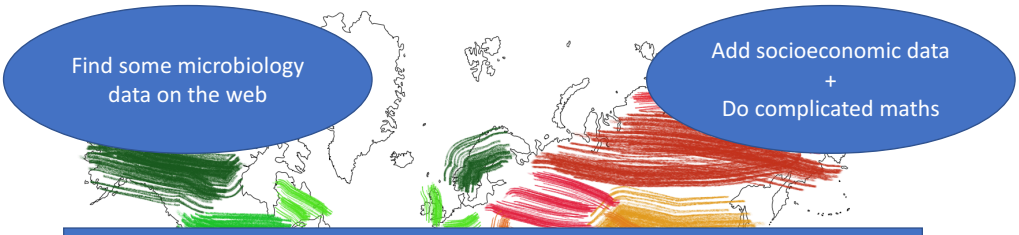
My Global AMR Map



14

Funding source: Not externally funded

My Global AMR Map



Conclude:

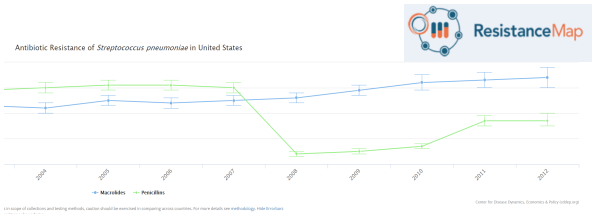
- Lots of gaps - we should do more surveillance
- Hard to interpret the data - there are lots of biases
- Hard to determine impact of AMR – no linked clinical-lab data
- Comparisons between countries difficult / impossible
- Cannot use the data for local decision making

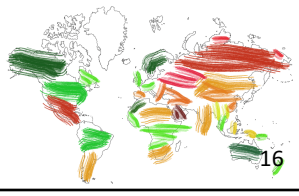
15

Funding source: Not externally funded

Things to ponder whilst looking at an AMR map

- What does country level resistance actually mean?
- Community acquired versus hospital acquired infections
  - Mash them together or keep separate?
- Sites of infection
  - Adults vs Children vs Neonates
  - Are bugs in urine the same as those in blood cultures?
- AMR data issues
  - Data quality – more coming on this
  - Changes in breakpoints over time
    - Fluoroquinolones and Enterobacterales
    - Penicillin and *Streptococcus pneumoniae*
  - Equivalence of breakpoints
    - CLSI vs EUCAST
    - What did they do with "I"?





16

AMR lab data quality…

Table 7 Percentage sensitivity patterns of most prevalent pathogens to selected antimicrobials

	Region	Africa		South-East Asia			
Organism	Antimicrobial	Adejuyigbe *et al* (20)	Muhe *et al* (27)	Mathur *et al* (37)	Panigrahi *et al* (39)	Darmstadt *et al* (35)	Tallur *et al* (41)
Escherichia coli	Amoxycillin (AMX)	60.0	–	–	–	–	–
	Ampicillin (AMP)	40.0	100.0	–	–	100.0	29.0
	Cefotaxime (CTX)	–	–	–	–	–	100.0
	Ceftazidime (CAZ)	–	100.0	–	–	100.0	–
	Ceftriaxone (CRO)	–	–	–	–	100.0	100.0
	Ciprofloxacin (CIP)	–	–	–	–	100.0	–
	Gentamicin (GEN)	80.0	100.0	–	–	100.0	71.0
	Imipenem (IMP)					100.0	–
Staphylococcus aureus	Amoxycillin (AMX)	73.0	–	–	–	–	–
							21.0
							–
							–
							–
							–
	Gentamicin (GEN)	85.8	–	–	–	90.0	29.0
	Imipenem (IMP)	–	–	–	–	90.0	–
Klebsiella species*	Amoxycillin (AMX)	0.0	–	–	–	–	–
	Ampicillin (AMP)	–	–	10.0	–	0.0	25.5
	Cefotaxime (CTX)	–	–	–	–	–	76.5
	Ceftazidime (CAZ)	–	–	–	22.0	33.3	–
	Ceftriaxone (CRO)	–	–	71.4	–	33.3	81.0
	Ciprofloxacin (CIP)	–	–	64.8	11.0	66.7	–
	Gentamicin (GEN)	100.0	–	42.8	–	66.7	59.5
	Imipenem (IMP)	–	–	100.0	–	100.0	–

*Averages were taken when more than one variant's sensitivity patterns were reported.

…there are issues to be aware of

J Glob Health. 2011;1(2):154-70

17

Klebsiella pneumoniae

Klebsiella species*	Amoxycillin (AMX)	0.0	–	–	–
	Ampicillin (AMP)	–	–	10.0	–
	Cefotaxime (CTX)	–	–	–	–
	Ceftazidime (CAZ)	–	–	–	22.0
	Ceftriaxone (CRO)	–	–	71.4	–
	Ciprofloxacin (CIP)	–	–	64.8	11.0
	Gentamicin (GEN)	100.0	–	42.8	–
	Imipenem (IMP)	–	–	100.0	–

Results look good?

"For interpretation of AST results, CLSI guideline (version X) was followed"

- Nothing to worry about then…
- Keep reading the CLSI doc until page 218…

Is this an isolated issue or part of a larger quality management problem?

