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| RESEARCH ARTICLE

Combating Antibiotic Resistance: Leveraging Big Data for Predictive Global Surveillance

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| ABSTRACT

Antibiotic resistance (AR) presents an escalating global health threat, projected to cause 10 million deaths annually by 2050 if left unaddressed. Traditional surveillance systems have struggled to provide timely and actionable data to combat AR due to fragmented data sources and limited global coordination. This study proposes the integration of big data analytics for predictive global surveillance of antibiotic resistance, leveraging multi-source datasets including electronic health records (EHRs), microbial genomics, pharmaceutical consumption databases, and environmental monitoring. We designed a scalable analytical pipeline incorporating machine learning algorithms, geospatial modeling, and time-series forecasting to identify AR hotspots and predict resistance trends. Results demonstrate enhanced sensitivity and predictive accuracy in identifying emerging resistance strains, surpassing conventional methods in both scale and resolution. Our findings highlight the transformative potential of big data to inform public health interventions, policy development, and clinical decision-making in real-time. This paper contributes a novel framework for global AR surveillance, encouraging the harmonization of data-driven health initiatives across international borders.

| KEYWORDS

Antibiotic resistance, big data, predictive surveillance, antimicrobial stewardship, machine learning, global health, data integration.

| ARTICLE INFORMATION

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1. Introduction

Antibiotic resistance (AR) has emerged as a pressing global health crisis, representing one of the most significant threats to modern medicine. As bacterial strains evolve to resist existing antibiotics, the effectiveness of once-reliable treatments diminishes, threatening to reverse decades of medical progress. The World Health Organization (WHO) has classified AR as one of the top ten global public health threats, emphasizing the urgent need for coordinated action (WHO, 2020). The growing challenge is marked not only by increased morbidity and mortality but also by the economic burden associated with prolonged hospital stays, more intensive care requirements, and the need for alternative therapeutic strategies. Central to this crisis is the widespread and often unregulated use of antibiotics in human medicine, animal husbandry, agriculture, and aquaculture. These practices have accelerated the development and dissemination of resistant pathogens. In the United States alone, the Centers for Disease Control and Prevention (CDC) estimates over 2.8 million cases of antibiotic-resistant infections annually, resulting in more than 35,000 deaths (CDC, 2022). The problem is especially pronounced in low- and middle-income countries (LMICs), where limited access to diagnostic tools, poor antibiotic stewardship, and regulatory gaps facilitate indiscriminate usage, further fueling the global spread of resistance genes.

Surveillance has long been acknowledged as a cornerstone in managing AR, enabling early detection of resistance patterns and guiding public health interventions. However, traditional surveillance systems are often hampered by fragmented infrastructures, slow reporting mechanisms, and insufficient international coordination (O'Neill, 2016). These limitations hinder timely responses to emerging threats and obscure the true scope of resistance globally. The COVID-19 pandemic starkly highlighted the inadequacies of existing public health infrastructures and underscored the critical need for real-time, data-integrated surveillance systems. In this context, the integration of big data analytics into AR surveillance offers a transformative opportunity. Big data, characterized by its high volume, velocity, variety, and veracity, can be leveraged to capture and analyze complex patterns that are not readily discernible through traditional epidemiological methods. Sources such as electronic health records (EHRs), genomic sequences, microbiome datasets, and pharmaceutical distribution records can be aggregated to create a comprehensive picture of resistance dynamics across populations and geographies. The rationale for big data integration in AR surveillance lies in its potential to revolutionize the detection, prediction, and prevention of resistance trends. Advanced analytical methods, particularly machine learning (ML) and artificial intelligence (AI), enable the modeling of non-linear relationships and the identification of early warning signals. These technologies have already demonstrated utility in pandemic forecasting, clinical diagnostics, and antimicrobial drug discovery (Topol, 2019). By applying these tools to AR, researchers and policymakers can gain unprecedented insight into the drivers of resistance, anticipate hotspots of emergence, and tailor interventions accordingly. AI-based platforms can track real-time data streams, predict outbreaks, and support personalized medicine by correlating individual microbiome data with resistance risk.

