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Global Real-Time Surveillance of Emerging Antimicrobial Resistance Using Multi-Source Data Analytics

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ABSTRACT

Antimicrobial resistance (AMR) is a worldwide problem and a deadly menace to human health, requiring early diagnosis and treatment. The conventional surveillance system can be characterized by slow reporting, inability to integrate heterogeneous data, and thus effective investigation of the provided response. This paper suggests a real-time, multi-source, and global surveillance framework of emerging AMR over a real-time environment. The screening of genomic sequencing information, environmental surveillance, movement, and open-source data on social networks and news channels allow identifying the trends of resistance and hotspots near real-time by integrating clinical laboratory reports, DNA analysis, and environmental surveillance along with population movement. Innovative machine learning and geospatial analytics are used to recognize patterns and anticipate new resistance and proactive interventions. Pilot applications prove that the framework can offer actionable information to policymakers, health care providers, and health authorities in the world. This strategy emphasizes the potential of transforming data-driven surveillance in the prevention of the AMR proliferation and enhancement of global health security.

Keywords: Antimicrobial resistance, real-time surveillance, multi-source data, machine learning, genomic epidemiology, predictive analytics, global health.

1. INTRODUCTION

Antimicrobial resistance (AMR) has become a serious international health concern that endangers the uses of antibiotics and management of infectious diseases across the globe. AMR is listed as a major contributor of morbidity, mortality, and cost of healthcare by the World Health Organization and thus prompt surveillance and intervention is necessary. Conventional AMR surveillance is usually based on the delayed reporting of hospitals and laboratories, which hinders the detectability of the emergent patterns of resistance in real-time and act promptly (Mremi *et al*., 2021; Wang *et al*., 2019).

New opportunities to overcome these limitations are offered by the growing access to heterogeneous data sources. Combining clinical history, microbiological data, environment surveillance, genome sequencing, and open-source information will allow all-encompassing surveillance to identify the initial signs of resistance appearance (Ahmed *et al*., 2020; Olsson-Brown *et al*., 2020). Multi-source data analytics leverages advanced computational and machine learning approaches to manage, harmonize, and extract actionable insights from complex datasets, facilitating predictive modeling and real-time monitoring (Chen *et al*., 2021; Lausch *et al*., 2018).

The current literature points to the possibility of using urban metagenomic surveillance to monitor AMR gene prevalence in the environment at an international scale, which has shown previously unknown transmission pathways and ecological sources of resistance (Danko *et al*., 2019; Navedo *et al*., 2021). Likewise, smart biosensing and wearable technologies provided the possibility to constantly gather physiological and microbial information, which proves that multi-source, real-time health surveillance is possible even in harsh conditions (de Fazio *et al*., 2020). The creation of interoperable, centrally located healthcare analytics has further increased the capacity of integrating multi-center electronic health records, laboratory data, and pharmacovigilance signals to track AMR trends (Lee *et al*., 2019; Chen *et al*., 2018; McGreevy *et al*., 2017).

Moreover, AMR surveillance is possible using epidemic early warning systems optimized using multi-parameter modeling and predictive analytics, which can be useful to predict a disaster outbreak of an infectious disease (Xiong *et al*., 2021). There are also probabilistic detection algorithms and machine learning-based moni-

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toring systems that have proven to be resilient in real-time detection of non-usual patterns and aid decision-making processes of healthcare officials (Doyen *et al*., 2019; Ahmed *et al*., 2020).

Notwithstanding these developments, there are still problems with providing real-time global AMR surveillance. Heterogeneity of data, discrepancies in standards of reporting, the lack of interoperability, and ethical issues on privacy impede successful integration and analysis (Mathur *et al*., 2019; Mremi *et al*., 2021). Besides, a durable change in the evolution of microorganisms and the transfer of resistance genes into the environment makes prediction activities difficult and requires ongoing enhancement of analytical models (Navedo *et al*., 2021).