Appendix B. Intrinsic Resistance

B1. *Enterobacteriaceae*

Organism \ Antimicrobial Agent	Ampicillin
Citrobacter freundii	R
Citrobacter koseri, ***Citrobacter amalonaticus* group**[a]	R
Enterobacter cloacae complex[b]	R
Escherichia coli	There is
Escherichia hermannii	R
Hafnia alvei	R
Klebsiella (formerly *Enterobacter*) *aerogenes*	R
Klebsiella pneumoniae, ***Klebsiella oxytoca, Klebsiella variicola***	R

18

Staphylococcus aureus

Staphylococcus aureus	Amoxycillin (AMX)	73.0	–	–	–	–	–
	Ampicillin (AMP)	–	–	–	–	0.0	21.0
	Cefotaxime (CTX)	–	–	–	–	–	–
	Ceftazidime (CAZ)	–	–	–	–	66.7	–
	Ceftriaxone (CRO)	–	–	–	–	90.0	–
	Ciprofloxacin (CIP)	–	–	–	–	80.0	–
	Gentamicin (GEN)	85.8	–	–	–	90.0	29.0
	Imipenem (IMP)	–	–	–	–	90.0	–

How much MRSA: no cefoxitin / oxacillin results?

- Could just guess from the imipenem or ceftriaxone data?
- But how were these results generated?

Ceftazidime for *S. aureus:* might be ok 2/3 of the time…really?

Are these isolated issues or part of a larger quality management problem?

19

"Antimicrobial resistance is a complex issue and is widely considered to be getting worse. However, the quality of the microbiology data that are being published to support this position could be substantially improved."

"Continued, non-standardised reporting of clinical microbiology data might impede efforts to quantify and control antimicrobial resistance."

20

MICRO

Microbiology Investigation Criteria for Reporting Objectively:
A framework for the reporting and interpretation of clinical microbiology data
BMC Medicine. 2019;17(1): 70

Tackling antimicrobial resistance (AMR) is a Global Health priority

Poor quality data hampers efforts to understand the burden of AMR

Use the MICRO framework to enhance the quality and scientific reporting of clinical microbiology data:

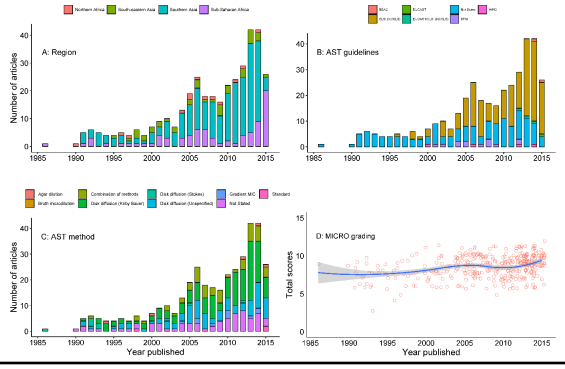
- Increase data utility and comparability
- Improve AMR surveillance
- Facilitate meta-analyses
- Inform policy and interventions from local to global levels

UNIVERSITY OF OXFORD

21

MICRO applied at scale

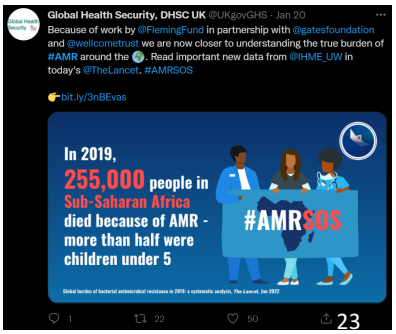
- Antimicrobial resistance patterns in bacteria causing febrile illness in Africa, South Asia and Southeast Asia: A systematic review of published aetiological studies from 1980-2015
  - 371 articles from 39 countries
  - Core MICRO checklist items scored
    - No study scored 13/13
    - Only 52% reported full information for their AST method



Roberts T et al. Submitted

22

Have we cracked it now?

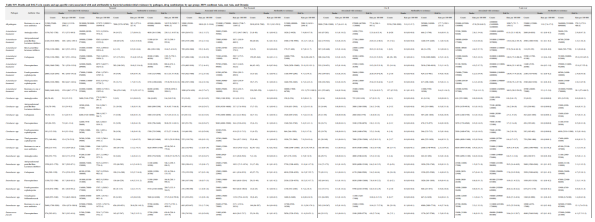


23

Lancet. 2022: doi.org/10.1016/S0140-6736(21)02724-0

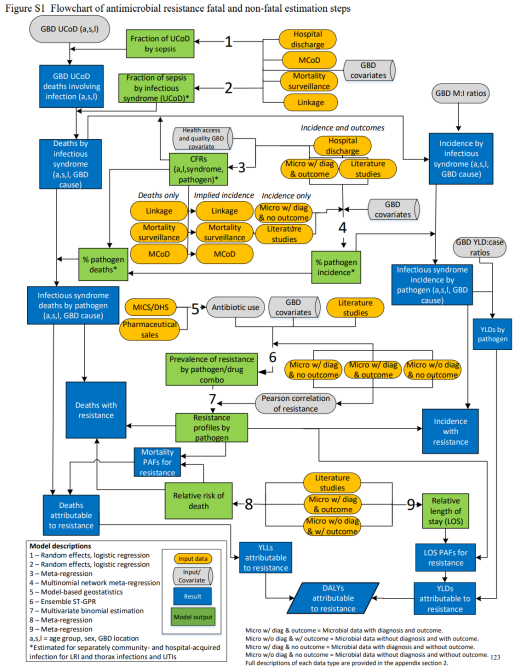
The data sources

- Could be best summarised as a little data went a long way for many locations
  - Impressive number of bacterial isolates / outcome data overall though
- Need to review all 130 pages of supplementary material to get a complete understanding of how it went down…bring your own magnifying glass:



24

The model…



…"is complicated"