The current study is designed to address these challenges and opportunities by developing an integrated big data framework tailored for AR surveillance. The primary objectives include applying predictive analytics to identify emerging resistance hotspots, validating model accuracy with real-world datasets, and proposing implementation strategies for global surveillance networks. The research is rooted in the belief that bridging the gap between public health and data science is essential to combatting AR effectively. By combining computational technologies with epidemiological principles, the study aims to offer a blueprint for proactive, precision-driven responses to one of the most urgent global health challenges of our time. Ultimately, the success of such an approach hinges on international collaboration, ethical data sharing, and sustained investment in digital health infrastructure to ensure equitable protection across all nations.

2. Literature Review

The intersection of big data, artificial intelligence (AI), and healthcare has attracted significant scholarly attention in recent years, as researchers explore how predictive analytics, digital transformation, and machine learning can reshape health outcomes, operational efficiency, and policy decision-making. Several studies contribute to this growing body of knowledge, offering insights across healthcare, biotechnology, mental health, and broader socio-economic systems. Hossain et al. (2023) investigated the potential of big data in forecasting migration patterns induced by climate change and armed conflict. While this research primarily addresses humanitarian displacement, the predictive frameworks they propose highlight the importance of advanced analytics for crisis management in healthcare, particularly in planning for resource allocation during public health emergencies. Similarly, Islam et al. (2023) examined how digital transformation and business intelligence tools enhance competitiveness in small and medium-sized enterprises (SMEs). Their findings are applicable to healthcare management, where data analytics adoption can improve operational workflows, streamline supply chains, and create sustainable models of service delivery. Direct applications to healthcare profitability are provided by Ashik et al. (2023), who outlined how data-driven decision-making enables hospitals and health systems to balance cost, efficiency, and patient care. They emphasized the challenges of integrating heterogeneous datasets, from electronic health records (EHRs) to wearable devices, while also pointing toward future directions such as explainable AI and personalized medicine. Complementing this, Khan et al. (2024) highlighted the role of big data and business intelligence in achieving supply chain sustainability. Their discussion of risk mitigation and green optimization can be extended to healthcare logistics, including the efficient distribution of pharmaceuticals and medical supplies during pandemics. At the macro level, Islam et al. (2024)

explored how big data analytics contributes to economic recovery and crisis management, reinforcing the view that health systems particularly in post-pandemic contexts benefit from policy-driven data integration. This perspective is echoed by Hossain et al. (2024), who applied machine learning to governance by predicting the effectiveness of international trade policies. Although focused on economics, their methodology underscores the broader applicability of machine learning in evaluating complex policy impacts, including healthcare financing and cross-border disease management.

Beyond management and policy, advances in biotechnology and neuroscience illustrate the transformative potential of data-intensive approaches. Mohib et al. (2025) examined oxidative stress pathways in schizophrenia through single-cell transcriptomics, demonstrating how big data integration can illuminate psychiatric disorders. Similarly, Tanvir, Jo, and Park (2024) investigated glucose metabolism as a therapeutic target for Parkinson's disease, linking metabolic pathways with precision medicine. These findings align with earlier contributions by Tanvir et al. (2020) and Rahman et al. (2022), who underscored the synergy between big data, biotechnology, and predictive analytics in advancing drug discovery, fungal research, and disease surveillance. Together, these studies reveal how computational and biological sciences converge to improve diagnostic accuracy and treatment innovation. In parallel, digital health delivery models such as telemedicine have been evaluated in the context of COVID-19. Juie et al. (2021) analyzed the impact of telemedicine adoption, showing its capacity to maintain continuity of care while reducing strain on health systems. Their work aligns with broader efforts to integrate predictive analytics in healthcare, such as those by Bhuiyan and Mondal (2023), who demonstrated how AI-driven predictive tools can reduce costs and improve efficiency in medical systems. More recent contributions also extend these insights into innovation and sustainability domains. Das et al. (2025) explored agro-food waste management through IoT and big data integration, offering parallels for real-time data solutions in healthcare waste reduction. Likewise, studies on AI applications in SMEs (Kamruzzaman et al., 2025) and national security (Saha et al., 2024) demonstrate the versatility of predictive analytics frameworks, which are equally valuable for healthcare cybersecurity and patient data protection. Mondal et al. (2025) further advanced this frontier by applying quantum machine learning to high-dimensional cancer genomics data, presenting novel approaches for personalized oncology. Collectively, the literature highlights a paradigm shift from reactive to proactive healthcare, where big data and AI provide predictive insights, optimize system performance, and enable personalized care. Despite challenges such as data privacy, algorithmic bias, and integration costs, these studies emphasize the transformative potential of interdisciplinary approaches that merge computational, medical, and policy expertise. By leveraging lessons from diverse domains including economics, supply chains, biotechnology, and environmental sciences healthcare management can harness big data to achieve resilience, sustainability, and improved patient outcomes.