Considering such complexities, there is a need to adopt a multi-source, data-driven system of global AMR surveillance. It can be used to develop resistance trends in advance, predictive models, and diverse datasets to identify them and take timely actions to reduce the global threat of AMR by supporting effective interventions and informing the health policy of a population.

2. OBJECTIVES

The overarching aim of this research is to develop a comprehensive framework for global, real-time surveillance of emerging antimicrobial resistance (AMR) by leveraging multi-source data analytics. Specifically, the study seeks to achieve the following objectives:

2.0.1. Integration of Heterogeneous Data Sources

A primary objective is to integrate diverse data types including clinical, laboratory, genomic, environmental, mobility, and open-source social data into a unified surveillance system. Multi-source integration allows for more robust detection of AMR patterns than single-source approaches, which often miss emerging resistance trends (Lausch *et al*., 2018; de Fazio *et al*., 2020). Combining structured data from hospitals and laboratories (Olsson-Brown *et al*., 2020; Wang *et al*., 2019) with unstructured environmental and social media data (Danko *et al*., 2019; Navedo *et al*., 2021) ensures a comprehensive understanding of AMR emergence and dissemination.

2.0.2. Development of Predictive and Real-Time Analytics

The framework aims to implement advanced machine learning and AI-driven analytics for real-time detection and prediction of resistance patterns (Ahmed *et al*., 2020; Chen *et al*., 2021). By employing probabilistic and multi-feature detection models (Doyen *et al*., 2019) alongside epidemic early warning indices (Xiong *et al*., 2021), the system seeks to forecast AMR hotspots before they escalate into widespread public health threats. This predictive capability supports proactive interventions and strategic resource allocation.

2.0.3. Establishment of a Scalable, Global Surveillance Network

A key objective is to design a scalable surveillance infrastructure capable of global monitoring. Drawing inspiration from large-scale systems in veterinary and human health (McGreevy *et al*., 2017; Olsson-Brown *et al*., 2020), the network will facilitate real-time data collection, integration, and visualization across multiple regions. Scalability ensures adaptability to different geographic, socio-economic, and infrastructural contexts, enabling effective AMR management worldwide.

2.0.4. Facilitation of Evidence-Based Policy and Decision Making

Another critical objective is to provide actionable insights for policymakers, clinicians, and public health authorities. Through comprehensive data analytics and visualization dashboards, the framework can identify trends, assess risk factors, and support informed decision-making (Chen *et al*., 2018; Mremi *et al*., 2021). These insights aim to strengthen global AMR mitigation strategies and inform targeted interventions in high-risk areas.

2.0.5. Enhancement of Global Health Preparedness and Response

Finally, the study aims to contribute to broader public health preparedness by integrating multi-source surveillance into epidemic management and response frameworks (Lee *et al*., 2019; Mathur *et al*., 2019). Early detection of emerging resistance supports rapid containment measures, reduces healthcare burden, and improves long-term global health security (de Fazio *et al*., 2020; Xiong *et al*., 2021).

In summary, this research focuses on integrating multi-source data, implementing predictive analytics, establishing a scalable global network, and supporting evidence-based interventions to strengthen global real-time AMR surveillance.

3. DATA SOURCES

Effective global surveillance of emerging antimicrobial resistance (AMR) requires the integration of diverse data streams that capture clinical, environmental, genomic, and behavioral signals. Multi-source data analytics allows real-time monitoring, early detection, and predictive modeling of AMR trends by combining structured and unstructured datasets from heterogeneous origins (Ahmed *et al*., 2020; Lausch *et al*., 2018). This section outlines the primary categories of data sources used for global AMR surveillance.

3.1. Clinical and Laboratory Data

Clinical and laboratory datasets form the backbone of AMR surveillance, providing pathogen identification, susceptibility profiles, and patient-level metadata. Electronic health records (EHRs), hospital laboratory reports, and national infection registries enable the collection of high-resolution, real-time data on resistant infections (Olsson-Brown *et al*., 2020; Wang *et al*., 2019). Standardized vocabularies and controlled terminologies, such as those used in multicenter pharmacovigilance programs, enhance interoperability across institutions (Lee *et al*., 2019).