25

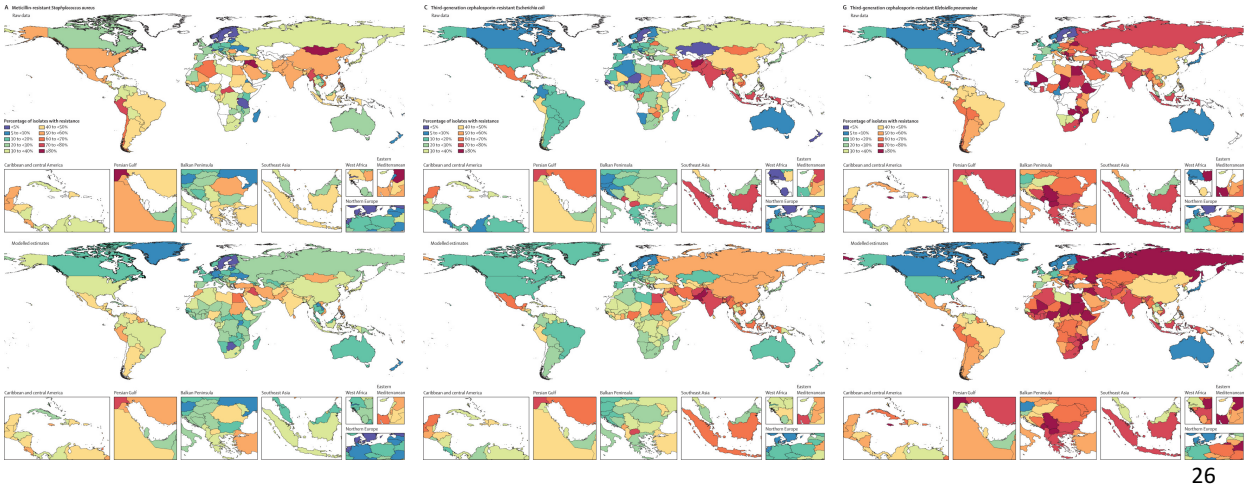
https://doi.org/10.1016/S0140-6736(21)02724-0

The maps

Methicillin R
S. aureus

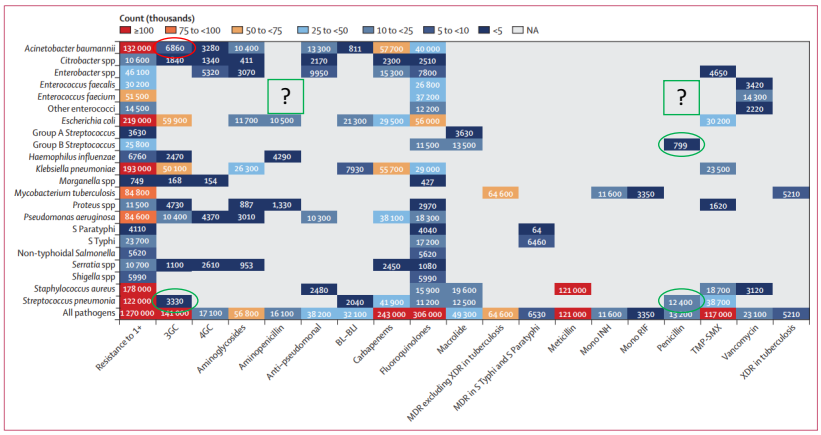
3rd gen cephalosporin R
E. coli

3rd gen cephalosporin R
K. pneumoniae



26

Antibiotic-level results…some interesting things



Major treatment drug

Intrinsic resistance?

Figure 6: **Global deaths (counts) attributable to bacterial antimicrobial resistance by pathogen–drug combination, 2019**
For this figure, only deaths attributable to resistance, not deaths associated with resistance, are shown due to the very high levels of correlation for resistance patterns between some drugs. 3GC=third-generation cephalosporins. 4GC=fourth-generation cephalosporins. Anti-pseudomonal=anti-pseudomonal penicillin or beta-lactamase inhibitors. BL-BLI=β-lactam or β-lactamase inhibitors. MDR=multidrug resistance. Mono INH=isoniazid mono-resistance. Mono RIF=rifampicin mono-resistance. NA=not applicable. Resistance to 1+=resistance to one or more drug. *S* Paratyphi=*Salmonella enterica* serotype Paratyphi. *S* Typhi=*S enterica* serotype Typhi. TMP-SMX=trimethoprim-sulfamethoxazole. XDR=extensive drug resistance.

27

Limitations

Not much data from LMICs

This study has several limitations, the most important being the sparsity of data from many LMICs on the distribution of pathogens by infectious syndrome, the prevalence of resistance for key pathogen–drug combinations, and the number of deaths involving infection; and the severe scarcity of data linking laboratory results to outcomes such as death.

CAI versus HAI – could not split out

In future iterations of the project, we hope to improve on the identification of community-acquired and hospital-acquired infections.

AMR data not standardised

Additionally, no universal laboratory standard exists to demarcate resistance versus susceptibility, and we often had to defer to laboratory interpretation to classify the isolates in our data, resulting in heterogeneous classification. Whenever possible, we classified resistance using the most recent CLSI guidelines based on the minimum inhibitory concentrations provided in the data; however, CLSI breakpoints have changed over time, and many datasets did not provide sufficient detail to allow for retrospective reanalysis of the data.[67]

Some of the lab data may not have been great quality

There are many well described barriers to good-quality clinical bacteriology in LMICs, and proper quality assurance and quality-control measures are crucial for quality care and accurate laboratory-based surveillance.[66]

28

Dame Sally's take

The study also demonstrates data disparities and the lack of infrastructure and capacity for surveillance that we need to detect and respond to pandemics.

https://www.flemingfund.org/

29

What does GRAM leave us with?

