GRAM
Global Research on Antimicrobial Resistance

Global Research on Antimicrobial Resistance (GRAM) project

Determining the global burden of antimicrobial resistance

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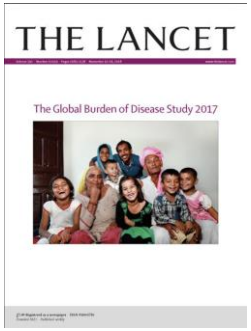
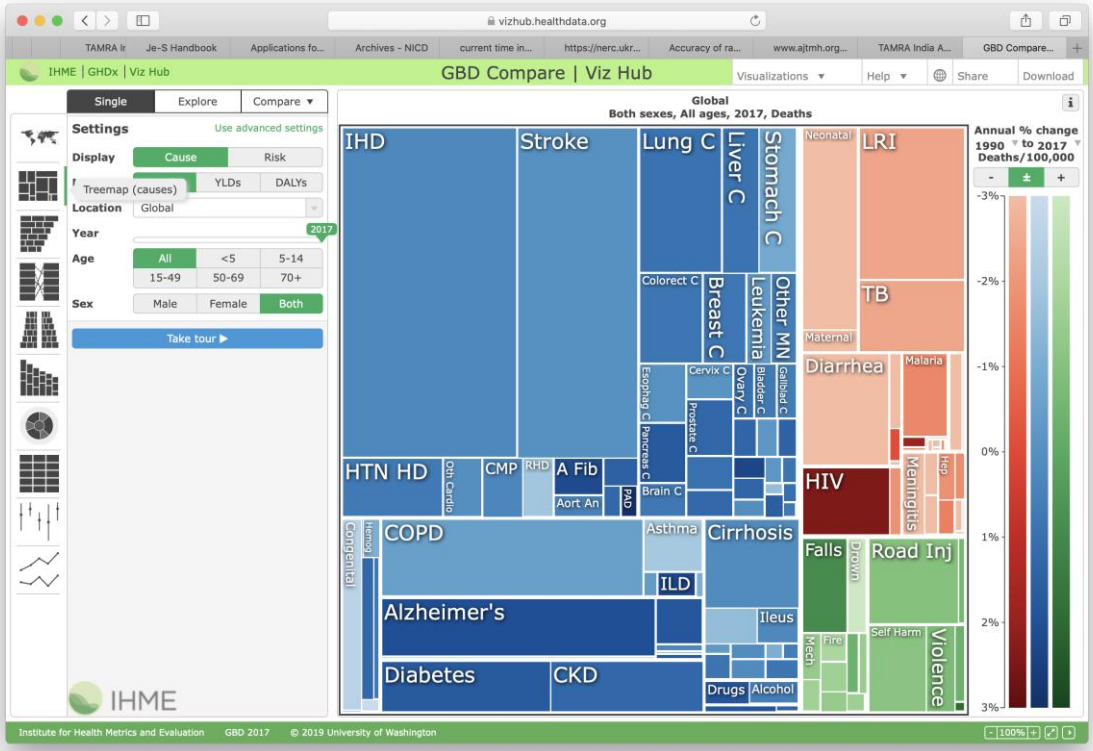
GRAM project objectives



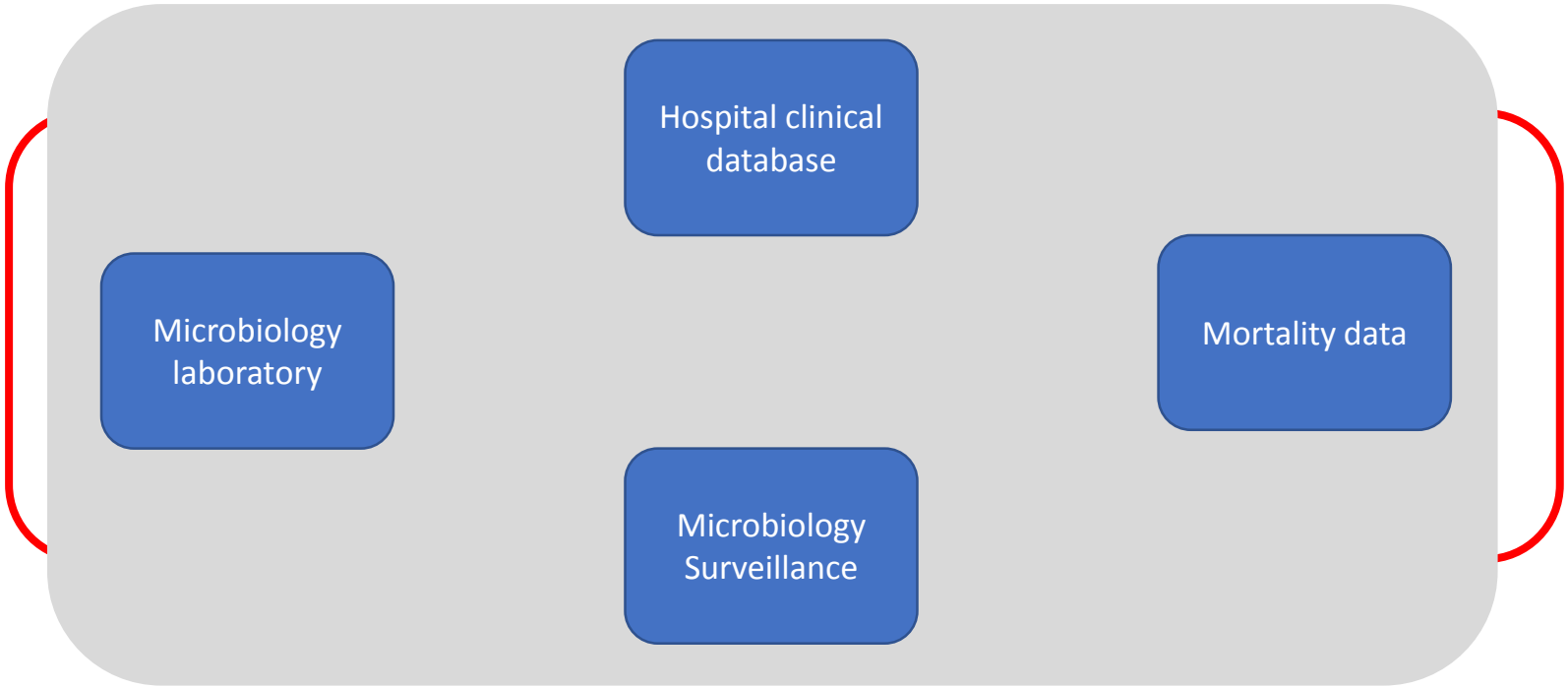
1. Comprehensive and up-to-date global data synthesis of AMR of (selected) bacterial pathogens
2. Geospatial mapping of the distribution of resistance of selected bug-drug combinations
3. Incorporation of the mortality and morbidity caused by these AMR bacterial pathogens into the Global Burden of Disease Study estimates



