

REVIEW

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The application of artificial intelligence in surveillance and control for antimicrobial resistance in hospital-acquired infections

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Abstract

Antimicrobial resistance (AMR) continues to undermine the effectiveness of modern medicine, with hospital-acquired infections (HAIs) as major contributors to morbidity and mortality. Traditional surveillance systems for AMR in HAIs are often fragmented, delayed, and reactive, limiting their ability to inform timely interventions. Emerging evidence demonstrates that artificial intelligence (AI) can transform AMR surveillance and control. AI can enable predictive modelling, risk stratification, and outbreak forecasting. This narrative review describes various AI applications for monitoring and evaluating antimicrobial resistance (AMR) among HAIs in hospital settings. We begin by discussing how machine learning models can predict the emergence and spread of antibiotic-resistant pathogens. This is achieved through the analysis of various datasets, including microbiological results, electronic health records, and hospital workflows. Patient-level risk scoring systems are examined, demonstrating their ability to identify individuals at increased risk of multidrug-resistant infections. We describe AI-powered early-warning systems that provide outbreak alerts, enabling timely infection prevention and control measures. Hospital applications, including predictive resistance models validated in European hospitals, such as those in Lower Saxony, Germany, and early-warning dashboards tested in Asia and Africa, illustrate the potential impact of these approaches. However, these studies vary substantially in their designs, validation methods, and implementation contexts. To ensure sustainability, we propose a roadmap for integrating AI into AMR programs. We discuss ethical, legal, and regulatory frameworks. We also discuss strategies for capacity building, cost-effectiveness, and scalability, particularly in low- and middle-income countries. Our findings suggest that AI has the potential to strengthen infection control, enhance stewardship, and provide resilient defences within hospital environments.

Keywords Antimicrobial resistance, Hospital-acquired infections, Machine learning, Artificial intelligence, Surveillance, Predictive analytics, Models



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1 Introduction

Antimicrobial resistance (AMR) is increasingly recognised as a critical global health crisis, threatening the effectiveness of treatments for infections and undermining hospital care. By 2019, over 4.95 and 1.27 million deaths globally were associated with and attributed to AMR, respectively, with sub-Saharan Africa bearing approximately 27.3 deaths per 100,000 population [1]. Hospital-acquired infections (HAIs) are a major contributor to AMR morbidity and mortality. HAIs across Europe, the US, and Australia are estimated at 6.5%, 3.2%, and 9.9%, respectively [2]. Across low-income countries, the risk of HAIs is estimated at 15%, which is double the average of 7% within high-income countries and is estimated to increase by 2050 [3]. Many HAIs are caused by pathogens that have developed resistance to first- and second-line antibiotics, complicating treatment and worsening outcomes. For example, in low- and middle-income countries (LMICs), hospital-associated drug-resistant infections (HARIs) are especially prevalent due to limited antimicrobial stewardship interventions [4]. Their persistence in healthcare environments arises from selective antibiotic pressure, horizontal gene transfer, environmental survival mechanisms, and adaptive virulence factors. Recent global estimates estimated the number of resistant HAI cases at 136 million annually, with the highest burden in China at 52 million [4]. Common MDR organisms include the urgent and high-priority pathogens *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter species*, also known as the ESKAPE pathogens [5]. It was estimated that the 90-day mortality rate among patients with HAIs increased by 80% compared to those without. Significantly, the 90-day mortality further increased by 90% among patients who had resistant HAIs, especially carbapenem-resistant gram-negative organisms [6]. Further evidence reported that resistant ESKAPE pathogens doubled the risk of death with significantly higher hospitalisation costs and longer stays, especially in the Asian region [7]. Effective surveillance is therefore essential for tracking the emergence and spread of AMR [5]. However, traditional surveillance systems are sometimes slow, fragmented, and under-used [8]. Additionally, they rarely include most of the Infection Control and Prevention (ICP) capacities, hindering efforts to address AMR.

The World Health Organisation's Global Antimicrobial Resistance and Use Surveillance System (GLASS) has made significant progress in combating AMR. Evidence demonstrates that 65.5% of the 194 WHO member states are enrolled on GLASS, with 55.2% of these enrolled (107 countries) actively submitting AMR surveillance data [9]. However, healthcare facilities reporting AMR data were variable within the WHO Mediterranean Region, with 9 countries reporting less than 5%, 8 countries reporting 5–50%, and only 2 countries reporting more than 50% by 2021 [9]. Evidence of the Eastern Mediterranean countries disaggregated by income status showed high-income countries (6) had reported approximately 92,081 isolates [10]. Middle-income countries (11) reported 104,329, and low-income countries (5) reported approximately 558 isolates [10]. Across Sub-Saharan Africa, 19 out of 54 countries had reported AMR data by 2022, demonstrating low participation [11]. Progress in many countries, especially LMICs, is hindered by inconsistent hospital-level testing, sparse data, and weak laboratory capacity. The GLASS strategy involves creating a national coordinating centre to manage and report surveillance data and establishing a national reference laboratory to support surveillance

efforts. The strategy also ensures that the reference laboratory adheres to quality assurance standards and complies with international laboratory standards [9].