- A better sense of the magnitude of the problem and can use this to encourage urgent high-level action
  - Prioritise antimicrobial drug development
  - Invest in better diagnostics
  - Work up and test interventions
- A need to fill in the massive national and local data gaps

30

Why are we really doing AMR surveillance?

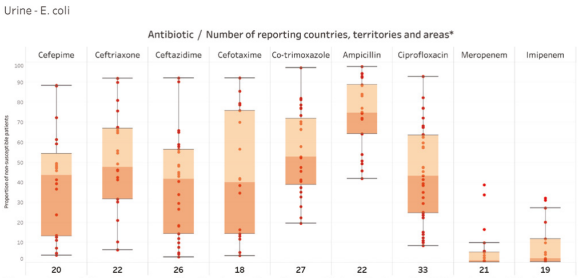
To ensure that patients with bacterial infections can be treated effectively

32

Something odd?

Hospital X

The World

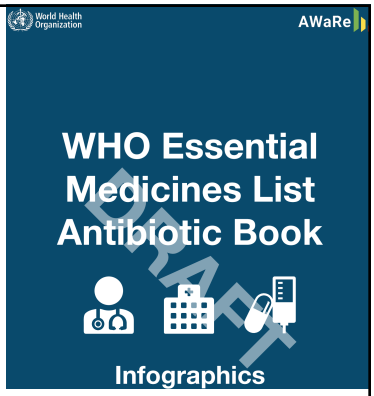


How do I treat Bob's UTI?

33

Treatment guideline development

- Complicated
  - Multiple possible pathogens
  - Syndrome specific considerations
  - Wide variations in AST prevalence



Wellcome Open Research

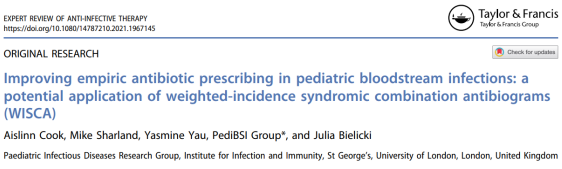
Wellcome Open Research 2018, 3:131 Last updated: 08 NOV 2018

Check for updates

RESEARCH ARTICLE

Using machine learning to guide targeted and locally-tailored empiric antibiotic prescribing in a children's hospital in Cambodia [version 1; referees: 1 approved]

Mathupanee Oonsivilai[1], Yin Mo[1,2], Nantasit Luangasanatip[1], Yoel Lubell[1], Thyl Miliya[3], Pisey Tan[3], Lorn Loeuk[3], Paul Turner[3,4], Ben S. Cooper[1,4]



EXPERT REVIEW OF ANTI-INFECTIVE THERAPY
https://doi.org/10.1080/14787210.2021.1967145

Taylor & Francis

ORIGINAL RESEARCH

Improving empiric antibiotic prescribing in pediatric bloodstream infections: a potential application of weighted-incidence syndromic combination antibiograms (WISCA)

Aislinn Cook, Mike Sharland, Yasmine Yau, PediBSI Group*, and Julia Bielicki

Paediatric Infectious Diseases Research Group, Institute for Infection and Immunity, St George's, University of London, London, United Kingdom

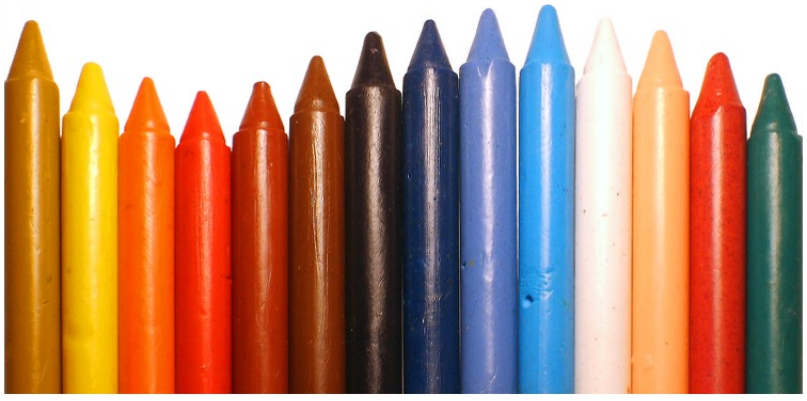
34

Ultimately, we need more of these

35

https://www.rotring.com/uk/

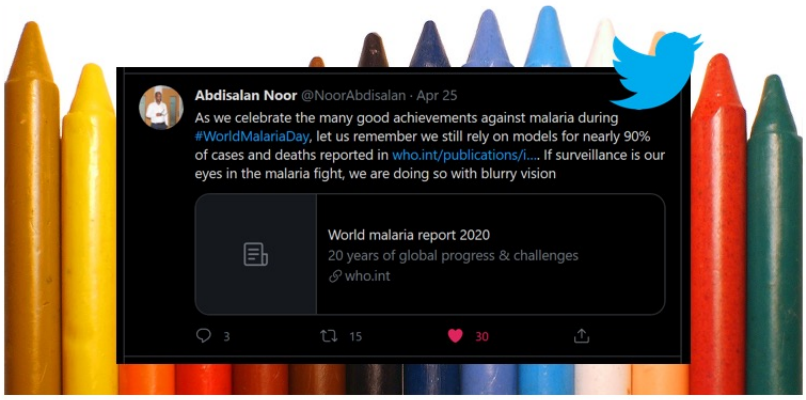
And less of these



36

https://commons.wikimedia.org/wiki/File:Crayones_cera.jpg

And less of these



37

https://commons.wikimedia.org/wiki/File:Crayones_cera.jpg

38

Better local clinical surveillance (in LMICs)

39

What tools are needed

- Money
- Good microbiology
  - Several excellent capacity building initiatives on-going
  - Important to connect labs to clinical services
- Human resources
  - Clinical staff require support to use microbiology effectively
  - In the absence of fully electronic patient, pharmacy, and lab information systems surveillance takes time and requires effort
- Case definitions
  - That are simple and do not require serial bloods / radiology

40

Lancet Infect Dis. 2018;18(8):e248-e58.