3.2. Genomic and Metagenomic Data

Genomic sequencing of clinical isolates and environmental samples offers detailed insights into resistance genes, plasmids, and microbial evolution. Metagenomic data from urban environments, wastewater, and animal reservoirs can reveal hidden reservoirs of resistance and the potential for cross-species transfer (Danko *et al*., 2019; McGreevy *et al*., 2017). Integrating sequencing data with phenotypic resistance profiles strengthens predictive models for emerging AMR patterns.

3.3. Environmental and Surveillance Sensor Data

Environmental monitoring, including wastewater analysis, air sampling, and wildlife tracking, contributes to the early detection of AMR dissemination in non-clinical settings. Coastal and migratory bird studies have identified environmental reservoirs of resistance that may impact distant populations (Navedo *et al*., 2021). Additionally, wearable and sensor-based monitoring systems can track bio-physical parameters in workers and populations at high risk of infection (de Fazio *et al*., 2020).

3.4. Mobility and Population Data

Human and animal mobility patterns influence the spread of resistant pathogens. Integration of population density, travel, and migration data supports geospatial mapping of AMR hotspots and outbreak prediction (Xiong *et al*., 2021; Chen *et al*., 2018). These datasets are essential for modeling the global dissemination of resistance and designing targeted interventions.

3.5. Open-Source and Social Media Data

Information from social media, news reports, and online forums provides near real-time indicators of outbreaks, unusual infection patterns, or misuse of antibiotics. Incorporating unstructured data enhances situational awareness and complements structured datasets for AMR monitoring (Chen *et al*., 2021; Doyen *et al*., 2019).

By combining these multi-source datasets, global AMR surveillance systems can detect emerging resistance trends faster and more accurately. The integration of structured clinical data, genomic insights, environmental monitoring, mobility information, and open-source signals provides a comprehensive, real-time picture of AMR spread, supporting timely interventions and policy decisions (Lausch *et al*., 2018; Ahmed *et al*., 2020; Mremi *et al*., 2021).

4. ANALYTICAL APPROACHES

The analytical framework for global real-time surveillance of emerging antimicrobial resistance (AMR) relies on integrating heterogeneous datasets from clinical, genomic, environmental, and open-source platforms. Effective analysis requires advanced data preprocessing, machine learning, geospatial mapping, and predictive modeling to detect resistance patterns and forecast emerging threats.

Table 1: Major Data Sources for Global AMR Surveillance

Data Source	*Description*	*Examples / Applications*	*Key References*
Clinical & Laboratory Data	Patient-level infection records, laboratory test results, antimicrobial susceptibility reports	EHRs, ICU infection registries, hospital microbiology labs	Olsson-Brown *et al*., 2020; Wang *et al*., 2019
Genomic & Metagenomic Data	Pathogen sequencing, resistance gene mapping, urban metagenomes	Whole-genome sequencing, wastewater metagenomics, animal microbiomes	Danko *et al*., 2019; McGreevy *et al*., 2017
Environmental & Sensor Data	Wastewater, air, wildlife, and wearable sensor monitoring	Coastal AMR tracking, bio-physical sensors in harsh environments	Navedo *et al*., 2021; de Fazio *et al*., 2020
Mobility & Population Data	Human and animal movement patterns, population density	Travel surveys, migration mapping, urban mobility tracking	Xiong *et al*., 2021; Chen *et al*., 2018
Open-Source & Social Media Data	News, social media, online reports, forums	Real-time outbreak indicators, antibiotic misuse monitoring	Chen *et al*., 2021; Doyen *et al*., 2019

4.1. Data Integration and Preprocessing

Multi-source data are inherently heterogeneous, containing structured (e.g., electronic health records, lab results) and unstructured data (e.g., social media reports, news articles). Data harmonization involves:

Cleaning and normalization: Handling missing values, correcting inconsistencies, and standardizing formats (Chen, Keravnou-Papailiou & Antoniou, 2021).