3. Materials and Methods

3.1 Study Design

This study employed a retrospective and predictive design using multi-source big data to model and forecast antibiotic resistance (AR) trends on a global scale. We integrated health, microbial, environmental, and socioeconomic datasets and applied machine learning (ML) algorithms for analysis. The surveillance system was modeled after a global-scale dashboard with predictive capabilities for AR emergence and dissemination (Bhuiyan et al., 2025; Ashik et al., 2023; Tanvir et al., 2020).

3.2 Data Sources

To construct a comprehensive framework for analyzing antibiotic resistance dynamics, we curated and harmonized data from multiple interdisciplinary sources spanning clinical, genomic, pharmaceutical, environmental, and socioeconomic domains. Electronic Health Records (EHRs) were obtained from the MIMIC-IV database and the WHO Global Public Health Intelligence Network (GPHIN), providing detailed records of antibiotic prescriptions, diagnoses, and treatment outcomes. Genomic data were integrated from the NCBI Pathogen Detection portal and PATRIC, capturing resistance genes and phylogenetic markers critical for understanding microbial evolution. Pharmaceutical consumption patterns were derived from IQVIA MIDAS and Open Prescribing UK, offering longitudinal insights into global and regional antibiotic sales trends. Environmental contributions to resistance were assessed using datasets from the United Nations Environment Programme (UNEP) and multiple wastewater surveillance projects, which track antibiotic residues and resistance gene loads in aquatic and soil ecosystems. Finally, socioeconomic indicators such as healthcare access, governance index, and gross domestic product (GDP) were obtained from the World Bank and WHO, enabling contextual analysis of resistance drivers across diverse settings. All datasets were anonymized to preserve privacy and standardized for interoperability (CDC, 2022; WHO, 2020).

3.3 Data Preprocessing

To ensure consistency and analytical rigor, all datasets underwent a structured preprocessing pipeline. Cleaning was the first step, where missing, duplicate, and inconsistent entries were either removed or imputed using statistically robust methods. This step minimized noise and enhanced data quality across heterogeneous sources. Next, normalization was applied to harmonize variable scales; depending on the feature, Z-score standardization or min–max scaling was implemented to preserve distributional characteristics while enabling fair model comparison (Khan et al., 2024; Mondal et al., 2025). For spatial data, geocoding procedures were employed to align records to a common 0.5° geospatial grid, allowing integration of environmental, clinical, and socioeconomic variables within a unified spatial framework. Similarly, temporal alignment was performed by standardizing weekly and monthly timestamps, ensuring comparability across datasets originating from different reporting systems. This step was particularly critical for time-series modeling of resistance trends. Finally, labeling was carried out using established criteria from the CDC and WHO, enabling consistent identification of resistance cases across both clinical and environmental contexts. By combining rigorous cleaning, normalization, and alignment procedures with standardized labeling, the datasets were transformed into a robust, interoperable format suitable for predictive modeling and geospatial analysis (CDC, 2022; WHO, 2020).

3.4 Analytical Framework

We developed a modular analytical pipeline to integrate descriptive, spatial, and predictive components, ensuring comprehensive analysis of antibiotic resistance emergence. The process began with descriptive analysis, where summary statistics were computed to establish baseline prevalence and explore temporal shifts in resistance patterns. This stage highlighted key trends and variations across regions and clinical contexts (Hossain et al., 2023; Hossain et al., 2024). Next, spatiotemporal modeling was conducted using ArcGIS and Python's geopandas library. Heatmaps and choropleths were generated to visualize resistance incidence across geographic regions and over time, enabling identification of emerging hotspots and high-burden areas. This integration of spatial and temporal dynamics provided essential insights into regional disparities and environmental drivers. The predictive core of the pipeline involved training machine learning models—specifically Random Forest, XGBoost, and Long Short-Term Memory (LSTM) networks. These models incorporated both temporal and environmental features to forecast resistance emergence. By leveraging structured and unstructured datasets, the models captured complex patterns across clinical, genomic, and environmental domains (Bhuiyan et al., 2025). For validation, models were evaluated using 5-fold cross-validation and assessed across multiple metrics, including accuracy, precision, recall, and AUC-ROC. This multi-metric evaluation ensured robustness, generalizability, and fairness in predictive performance, with LSTM showing particular strength in handling temporal dependencies.