What tools are needed

3.3 Pneumonia (PN1–PN5)

X-ray

Two or more serial chest X-rays or CT-scans with a suggestive image of pneumonia for patients with underlying cardiac or pulmonary disease. In patients without underlying cardiac or pulmonary disease, one definitive chest X-ray or CT-scan is sufficient.

And at least one of the following:

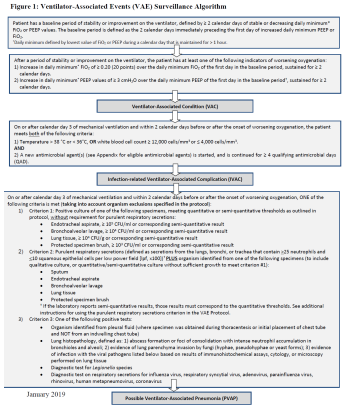
- fever > 38 °C with no other cause
- leukopenia (< 4 000 WBC/mm^3) or leucocytosis (≥ 12 000 WBC/mm^3).

Symptoms

and

at least one of the following (or at least two, if clinical pneumonia only = PN4 and PN5):

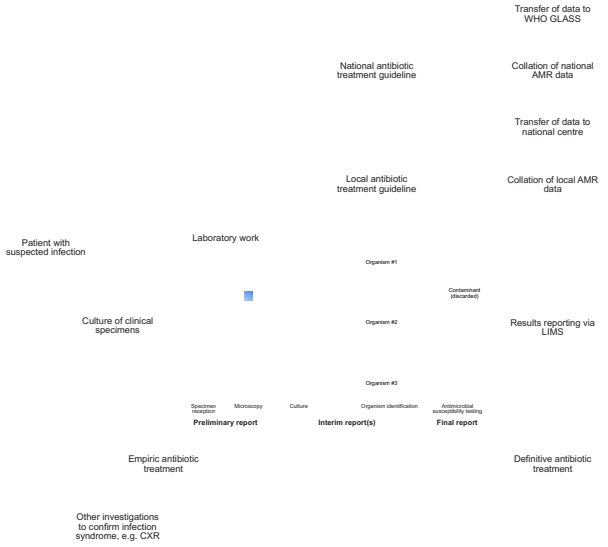
- new onset of purulent sputum, or change in character of sputum (colour, odour, quantity, consistency)
- cough or dyspnea or tachypnea
- suggestive auscultation (rales or bronchial breath sounds), rhonchi, wheezing
- worsening gas exchange (e.g. O_2 desaturation or increased oxygen requirements or increased ventilation demand).



What tools are needed

- Money
- Good microbiology
  - Several excellent capacity building initiatives on-going
  - Important to connect labs to clinical services
- Human resources
  - Clinical staff require support to use microbiology effectively
  - In the absence of fully electronic patient, pharmacy, and lab information systems surveillance takes time and requires effort
- Case definitions
  - That are simple and do not require serial bloods / radiology
- IT infrastructure

Better AMR surveillance IT tools



Using information technology to improve surveillance of antimicrobial resistance in South East Asia

Sirenda Vong and colleagues argue that investing in information technology surveillance systems to detect trends is an essential first step in tackling antimicrobial resistance in South East Asian countries

- Lack of IT infrastructure is often cited as a barrier to comprehensive AMR surveillance and antibiotic usage stewardship programmes in LMICs
- Few open access software options that might support an IT infrastructure for AMR surveillance are available

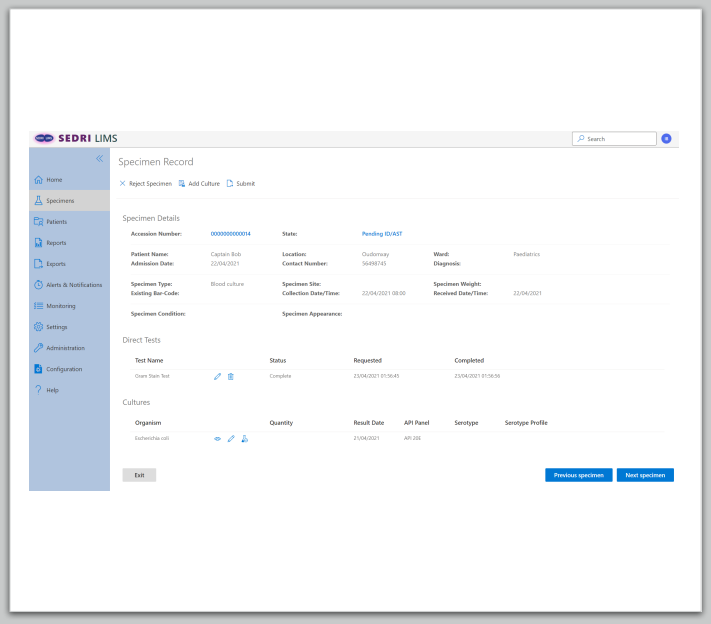
Lancet Infect Dis. 2021; 10.1016/s1473-3099(20)30835-5

43

BMJ. 2017;358:j3781

SEDRI-LIMS

- Open-source laboratory information system
- Progressive web app
  - Works on tablets, laptops, workstations
- Laptop, local server, cloud-based
- Microbiology focused
  - User-friendly
  - Flexible
  - Interoperability built in
- Coming soon



44

Better AMR data analysis tools

The microbiology laboratory database software.