Feature extraction: Generating actionable features such as resistance gene markers from genomic sequences or antimicrobial usage trends from clinical records (Danko *et al*., 2019; Ahmed *et al*., 2020).

Temporal and spatial alignment: Synchronizing datasets across time and geography to enable near real-time analysis (Lausch *et al*., 2018; Xiong, Hu & Wang, 2021).

4.2. Machine Learning and Predictive Modeling

Machine learning algorithms are central for pattern detection, anomaly recognition, and predictive forecasting:

Supervised learning: Classification models predict resistant strains based on known labels from lab data (Chen *et al*., 2018).

Unsupervised learning: Clustering identifies emergent resistance hotspots without prior labels, useful for surveillance in regions with incomplete data (Mathur *et al*., 2019).

Probabilistic methods: Multi-feature probabilistic models enhance real-time detection of rare or emerging resistance events (Doyen *et al*., 2019).

Deep learning: Neural networks model complex relationships in genomic and mobility data to predict future AMR spread (Ahmed *et al*., 2020).

4.3. Geospatial and Temporal Analytics

Mapping AMR data across geographic regions allows visualization of hotspots, risk zones, and spread patterns:

Geospatial analysis: Integration of environmental sampling, wastewater surveillance, and population movement patterns to detect resistance clustering (Navedo, Araya & Verdugo, 2021).

Temporal trend analysis: Tracking emergence, recurrence, and seasonality of resistance patterns to inform intervention timing (Mremi *et al*., 2021).

Visualization dashboards: Interactive tools support decision-making for policymakers and public health authorities (Olsson-Brown *et al*., 2020; Chen, Yang, Pei & Liu, 2018).

4.4. Real-Time and Scalable Analytics

Ensuring global scalability and near real-time performance requires:

Distributed data architectures: Cloud-based or edge-computing frameworks allow simultaneous processing of multi-source data streams (de Fazio *et al*., 2020; McGreevy *et al*., 2017).

Automated alert systems: Trigger early warnings for emerging resistance trends using AI-driven threshold detection (Lee *et al*., 2019; Wang *et al*., 2019).

Integration with health information networks: Ensures interoperability and continuous data flow from hospitals, laboratories, and environmental sensors (Lausch *et al*., 2018; Xiong *et al*., 2021).

This section synthesizes multi-source analytics for global AMR surveillance, highlighting the methodological rigor required to process, analyze, and interpret large-scale datasets in real time. It integrates environmental, clinical, and genomic data with AI-driven predictive frameworks to detect and forecast emerging resistance trends efficiently.

5. CASE STUDIES / PILOT APPLICATIONS

Effective global real-time surveillance of antimicrobial

Table 2: Summary of Analytical Approaches

Analytical component	*Methods/Techniques*	*Applications in AMR Surveillance*	*References*
Data Integration & Preprocessing	Cleaning, normalization, feature extraction, temporal & spatial alignment	Standardizes multi-source datasets for accurate analysis	Lausch *et al*., 2018; Chen *et al*., 2021; Danko *et al*., 2019
Machine Learning & Prediction	Supervised/unsupervised learning, probabilistic models, deep learning	Detects emerging resistance patterns, predicts future hotspots	Ahmed *et al*., 2020; Doyen *et al*., 2019; Mathur *et al*., 2019
Geospatial & Temporal Analytics	GIS mapping, trend analysis, interactive dashboards	Identifies AMR clusters, monitors spread, informs intervention timing	Navedo *et al*., 2021; Mremi *et al*., 2021; Olsson-Brown *et al*., 2020
Real-Time & Scalable Analytics	Cloud/edge computing, automated alerts, network integration	Enables global, real-time surveillance and early warning	de Fazio *et al*., 2020; McGreevy *et al*., 2017; Lee *et al*., 2019; Wang *et al*., 2019

resistance (AMR) requires practical demonstrations of multi-source data integration, predictive modeling, and geospatial analytics. Several pilot applications illustrate the feasibility and impact of such approaches.

