Major disparities between burden of antimicrobial resistance and availability of genomic data

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ABSTRACT

The issue of antimicrobial resistance (AMR) and its burden on human health, animal health, and food safety are discussed in this poster. In order to address AMR, the World Health Organisation (WHO) has created international action plans, with genomics playing a key role in the identification of resistant bacteria. However, efforts to tackle AMR are hampered by the lack of sequencing capability in low- and middle-income nations. The Sequence Read Archive (SRA) database, created by the National Centre for Biotechnology Information (NCBI) to address this problem, is a useful tool for academics and medical professionals looking into the molecular causes of AMR.

INTRODUCTION

Antimicrobial resistance (AMR) is a critical global issue that imposes a significant burden on public health, animal health, and food safety, with an estimated 1.27M deaths attributable to bacterial AMR globally each year. If no action is taken, the global burden of AMR is projected to increase to 10 million deaths per year by 2050.[1] Calculating the burden of AMR involves analyzing mortality rates, disability-adjusted life years, and economic costs, among other factors. To alleviate AMR, the World Health Organization (WHO) has developed global action plans that emphasize the importance of diagnostics and surveillance, with genomics playing a crucial role in the diagnosis of resistant bacteria. However, accurate metadata, including clinical and epidemiological data, is essential for genomic data to be useful in understanding and managing AMR.[2]

Despite its potential benefits, there are significant global inequities in access to sequencing capacity, hindering efforts to combat AMR. Several studies have highlighted the lack of sequencing capacity in low- and middle-income countries, with limited resources to perform genomic analysis.[3,4]

To support genomic analysis for AMR surveillance and research, the National Center for Biotechnology Information (NCBI) at the National Institutes of Health (NIH) has developed the Sequence Read Archive (SRA) database. This database provides a central repository for raw sequence data from high-throughput sequencing platforms, including data generated by next-generation sequencing technologies. SRA is a valuable resource for researchers and clinicians investigating the molecular mechanisms of AMR, as well as for surveillance and outbreak investigation. The SRA database contains a vast collection of raw sequencing data, including data from bacterial, viral, and eukaryotic genomes, as well as metagenomic datasets.

MATERIALS & METHODS

In this study, Mycobacterium tuberculosis (MTB), Streptococcus pneumoniae, Staphylococcus aureus, Klebsiella pneumoniae, and Escherichia coli were the five pathogens for which data were gathered as these five pathogens cause the most global burden. Data for various infectious syndromes, disability-adjusted life years (DALYs), rates per 100,000 people, and all ages were gathered from the Institute for Health Metrics and Evaluation (IHME) in the form of choropleth maps. The data was downloaded for all nations globally from the IHME website.[5]

Jupyter Notebook was used for all data processing. The prior data was combined to construct plots, and the choropleth maps for each of the five diseases were imported into the notebook. The notebook was updated with pathogen data from IHME, and SRA metadata description was added via GitHub (git@github.com:zzeinou/amr_metadata_project.git). Graphs were then generated utilizing the data that had been processed.

RESULTS

Unequal Global AMR Health Burden
Antimicrobial resistance (AMR) poses a threat to global health, yet its consequences aren't felt equally everywhere. Some communities may be more at danger than others within a country, and certain regions are more affected than others. (Figure 1)

Poor Metadata Availability
Accurately tracking the effect and spread of AMR is challenging due to a lack of easily accessible metadata (Figure 2).

Most countries lack any available genomes
Our awareness of the issue is further limited by the absence of available genomes in the majority of countries (Figure 3).