AMR (for R) | Home | How to | Manual | Authors | Changelog

AMR (for R)

Note: the rules of 'EUCAST Clinical Breakpoints v11.0 (2021)' are now implemented.

What is **AMR** (for R)?

(To find out how to conduct AMR data analysis, please continue reading here to get started.)

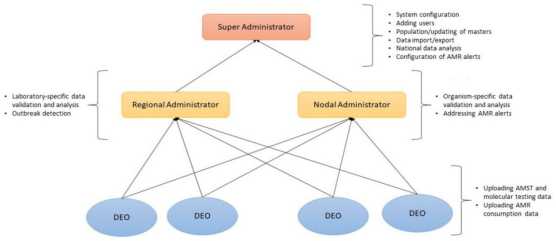
AMR is a free, open-source and independent R package to simplify the analysis and prediction of Antimicrobial Resistance (AMR) and to work with microbial and antimicrobial data and properties, by using evidence-based methods. **Our aim is to provide a standard** for clean and reproducible AMR data analysis, that can therefore empower epidemiological analyses to continuously enable surveillance and treatment evaluation in any setting.

JAC Antimicrob Resist
doi:10.1093/jacamr/dlab023

JAC-Antimicrobial Resistance

ICMR's Antimicrobial Resistance Surveillance system (*i*-AMRSS): a promising tool for global antimicrobial resistance surveillance

Jasmine Kaur[1,2,3]†, Ajay Singh Dhama[1]†, Harish Buttolia[1]†, Jasleen Kaur[1], Kamini Walia[4], Vinod Ohri[4], Vinit Kumar[1], Andrew M. Lynn[2], Alok Srivastava[3,5] and Harpreet Singh[1]*



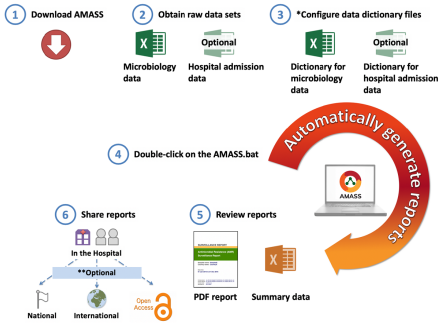
Clinical data analysis?

- Guideline development
- Outcomes / Risk factors

Joining up clinical and lab data… and putting in the hands of local clinicians

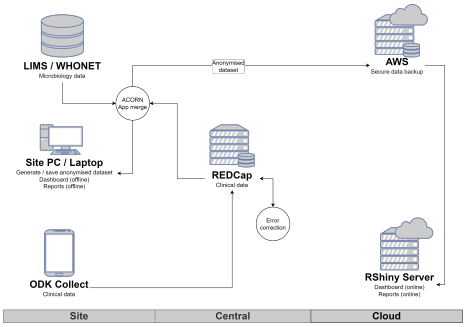
AMASS

- Automated reports using existing hospital data



ACORN

- Prospective pragmatic clinical surveillance

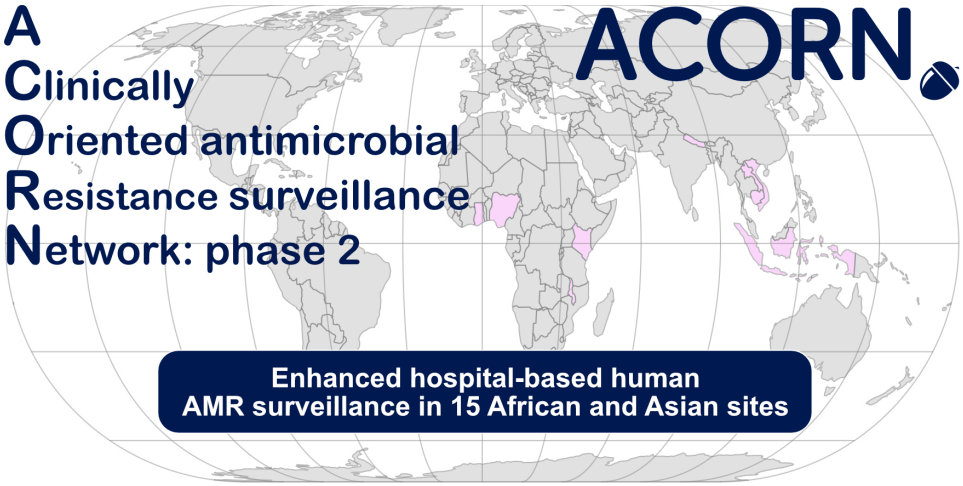


J Med Internet Res. 2020;22(10):e19762.

www.acornamr.net

A Clinically Oriented antimicrobial Resistance surveillance Network: phase 2

ACORN



Enhanced hospital-based human AMR surveillance in 15 African and Asian sites

Patients treated for suspected bacterial infection
- Daily ward review for community acquired infections
- Weekly point-prevalence survey for hospital acquired infections