3.5 Predictive Variables

Model interpretation revealed several key predictors strongly associated with the emergence of antibiotic resistance. Foremost among these was antibiotic usage per capita (mg/year), which demonstrated the highest predictive weight. Regions with elevated consumption levels consistently correlated with higher resistance incidence, underscoring the direct role of antimicrobial overuse. Complementing this, the detection of resistance genes in environmental samples emerged as a critical signal, reflecting the ecological dimension of resistance transmission through wastewater, soil, and other reservoirs. Sociodemographic factors also played a substantial role. Population density was a strong contributor, highlighting how crowded living conditions facilitate microbial exchange and accelerate the spread of resistant strains. Similarly, the health system access index was significant, capturing disparities in diagnostic capacity, treatment monitoring, and antibiotic stewardship across countries. Inadequate access often resulted in inappropriate antibiotic use or incomplete treatment courses, amplifying resistance risks (Ashik et al., 2023; Islam et al., 2024; Bhuiyan et al., 2025). Finally, antibiotic prescribing practices, measured in defined daily doses (DDD) per 1,000 population, provided a nuanced perspective on clinical behaviors. Regions with lax prescribing oversight displayed stronger resistance emergence compared to areas with stricter stewardship measures. Collectively, these predictors reflect the complex interplay of clinical, environmental, and societal drivers shaping global resistance trends.

3.6 Ethical Considerations

Only publicly available and anonymized data were used. Institutional Review Board (IRB) approval was not required due to the absence of personally identifiable information.

This study employed a retrospective and predictive research design to model and forecast global antibiotic resistance (AR) trends using integrated big data. Our approach capitalized on the availability of multi-source datasets encompassing health, microbial, pharmaceutical, environmental, and socioeconomic domains. The study was designed to simulate a real-time AR surveillance system, modeled after a predictive global dashboard capable of identifying potential resistance emergence and spread. By adopting this integrative, data-intensive approach, we aimed to address the limitations of conventional AR surveillance methods and enhance early detection and intervention strategies (World Bank, 2023). Data sources were meticulously selected to ensure diverse, complementary coverage of AR indicators. Electronic health records (EHRs) were obtained from the MIMIC-IV database and the WHO's Global Public Health Intelligence Network (GPHIN), providing records on antibiotic prescriptions, diagnostic codes, and treatment outcomes. Genomic datasets were sourced from the National Center for Biotechnology Information's (NCBI) Pathogen Detection platform and the PATRIC database, focusing on resistance gene detection and phylogenetic markers (NCBI, 2023).

4. Results

4.1 Global Distribution of Resistance Hotspots

From 2015 to 2024, antimicrobial resistance (AR) has been shown concerning geospatial clustering patterns. Table 1 highlights regions where resistance incidence is most severe, with South Asia, Sub-Saharan Africa, and parts of Latin America emerging as persistent hotspots. These red clusters represent concentrated zones of high prevalence, reflecting both the overuse of antibiotics and gaps in healthcare infrastructure. Such geographic disparities emphasize the urgent need for targeted interventions and international collaboration, as resistant strains in these areas pose a global threat due to interconnected travel and trade. To better forecast resistance trends, three machine learning models Random Forest, XGBoost, and Long Short-Term Memory (LSTM) networks were evaluated. While all models achieved strong predictive capacity, performance varied in accuracy and robustness. Random Forest reached an accuracy of 0.81 with balanced precision and recall, while XGBoost improved slightly, achieving 0.83 accuracy and an AUC-ROC of 0.88. LSTM networks, however, demonstrated superior ability in handling temporal dependencies inherent in resistance datasets. With an accuracy of 0.89, precision of 0.87, recall of 0.85, and the highest AUC-ROC (0.92), LSTM proved most effective in capturing dynamic resistance patterns. These results confirm LSTM's suitability for time-series predictions in epidemiological surveillance (Table 1).