No relationship between between intensity of sequencing and burden
Additionally, it appears that there is no direct correlation between the level of sequencing and the prevalence of AMR in a particular community (Figure 3).
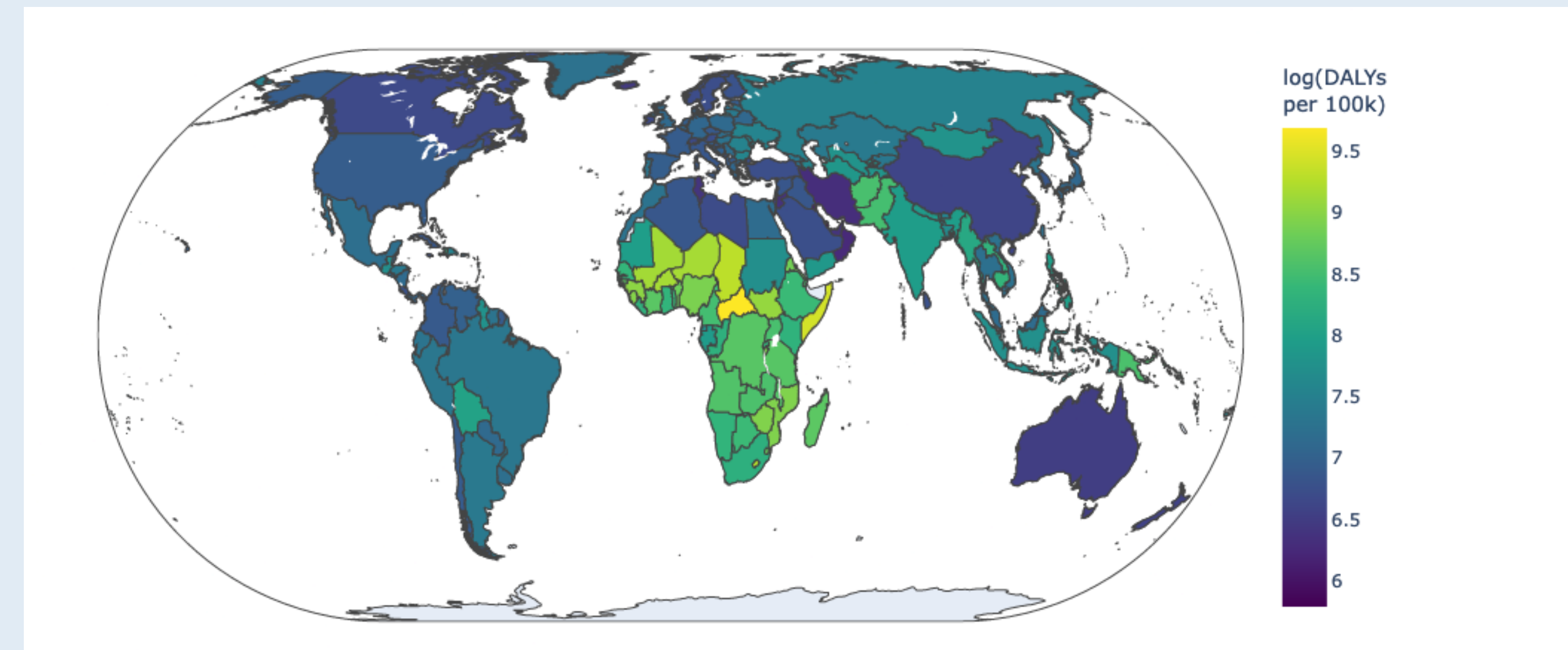
Figure 1: Global Antimicrobial Resistance Health Burden for 5 Highest Burden Pathogens. Chloropleth map indicating the highly unequal population normalised national burden attributable to Bacterial AMR from 5 highest burden pathogens (Mycobacterium tuberculosis, Streptococcus pneumoniae, Staphylococcus aureus, Klebsiella pneumoniae, and Escherichia coli). Burden is indicated as per the color bar in log Disability Adjusted Life Years (DALYs) lost per 100,000 population in 2019 and is derived from IHME database. The lowest national burden (dark blue) is found in countries; Iran, Oman, Tunisia and the highest (yellow) in countries; Central African Republic, Somalia, Tchad.
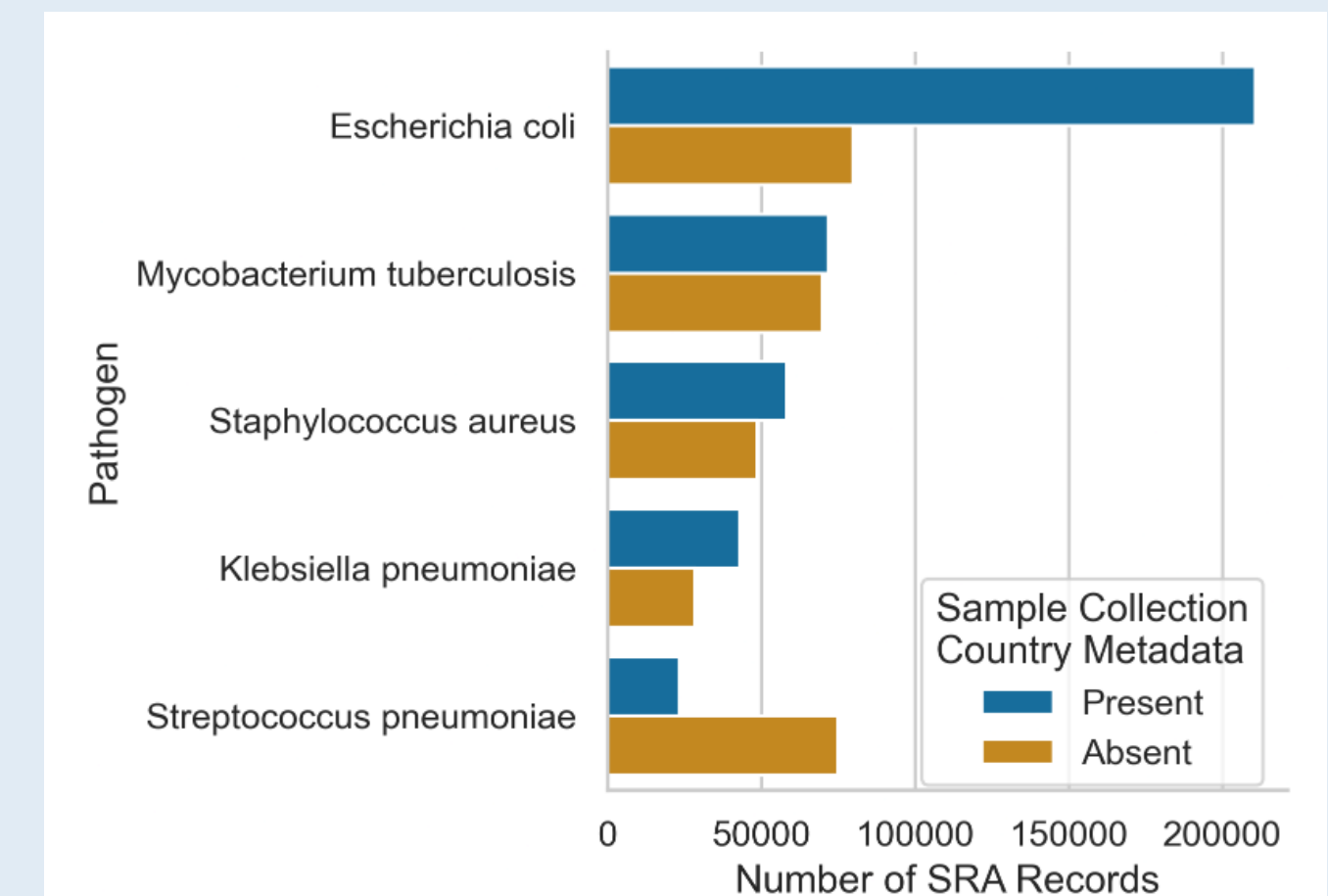