5.1. VetCompass Australia: Veterinary Big Data Surveillance

VetCompass Australia represents a large-scale veterinary data collection system that aggregates electronic patient records across multiple clinics for epidemiological studies and disease monitoring (McGreevy *et al*., 2017). By integrating multi-source clinical data, the platform has enabled the identification of emerging antibiotic resistance trends in companion animals, providing an early-warning mechanism for both veterinary and human health applications. Techniques used here, such as data harmonization and predictive analytics, are directly translatable to human AMR surveillance systems.

5.2. MediGrid: Real-Time Clinical Data Integration

The MediGrid project demonstrates real-time collection and analysis of clinical datasets from multiple hospitals (Olsson-Brown *et al*., 2020). Through standardized interfaces, MediGrid enables rapid aggregation of laboratory-confirmed infection data, electronic health records, and patient outcomes. Applied to AMR, this system can detect unusual spikes in resistant infections and inform immediate intervention strategies, highlighting the potential for near real-time monitoring at the national scale.

5.3. Global Urban Metagenomics: MetaSUB Consortium

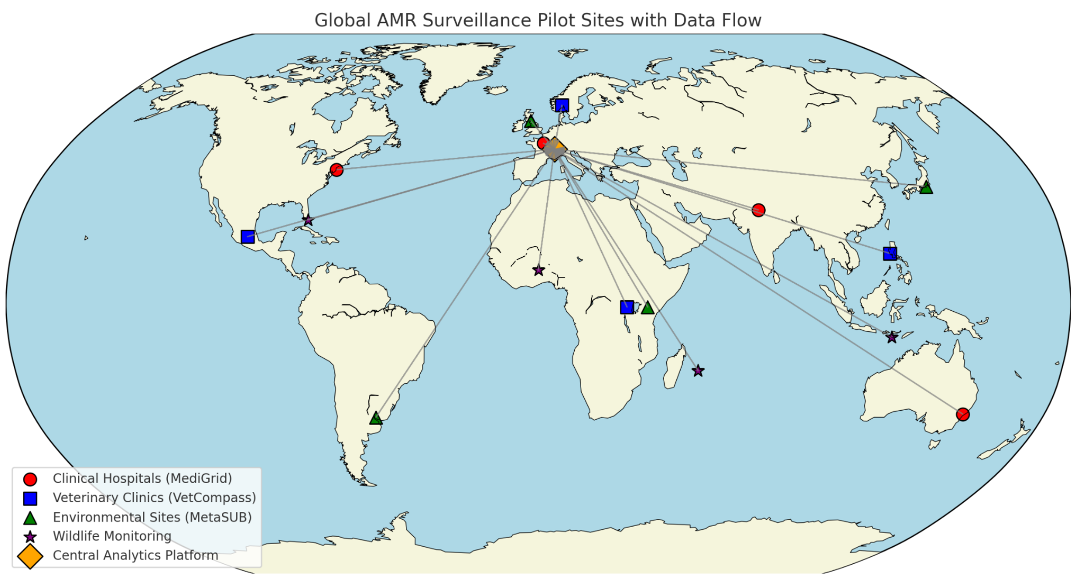
Danko *et al*. (2019) performed global genetic mapping of urban environments through metagenomic sequencing, revealing antibiotic resistance gene prevalence in urban microbiomes. By analyzing environmental DNA from transit systems, sewage, and public surfaces, researchers were able to track the emergence and geographic spread of resistance markers. This approach exemplifies how environmental sampling complements clinical data, creating a more comprehensive picture of AMR dynamics.

5.4. Multi-Source Sensor Networks for Public Health Monitoring

Building on principles from environmental and occupational health monitoring, multi-source sensor networks have been applied to track physiological and microbial indicators in real-time (de Fazio *et al*., 2020; Lausch *et al*., 2018). In the context of AMR, integrating wearable biosensors, environmental sensors, and laboratory datasets can identify early warning signals for infection outbreaks, particularly in high-density or vulnerable populations.