Bacteria	Antibacterial drug(s)
Escherichia coli	Third-generation cephalosporins, fluoroquinolones
Shigella	Fluoroquinolones
Klebsiella pneumoniae	Third-generation cephalosporins, carbapenems
Streptococcus pneumoniae	Penicillin
Staphylococcus aureus	Methicillin
Salmonella Typhi and Paratyphi	Fluoroquinolones, chloramphenicol
Non-typhoidal *Salmonellae*	Fluoroquinolones
Neisseria gonorrhoeae	Third-generation cephalosporins
Mycobacterium tuberculosis	First-line – isoniazid, rifampicin, second-line – fluoroquinolones, amikacin, capreomycin, kanamycin

The Challenge

To estimate the global burden of AMR, we are seeking:



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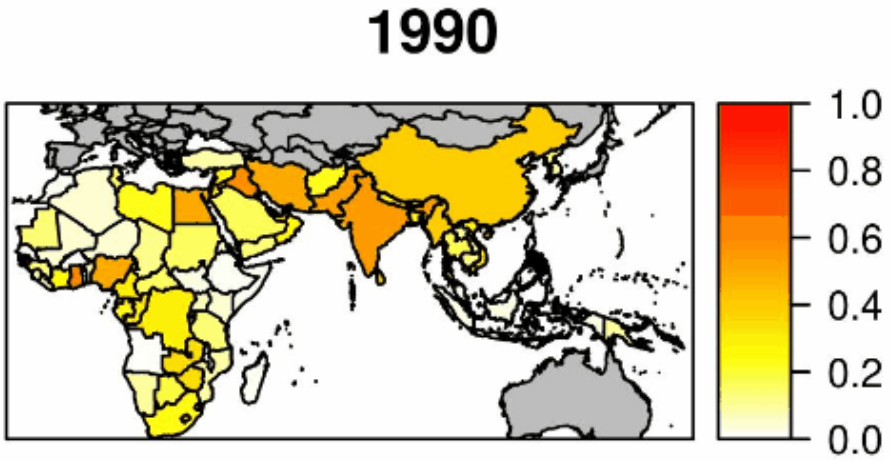
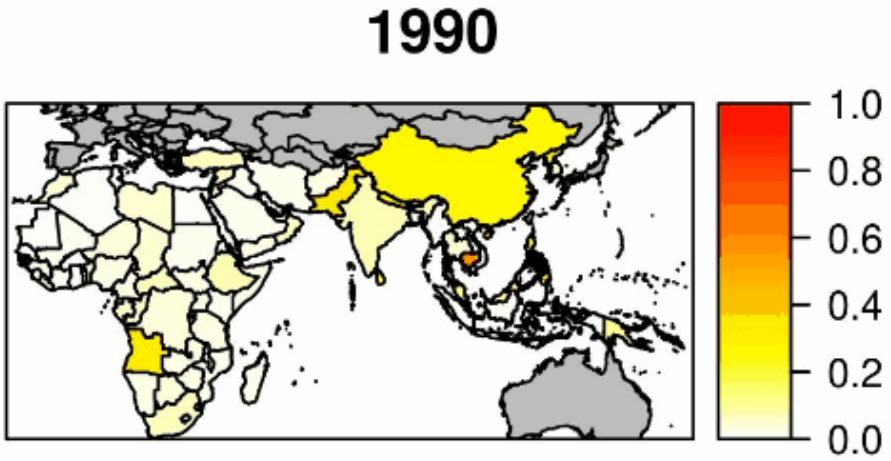
Preliminary results – *Salmonella enterica* serovar Typhi

Proportion of MDR Typhi



Proportion of FQNS Typhi



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Conclusions

- GRAM aims to produce an estimate that is as accurate as possible
- The data and the modelling assumptions are central
- We are learning where data is available and where the gaps exist
- In collaboration with researchers we are able to understand their data and their needs
- Global surveillance systems need to be built up in more countries
- Identification of knowledge and skills gaps will be a key output
- We seek to provide a framework for collaboration and drive support for strategies to fight AMR

Thank you

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The GBD-AMR team

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