Figure 2: Availability of Sampling Location Metadata in SRA. Bar chart illustrating the total number of SRA records (both present and absent) across the globe for the following five pathogens; Escherichia coli, Mycobacterium tuberculosis, Staphylococcus aureus, Klebsiella pneumoniae, and Streptococcus pneumoniae. The quantity of metadata for each disease that is accessible in the countries where the data was sampled is displayed. Streptococcus pneumoniae has fewer than 25,000 SRA records, whereas Escherichia coli has over 200,000, showing a nearly global prevalence.
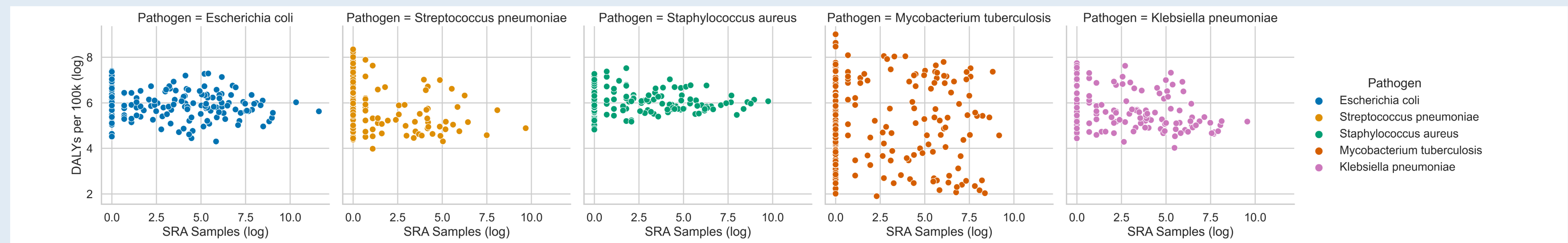
Figure 3: Burden and Sequencing data for each of the 5 Highest Burden Pathogens. The top 5 pathogens with the highest burden are shown along with their sequencing data. The graphic shows that the quantity of sequencing samples available and the burden of each infection are unrelated. This absence of a correlation emphasizes the need for better accessibility and availability of sequencing data for all diseases, regardless of their burden, to support effective disease surveillance and control initiatives in a timely manner.