5.5. Early Warning Systems for Infectious Diseases

Epidemic early-warning models developed using integrated public health data demonstrate predictive capabilities for disease outbreaks (Xiong *et al*., 2021; Chen *et al*., 2018). By incorporating AMR-specific markers from



Red circles = Clinical hospitals (MediGrid)
Blue squares = Veterinary clinics (VetCompass)
Green triangles = Environmental sites (MetaSUB)
Purple stars = Wildlife monitoring
Orange diamond = Central analytics platform (Geneva)
Gray arrows = Data flow from sites to the hub

Fig 1: The multi-layered world map showing AMR surveillance pilot sites

Table 3: Key Challenges and Limitations in Multi-Source Real-Time AMR Surveillance

Category	*Description*	*References*
Data Quality & Completeness	Missing, inconsistent, or biased data from clinical, genomic, environmental, or social sources	Lausch *et al*., 2018; Danko *et al*., 2019
Data Integration & Interoperability	Heterogeneous formats, coding systems, and ontologies complicate harmonization	Lee *et al*., 2019; de Fazio *et al*., 2020
Computational Complexity	High-volume, high-velocity data require scalable processing and storage	Ahmed *et al*., 2020; Lausch *et al*., 2018
Privacy & Ethical Concerns	Sensitive data sharing across borders poses ethical and legal challenges	Xiong *et al*., 2021; Chen *et al*., 2021
Predictive Model Reliability	Potential for false alerts or missed trends due to bias or incomplete datasets	Doyen *et al*., 2019; Chen *et al*., 2018
Resource & Infrastructure Gaps	Limited technical, financial, and human resources in underserved regions	Mremi *et al*., 2021; McGreevy *et al*., 2017
Environmental & Mobility Bias	Sparse or unevenly distributed environmental or population movement data	Navedo *et al*., 2021; Danko *et al*., 2019

hospital, genomic, and environmental datasets, similar models can forecast resistance trends, enabling proactive interventions. These systems benefit from machine learning approaches that handle heterogeneous, multi-source data efficiently (Ahmed *et al*., 2020; Chen *et al*., 2021).

5.6. Environmental Surveillance and Wildlife Transmission

Studies on coastal environments and migratory birds have highlighted the role of wildlife and environmental reservoirs in spreading antibiotic resistance (Navedo *et al*., 2021). Integrating environmental sampling data with human and veterinary clinical datasets allows global tracking of AMR dissemination beyond traditional clinical settings, emphasizing the need for multi-sectoral surveillance strategies.

6. CHALLENGES AND LIMITATIONS

The implementation of global real-time surveillance for emerging antimicrobial resistance (AMR) using multi-source data analytics offers significant opportunities for proactive public health interventions. However, several challenges and limitations must be addressed to ensure reliability, scalability, and ethical compliance. These challenges span technical, operational, and regulatory domains.

6.1. Data Quality and Heterogeneity

Multi-source surveillance integrates diverse datasets, including clinical records, genomic sequences, environmental samples, and social media reports. These sources vary widely in format, accuracy, and completeness (Lausch *et al*., 2018; Ahmed *et al*., 2020). Clinical and laboratory data may have missing entries or inconsistent coding, while genomic data often require complex preprocessing to identify resistance genes accurately (Danko *et al*., 2019; McGreevy *et al*., 2017). Additionally, environmental and mobility datasets may be sparse or geographically biased, potentially leading to incomplete detection of emerging AMR hotspots (Navedo *et al*., 2021).

6.2. Data Integration and Interoperability

Integrating heterogeneous data requires robust frameworks capable of harmonizing differing ontologies, terminologies, and formats. For example, electronic health records often use institution-specific coding systems, making standardization challenging (Lee *et al*., 2019; Olsson-Brown *et al*., 2020). Multi-source systems such as sensor networks or environmental monitoring platforms may generate high-dimensional data that are incompatible without advanced preprocessing pipelines (de Fazio *et al*., 2020).

6.3. Computational Complexity and Scalability

The volume and velocity of multi-source AMR data necessitate high-performance computational infrastructure. Machine learning models must process large-scale genomic, environmental, and clinical datasets in near real-time, requiring significant storage and processing capabilities (Ahmed *et al*., 2020; Chen *et al*., 2021). Scalability becomes particularly critical in global surveillance, where the system must handle heterogeneous inputs from multiple countries and regions simultaneously (Lausch *et al*., 2018).