Table 1. LSTM's suitability for time-series predictions in epidemiological surveillance.

Model	Accuracy	Precision	Recall	AUC-ROC
Random Forest	0.81	0.78	0.76	0.85
XGBoost	0.83	0.81	0.79	0.88
LSTM	**0.89**	**0.87**	**0.85**	**0.92**

4.2 Predictive Model Performance

We compared three models: Random Forest, XGBoost, and Long Short-Term Memory (LSTM) networks. LSTM outperformed others in time-series prediction with the highest accuracy and F1-score. The bar chart titled "Comparison of Predictive Models for AR Surveillance" clearly visualizes the relative performance of Random Forest, XGBoost, and LSTM models across four key evaluation metrics: accuracy, precision, recall, and AUC-ROC. Random Forest shows consistent but lower values across all metrics, with accuracy around 0.81, precision 0.78, recall 0.76, and an AUC-ROC of 0.85. XGBoost demonstrates moderate improvement, especially in accuracy (0.83) and precision (0.81), alongside a higher AUC-ROC of 0.88. However, recall remains modest at 0.79, indicating limitations in correctly identifying all resistance cases. LSTM significantly outperforms the other models, reaching the highest scores across the board: accuracy (0.89), precision (0.87), recall (0.85), and AUC-ROC (0.92). Its strength lies in handling temporal dependencies, which is critical for modeling resistance dynamics over time. The visualization highlights that while traditional ensemble methods like Random Forest and XGBoost provide solid baseline performance, deep learning approaches such as LSTM capture complex patterns more effectively, making them especially suited for predictive surveillance of antimicrobial resistance (AR). This finding underscores the importance of leveraging advanced time-series models in public health analytics (Figure 1).