Artificial intelligence (AI) and machine learning (ML) have been proposed as potential tools to enhance AMR surveillance and accelerate detection, prediction, and control of resistant HAIs. These AI tools have multiple merits and limitations, despite their promising prospects, as summarised in Table 1.

ML models can forecast resistance trends using hospital-level historical antibiotic use and resistance data. For example, these models can predict year-to-year changes in resistant bloodstream pathogens with good performance [25]. Also, interpretable ML applied to Intensive Care Unit (ICU) admission data can help predict bloodstream infections and their resistance profiles, supporting more timely empirical therapy [26]. These applications directly contribute to Sustainable Development Goal 3, which focuses on the Health and well-being of individuals [27, 28].

However, there is fragmented information on the application of AI models across hospital settings to combat the rising AMR threat. This study describes and critically synthesises existing applications of AI in hospital-based AMR surveillance and identifies emerging trends, limitations, and research gaps. The goal is to support antimicrobial stewardship and infection prevention/control policies with real-time and actionable intelligence.

2 Methods

This narrative review synthesised published evidence on the application of AI and ML methods for AMR surveillance and HAIs monitoring in hospital settings. Although not conducted as a systematic review, structured search and selection procedures were applied to enhance transparency and reproducibility. We searched multiple databases, including PubMed, Scopus, and Google Scholar. We also included other databases, such as the World Health Organisation website and other credible sources that have developed AI-based AMR tools, such as the Wellcome Trust. Search terms included “*AI-surveillance framework*”, “*Hospital Acquired Infections*”, “*Hospital Infections Resistance*”, “*AMR in hospitals*”, “*AI in AMR*”, and “*Predictive Modelling in Hospital Infections*”. The search strategy combined MeSH terms and free-text terms using Boolean operators. An example of the PubMed search string used was; (“*artificial intelligence*”[MeSH Terms] OR “*machine learning*” OR “*deep learning*” OR “*predictive modelling*” OR “*algorithm*” OR “*neural network*”) AND (“*antimicrobial resistance*” OR “AMR” OR “*drug resistance, microbial*”[MeSH Terms] OR “*healthcare-associated infection*” OR “*hospital-acquired infection*” OR “*nosocomial infection*” OR “HAI”) AND (“*surveillance*” OR “*early warning*” OR “*forecast*” OR “*risk prediction*” OR “*clinical decision support*” OR “*outbreak detection*”) AND (“*hospital*” OR “*inpatient*” OR “*tertiary care*” OR “*clinical setting*”). Equivalent search terms were adapted for Scopus and Google Scholar. Snowballing was used, with the reference lists of included articles manually screened to identify additional relevant studies. Approximately 70 articles were included with the last date of literature review on 27 February 2026.

Studies were included if they described the development, validation, implementation, or evaluation of AI or machine learning methods applied to antimicrobial resistance surveillance or healthcare-associated infection monitoring in hospital settings. These inclusion criteria followed the intervention, outcome, and setting constructs. Full-text

Table 1 The different AI models, their applications, merits, and limitations in enhancing the detection, identification, and management of HAIs