DISCUSSION

The effectiveness of antibiotics and other antimicrobial treatments is at risk because of the serious global public health problem of antimicrobial resistance (AMR). The incidence and severity of resistant infections vary greatly across the globe, with some areas bearing a disproportionately high burden of AMR. For instance, a number of LMICs have high rates of AMR because of things like limited healthcare infrastructure, poor sanitation, and excessive antibiotic use. Additionally, within nations, specific populations, such as those who are immunocompromised or who live in crowded conditions, may be more susceptible to resistant illnesses. Even though precise statistics on the prevalence and effects of AMR are urgently needed, the lack of easily accessible metadata continues to be a major problem. It is challenging to create efficient prevention and treatment plans without thorough knowledge about the frequency, prevalence, and outcomes of resistant illnesses. Furthermore, most nations do not have any analysis-ready genomes, which further restricts our understanding of the genetic pathways generating AMR. Furthermore, it doesn't seem as though there is an immediate relationship between the level of sequencing and the prevalence of AMR in a particular community. The transmission of AMR may be significantly influenced by variables other than the genetic makeup of resistant strains, such as environmental and socioeconomic determinants of health. Increased funding is urgently needed for surveillance systems, data exchange infrastructure, and targeted research projects that concentrate on the distinct causes of AMR in various populations in order to solve these difficulties.[6,7]

CONCLUSION

Finally, it should be noted that the burden of antimicrobial resistance (AMR) continues to pose a serious risk to global public health, and that the lack of complete genetic data on AMR presents a substantial obstacle to understanding and addressing this issue. Having access to sequencing capacity and reliable metadata are essential for creating strategies that effectively combat AMR. Therefore, there is an urgent need for international efforts to increase genomic data accessibility, produce accurate metadata, and create efficient AMR understanding and management techniques. By collaborating, we can increase our understanding of the issue and put evidence-based strategies into action that can help us stop the spread of AMR.

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