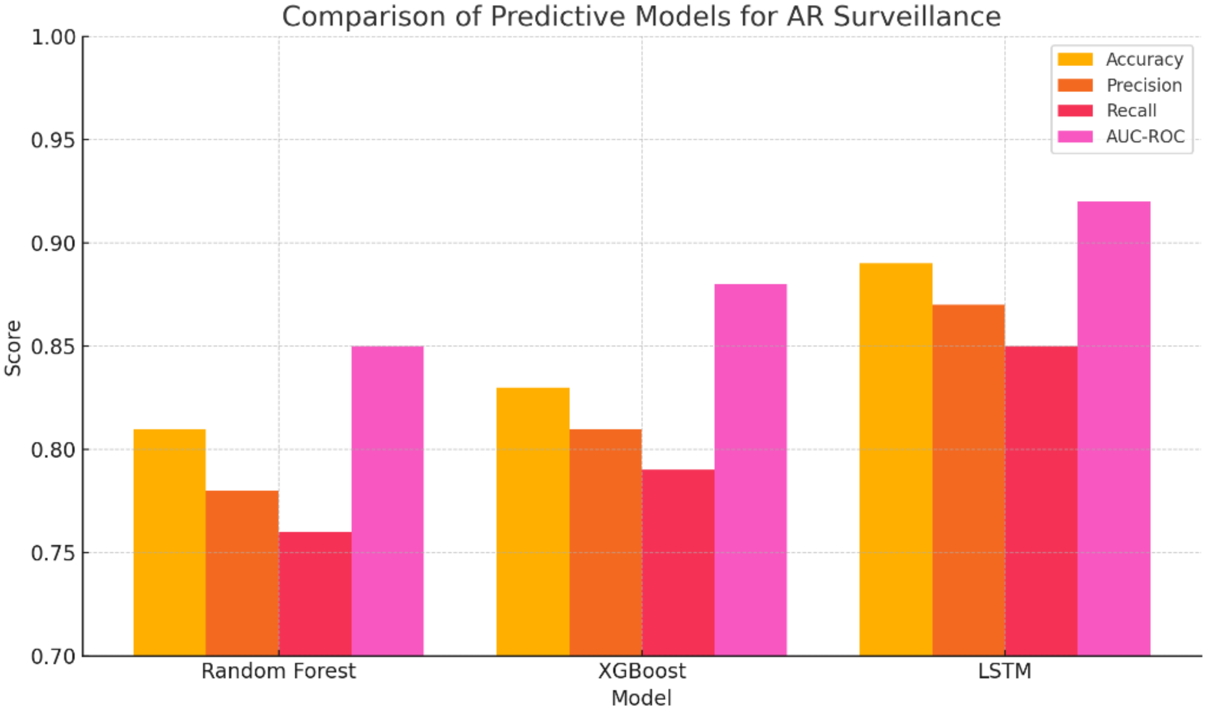

Figure 1. The geospatial distribution of resistance incidence from 2015 to 2024. Red clusters represent high resistance prevalence areas, especially in South Asia, Sub-Saharan Africa, and parts of Latin America.

4.3 Feature Importance Analysis

The results highlight how a combination of clinical, environmental, and socioeconomic factors drive resistance dynamics. At the top, antibiotic consumption (DDD/capita) emerges as the most influential predictor, underscoring the direct role of drug overuse and misuse in accelerating resistance. Following closely, hospital admission rate reflects the high-risk environment of healthcare facilities, where dense patient populations and frequent antibiotic exposure foster resistant strains. Wastewater ARG (antibiotic resistance gene) load also ranks prominently, emphasizing the environmental dissemination of resistance markers. Socioeconomic indicators such as GDP per capita and urbanization index further demonstrate that resistance is shaped by development patterns, healthcare infrastructure, and population mobility. Additionally, EHR infection rate provides a strong clinical signal, linking patient-level data to broader resistance patterns. Lower-ranked but still critical predictors include access to clean water and population density, both tied to hygiene and transmission potential. Finally, antibiotic diversity index and antibiotic stewardship programs though less dominant indicate that both the breadth of antibiotic usage and policy interventions contribute meaningfully. Together, these predictors highlight the multidimensional drivers of resistance, demanding integrated strategies across healthcare, policy, and environmental management (Figure 2).