AI Model Type and Examples	Main Healthcare Use	Advantages	Limitations
Traditional ML, e.g., Random Forest, Gradient boosting (XGBoost/LightGBM), logistic regression, Support Vector Machines (SVM)	Risk prediction, AMR prediction, Patient deterioration scoring, and Early sepsis identification [12]	Simple, interpretable, fast to train, works well with tabular clinical data, and performs well on small to medium datasets	Limited in the quantity of datasets to consider, and it can be complex to execute and interpret [13] Requires feature engineering, performance plateaus with large datasets, and may fail to capture complex patterns, such as those in images and genomic data.
Deep Learning (Neural Networks) Feedforward Neural Networks (FNN), Convolutional Neural Networks (CNNs), and Recurrent Neural Networks (RNNs).	Imaging-based infection detection from Chest X-rays and CT scans Automated pathogen identification from microscopy images Predicting patient deterioration using Electronic Health Records time series [14] Outbreak prediction using sequence data	High accuracy on complex datasets like images, genomic data, and signals [15] Learns patterns automatically No feature engineering required Useful for real-time monitoring and automated triage	Needs big/large datasets Risk of overfitting High Computational cost [14] Low interpretability [16]
Recurrent Models: Long Short-term Memory (LSTM) and Gated Recurrent Unit (GRU), and Time-series models	ICU monitoring, outbreak prediction [17] Early sepsis detection Predicting hospital outbreaks from patient flow data [18]	Temporal learning Effective for continuous monitoring	Hard to interpret Require high-quality and continuous data [18] Can struggle with long-term dependencies
Transformer Models, such as Bidirectional Encoder Representations from Transformers (BERT), ClinicalBERT, BioBERT, Med-BERT)	Text mining, EHR analytics [19] Predicting AMR from clinical notes Automated generation of infection-control alerts Guideline extraction of clinical decision support	Best for text & sequence Handles long-range dependencies Pretrained medical models reduce data needs	Computationally heavy and data-intensive Huge model sizes Can hallucinate (generation of fluent but factually incorrect or unverified content arising from probabilistic next-token prediction in the absence of grounded evidence) if not trained on domain-specific datasets [19]
Generative Models, such as Generative Adversarial Networks (GANs)/Diffusion models, Variational Autoencoders (VAEs)	Data augmentation for rare infections Generating synthetic microbiology data when samples are limited [20] Improving image quality	Solves data scarcity Reduces dependence on hard-to-collect infection datasets Enhances image clarity for better diagnostics	Risk of artefacts, unrealistic, and biased data [20] Lack of clinical interpretability Ethical concerns
Topological Data Analysis (TDA)	Patient movement tracking [21] Molecular analysis and prediction of resistant strain evolution [22] Prediction of gene transfer between strains [23]	Predictive accuracy with small data samples [21] Robust to missing, erroneous, or sparse data Gives an interpretable model [24]	Computational limits for high-dimensional topological features

articles in English were considered, while those in other languages were excluded due to the limitations of language translation. Preprints were also excluded, especially because they are not peer-reviewed. Titles and abstracts were screened for relevance, followed by full-text review of potentially eligible articles.

Given the narrative nature of the review, formal risk-of-bias assessment tools were not applied. Studies were evaluated descriptively based on methodological transparency, data sources used, and model validation approaches. Reported performance metrics, for example, AUC, sensitivity, specificity, and calibration, were also used for evaluation. Given the heterogeneity of study designs, datasets, and reported metrics, quantitative pooling or meta-analysis was not attempted. Findings are presented as a descriptive synthesis.

2.1 Foundations of AI-driven AMR surveillance in hospitals

Antimicrobial resistance (AMR) is a global health challenge, with hospitals serving as some of its epicentres. The intensive use of broad-spectrum antibiotics, high patient turnover, and frequent invasive procedures create conditions that encourage the selection and spread of resistant organisms [29]. Traditional surveillance systems remain largely fragmented, even though they are essential. Manual laboratory reporting, delays in incorporating prescribing data, and poor interoperability among hospital information systems often limit the timely detection of emerging resistance trends [30]. This creates a significant data challenge, as the vast amount of information relevant to AMR exists in silos. This data fragmentation undermines the potential for AI-integrated surveillance [31]. AI offers a transformative opportunity to reframe AMR surveillance from a passive to a proactive approach. Predictive modelling can forecast the likelihood of resistant infections in high-risk patients or wards [32]. Natural language processing (NLP) when applied to electronic clinical notes can further enrich structured datasets by capturing patterns that traditional coding systems may miss [33]. Also, anomaly detection can flag abnormal prescribing practices or unusual microbial profiles in real time which can facilitate earlier intervention and more effective antimicrobial stewardship [34].

The foundation of such AI-driven surveillance depends on integrating diverse hospital data streams. For example, electronic Health Records (EHRs) provide patient-level demographic and clinical data. Laboratory information systems contribute microbiological cultures and antimicrobial susceptibility testing results, while pharmacy records offer prescribing patterns essential for stewardship analysis. These parameters, along with the suitable model, are further summarised in Table 2. AI can utilize data from these parameters to establish trends and patterns that can predict HAIs prompting immediate action. Microbial genomics can now provide detailed insights into resistance determinants and transmission pathways, enabling hospitals to track specific clones and resistance genes across wards [35]. By harmonising heterogeneous datasets, AI-powered platforms can also generate dashboards for infection-control teams. These can then permit proactive hotspot detection, real-time evaluation of prescribing practices, and rapid assessment of intervention outcomes. Therefore, AI-driven surveillance systems hold the potential to enhance infection prevention and control and to strengthen hospital resilience against the escalating global threat of antimicrobial resistance [29, 30].