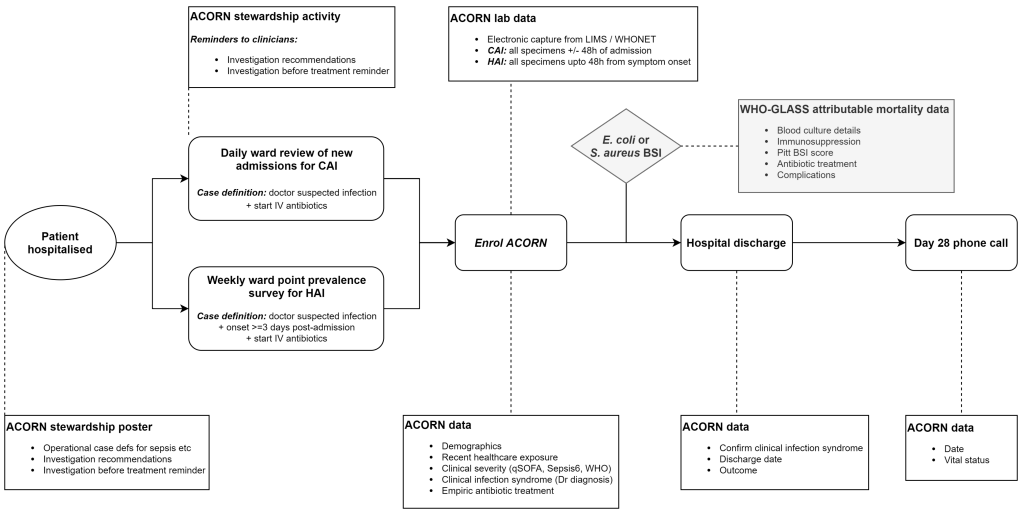
Efficient clinical and lab data capture
- WHO GLASS pathogens
- Linkage to WHO attributable mortality protocol

Generation of locally useful data
backed up by user friendly analysis and reporting tools