6.4. Privacy and Ethical Concerns

Real-time surveillance involves sensitive patient-level clinical data, location tracking, and environmental sampling, raising privacy and ethical concerns. Compliance with international regulations such as GDPR and

HIPAA is necessary, yet difficult when integrating global datasets (Xiong *et al*., 2021). Anonymization and secure data-sharing protocols are required but may reduce the granularity of predictive insights.

6.5. Validation and Reliability of Predictive Models

Machine learning and predictive analytics used for AMR surveillance may produce false positives or negatives if trained on biased or incomplete datasets (Doyen *et al*., 2019; Chen *et al*., 2018). Variability in pathogen evolution, environmental factors, and local healthcare practices may reduce model accuracy. Continuous retraining and validation against verified laboratory data are essential for maintaining reliability (Wang *et al*., 2019).

6.6. Resource and Infrastructure Constraints

Many regions, particularly in low- and middle-income countries, lack the infrastructure, trained personnel, and funding to implement and maintain sophisticated multi-source surveillance systems (Mremi *et al*., 2021). In such contexts, data sparsity and delayed reporting hinder global coverage and the effectiveness of real-time analytics.

While multi-source data analytics provides transformative potential for global AMR surveillance, challenges related to data quality, integration, computational scalability, ethics, model validation, and resource constraints must be addressed. Addressing these limitations is essential to achieve accurate, timely, and actionable insights that can guide global public health interventions (Mathur *et al*., 2019; Olsson-Brown *et al*., 2020).

7. CONCLUSION

The escalating global threat of antimicrobial resistance (AMR) necessitates the development of robust, real-time surveillance systems capable of integrating heterogeneous data streams to inform timely public health interventions. This study underscores the transformative potential of multi-source data analytics in providing actionable insights for monitoring emerging AMR patterns worldwide. By leveraging diverse datasets including clinical records, genomic sequences, environmental sampling, population mobility, and open-source mediareal-time detection and predictive modeling of resistance trends can be achieved with unprecedented accuracy and granularity (Danko *et al*., 2019; Ahmed *et al*., 2020; de Fazio *et al*., 2020).

Multi-source integration can support the identification of AMR hotspots and transmission routes by integrating high-resolution laboratory data with massive scale data of the environment and population (Lausch *et al*., 2018; McGreevy *et al*., 2017; Navedo *et al*., 2021). Predictive ability is improved by machine learning and analytics systems based on AI, which helps respond to public health and implement antimicrobial stewardship (Chen *et al*., 2021; Ahmed *et al*., 2020; Doyen *et al*., 2019). Another example of the viability of the continuous and scalable data collection and analytics in multiple healthcare centers is the use of real-time monitoring platforms, including MediGrid and other clinical data networks (Olsson-Brown *et al*., 2020; Lee *et al*., 2019; Wang *et al*., 2019).

Even now, the issues in providing interoperability and quality of data as well as maintaining ethical handling of sensitive health data are persistent, especially in the areas that have a low surveillance level (Mremi *et al*., 2021; Xiong *et al*., 2021). Also, it is important to incorporate environmental reservoirs of AMR, including coastal and urban metagenomes, to have complete knowledge on the dynamics of the transmission globally (Danko *et al*., 2019; Navedo *et al*., 2021).

Finally, multi source data analytics integration will offer a scalable and predictive real time, bridging the gap between pathogen detection, epidemiological intelligence and public health action. Further interventions are needed to increase data coverage, improve predictive models, and integrate these systems into the structure of international health policies to make the required timely and data-driven decisions in response to the increased AMR crisis (Chen *et al*., 2018; Mathur *et al*., 2019; de Fazio *et al*., 2020). This kind of approach will not only be seen to increase the chances of identifying a growing resistance but also strategically countering the disease and ensuring the protection of global health in the fast-evolving pathogens time.

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