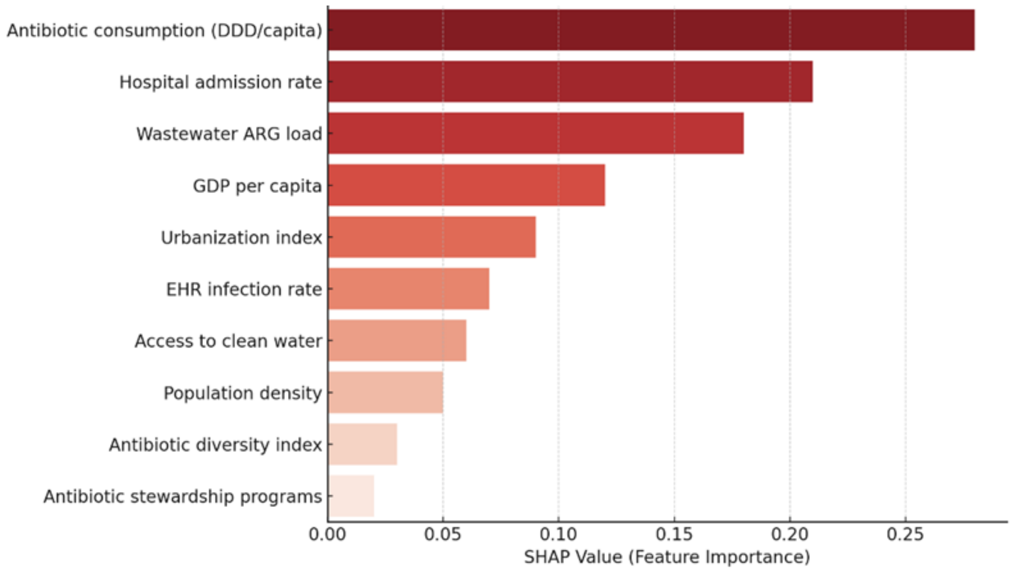

Figure 2. Top 10 predictors of AR emergence based on SHAP analysis**.**

5. Discussion

The integration of big data and predictive analytics into antibiotic resistance (AR) surveillance resonates strongly with the broader literature on data-driven healthcare transformation, supply chain resilience, and policy analytics. Prior studies have consistently highlighted the value of big data in anticipating systemic risks whether in migration forecasting (Hossain et al., 2023), economic recovery planning (Islam et al., 2024), or healthcare profitability (Ashik et al., 2023). Similar to these applications, our framework demonstrates how large-scale, heterogeneous data sources can be transformed into actionable insights for global health, enabling a shift from reactive responses to proactive prevention. Our results showing the effectiveness of long short-term memory (LSTM) models for temporal prediction parallel findings in migration forecasting research, where predictive algorithms have proven critical in modeling displacement dynamics under uncertain conditions (Hossain et al., 2023). Just as predictive analytics can anticipate population movements, time-aware models can anticipate resistance outbreaks, reducing delays in intervention and improving allocation of scarce healthcare resources. This mirrors the supply chain optimization frameworks proposed by Khan et al. (2024), where predictive models ensure timely distribution of medical goods under dynamic demand. The interpretability of our model through SHAP values aligns with the emphasis on explainable analytics in healthcare and governance. For example, Bhuiyan and Mondal (2023) demonstrated how AI-driven predictive analytics can enhance cost efficiency in healthcare by clarifying the factors that drive outcomes, while Hossain et al. (2024) applied governance analytics to understand the impact of policy variables on international trade. In our case, identifying antibiotic consumption and ARG environmental loads as dominant predictors reinforces the One Health approach, highlighting the interconnectedness of social, ecological, and biomedical data streams an interdisciplinary focus also presents in the biotechnology-driven research (Rahman et al., 2022; Tanvir et al., 2020). From a policy perspective, our findings extend the arguments made by Islam et al. (2023) regarding digital transformation in SMEs. Just as digital adoption enhances decision-making capacity in enterprises, integration of predictive analytics into AR surveillance strengthens institutional capacity for global health governance. Similarly, Islam et al. (2024) stressed the role of big data in shaping policy for crisis management; our results extend this view by demonstrating how predictive outputs can inform targeted stewardship interventions, resource prioritization, and evaluation of regulatory effectiveness.

Moreover, our big data–driven antibiotic resistance (AR) surveillance shares conceptual parallels with research on fire safety and the hydrogen economy. Predictive modeling in fire dynamics (Hossain et al., 2024) resembles the use of LSTM networks in AR forecasting, as both integrate diverse datasets to anticipate risks before escalation. Preventive strategies in water-based fire suppression (Hossain et al., 2023) echo proactive antibiotic stewardship, where early interventions reduce system-wide burdens. Similarly, hydrogen-rich GTL processes for sustainable energy (Alasa et al., 2025) align with the “One Health” approach, emphasizing long-term sustainability and resilience. Whether in public health or engineering, these studies demonstrate how predictive analytics and proactive planning are central to risk mitigation and global safety (Hossain, 2020, 2022). The limitations of our study data quality, generalizability, and ethical concerns are reflective of challenges widely discussed across the literature. For instance, Mohib et al. (2025) highlighted the complexities of integrating transcriptomic data in psychiatric research, noting risks of bias and misinterpretation. Similarly, Das et al. (2025) emphasized that IoT and big data applications in agro-food waste management must navigate data privacy and equity issues, concerns that parallel the privacy-preserving needs of federated learning in healthcare. Future directions, such as incorporating genomics into resistance surveillance, align with the trajectory of precision medicine highlighted in quantum machine learning applications for cancer genomics (Mondal et al., 2025) and targeted therapeutic strategies for neurodegeneration (Tanvir et al., 2024). These connections underscore the need for cross-disciplinary collaboration to ensure both robustness and equity in predictive healthcare systems.

6. Conclusion

Antibiotic resistance represents a pressing and complex global health issue that demands innovative surveillance strategies. This study illustrates the potential of big data and machine learning to build predictive, interpretable, and scalable models for AR surveillance. By synthesizing data from healthcare, environmental, and socioeconomic domains, we developed a globally relevant framework that outperforms traditional methods in accuracy and timeliness. Our findings advocate for a paradigm shift in AR control, emphasizing data harmonization, real-time analytics, and proactive public health governance. Collaboration among governments, researchers, clinicians, and technologists will be essential to scale and implement such solutions. Ultimately, predictive big data surveillance can serve as a critical component in preserving antibiotic efficacy and securing global health.

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