https://acornamr.net/

47

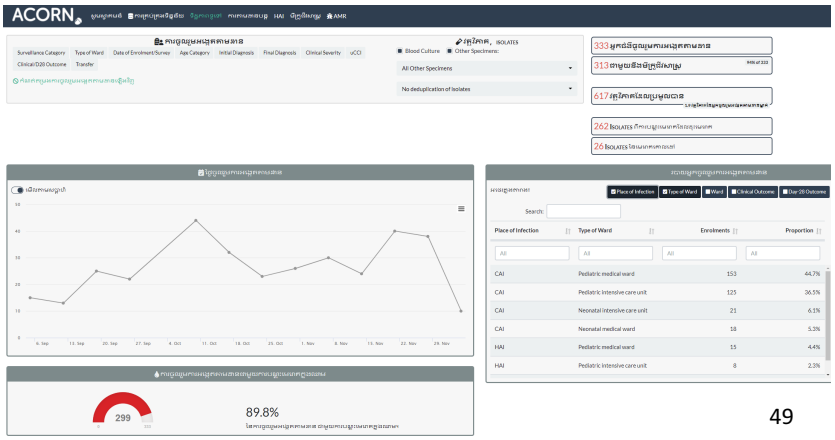
ACORN surveillance work flow



48

The ACORN Dashboard

- Real-time flexible data access
- Online and offline

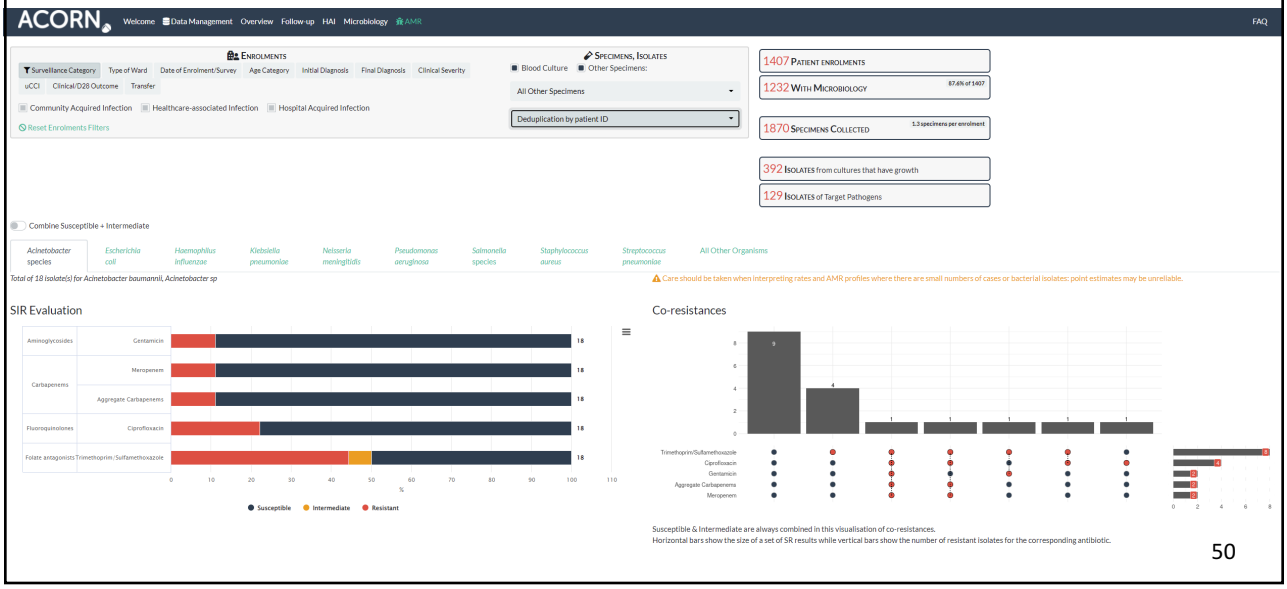


Give it a try

- Fully functional online demo
- https://moru.shinyapps.io/acorn2/

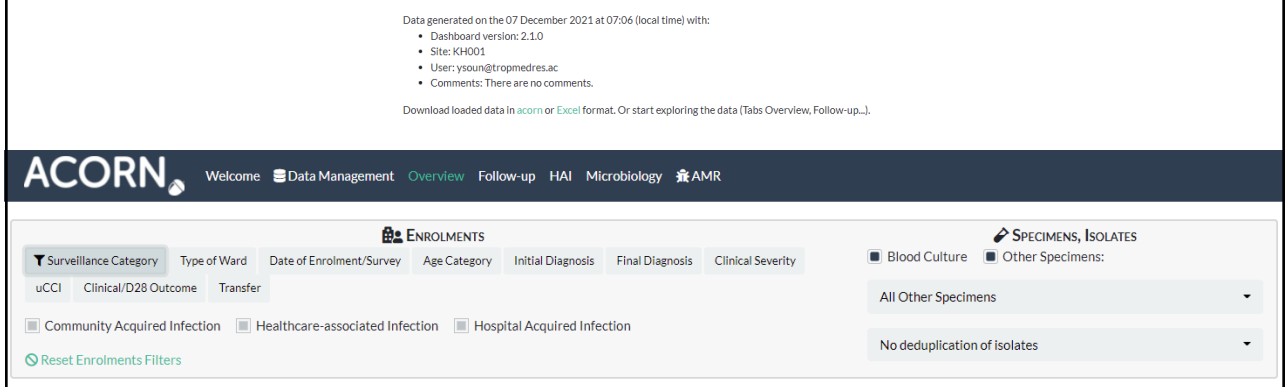
49

Useful AMR data summaries



50

It's your data…what do you want to know?



Filter clinical and lab data to generate the summary that you need

All data and graphs are immediately downloadable for incorporation into PowerPoint slides and reports

51

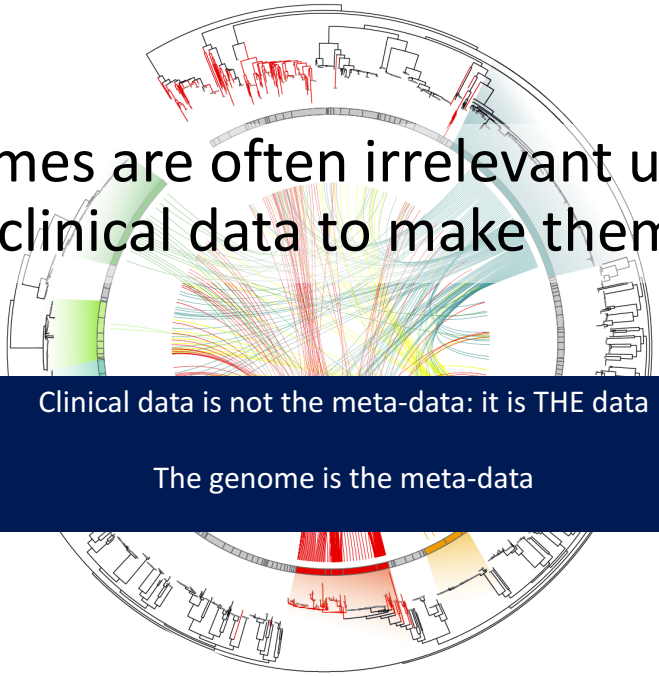
A word about genomes

- Clearly have the potential to add considerable value to AMR surveillance efforts

- Key issues to resolve
  - Scope of WGS-based surveillance
  - Discordances between phenotypic and genotypic AMR data
  - Decentralisation to ensure clinical utility is not lost
    - Cost and logistics issues are challenging
  - Access to easy-to-use surveillance-appropriate bioinformatics tools
    - Pathogenwatch / CGE-DTU (online) and FlowCraft / Bactopia (local) are all available now

52

Genomes are often irrelevant unless there is clinical data to make them useful



Clinical data is not the meta-data: it is THE data

The genome is the meta-data

53

Nat Genet. 2014;46(3):305-9

To sum up…

- Generation and interpretation of AMR burden data is complicated
- There are still large data (+ data quality) and knowledge gaps
- Data management is a major road block to progress
  - Urgently need better LIMS and IT infrastructure to support this
  - User friendly analysis tools would unlock local data use
- Not enough attention is being paid to local use of data
- More focus on the local situation will improve uptake and usefulness of global surveillance
  - If we don't get the site level data sorted, then the global data will be wrong anyway

54

Thanks for listening:
any questions?

55

www.webbertraining.com/schedulep1.php	
June 8, 2022	PULLING THE PLUG ON THE SINK DRAIN Speaker: **Prof. Jean-Yves Maillard**, Cardiff University, Wales
June 21, 2022	*(European Teleclass)* HOW EFFECTIVE ARE INTERVENTIONS TO IMPROVE CLEANING OF HEALTHCARE ENVIRONMENTS IN LOW-RESOURCED SETTINGS? Speaker: **Prof. Giorgia Gon**, London School of Hygiene and Tropical Medicine, UK
June 30, 2022	*(FREE Teleclass)* SHARING KNOWLEDGE: LEARNING FROM THOSE WHO HAVE CHALLENGED THE CIC Speaker: **Sam MacFarlane**, Public Health Ontario, **Sandra Petersen**,Ottawa Public Health, and **Jeff Lee,** Canadian Armed Forces Health Services Headquarters
July 14, 2022	HEALTHCARE INFORMATICS LESSONS FROM THE PANDEMIC Speaker: **Prof. Keith Woeltje**, Medical College of Wisconsin
	(European Teleclass)

Hosted by Jane Barnett jane@webbertraining.com
www.webbertraining.com

Thanks to Teleclass Education

PATRON SPONSORS

diversey.com

virox.com

gojo.com

gamahealthcare.com