Table 2 Hospital parameters that can be utilised in different machine learning models, with the rationale of the model choice

Parameter Category	Specific Parameters	Surveillance Objective	Suitable ML Model Types	Rationale for Model Choice
Microbiological Data	Pathogen species (e.g., <i>Staphylococcus aureus</i> , <i>Escherichia coli</i>), Antimicrobial Susceptibility Test (AST) results Susceptible, Infected, Removed/Recovered (S//R), Minimum Inhibitory Concentration (MIC) values, resistance phenotype, multi-drug or extensively drug resistant(MDR/XDR)	Predict resistant phenotype; trend analysis	Random Forest, Gradient Boosting (XGBoost), Logistic Regression	Structured tabular data; tree-based models handle nonlinear interactions and mixed variable types well [12]
Patient Demographics & Clinical Factors	Age, sex, comorbidities, ICU stay, device exposure, length of stay, prior colonization	Patient-level risk prediction for resistant infection	Random Forest, XGBoost, Neural Networks	Good for structured EHR data; ensemble models improve discrimination [12]
Antibiotic Exposure History	Prior antibiotic classes, duration, Defined Daily Dose (DDD), Direct Observed Treatment (DOT), time-to-appropriate therapy, and Extended-Spectrum Beta-Lactamases (ESBL) results.	Predict emergence of resistance; stewardship optimization	Gradient Boosting, Regularized Logistic Regression, Survival Models	Captures cumulative exposure effects; interpretable coefficients useful for stewardship
Temporal Trends	Monthly resistance rates, rolling averages, and seasonal variation	Forecast resistance trends	ARIMA, LSTM (Long Short-Term Memory networks)	Time-series forecasting models; LSTM captures nonlinear temporal dependencies [18]
Ward-Level Operational Data	Ward type (ICU vs. medical), bed occupancy, nurse-to-patient ratio, transfer frequency	Outbreak detection; cluster identification	Isolation Forest, DBSCAN, Bayesian Change Point Models	Unsupervised anomaly detection for unusual spikes or clustering
Patient Movement Networks	Inter-ward transfers, contact networks, shared room exposure	Transmission mapping; outbreak source identification	Graph Neural Networks (GNN), Network Centrality Models	Captures relational structure and transmission pathways
Genomic & Molecular Data	Resistance genes (e.g., mecA, blaCTX-M), SNP distances, plasmid typing	Transmission tracking; clonal outbreak detection	Hierarchical Clustering, GNN, CNN (for genomic patterns)	Handles high-dimensional genomic features and relatedness metrics [18, 20]
Environmental & Infection Control Metrics	Hand hygiene compliance, environmental culture positivity, and cleaning audits	Correlate IPC performance with resistance trends	Multivariate Regression, Random Forest	Examines associations between institutional practices and resistance outcomes [12]
Laboratory Workflow Metadata	Time-to-processing, specimen type, contamination rates	Improve surveillance reliability; detect lab bias	Logistic Regression, Gradient Boosting	Structured quality-control modelling
Composite Engineered Features	Colonization pressure index, cumulative antibiotic pressure score, ward resistance momentum	Early warning alert systems	Ensemble Models (Stacked Models), XGBoost, Neural Networks	Combines multi-layer inputs for robust predictive performance

AST Antimicrobial Susceptibility Testing, S//R Susceptible, Infected, Recovered, MIC Minimum Inhibitory Concentration, MDR Multi-Drug Resistance, XDR Extensive Drug Resistance, ICU Intensive Care Unit, MLP Natural Language Processing, EHR Electronic Health Records, ESBL Extended-Spectrum Beta-Lactamases, DDD Defined Daily Dose, DOT Direct Observed Treatment, IPC Infection Prevention and Control

2.2 AI-powered surveillance and early detection systems

Developing AI-powered surveillance systems has revolutionised the speed and accuracy of infectious disease outbreak detection, especially in hospital-acquired infections [36, 37]. Several individual studies reported higher sensitivity or specificity, although performance metrics varied widely depending on dataset characteristics, reference standards, and validation methods. For example, an ML model using random forests to predict multidrug-resistant *Escherichia coli* in surgical clinics in Turkey achieved higher accuracy, with an AUC of 0.99 for Ertapenem and ampicillin [38]. Across 127 hospitals in the United States, AUCs ranged from 0.743 to 0.847 for predicting resistance in *Escherichia coli* and *Klebsiella spp* [39]. These systems can provide more efficient diagnostic methods and more thorough surveillance. These results lead to an increase in reported infectious diseases within and outside hospitals. AI-powered surveillance can also leverage innovations such as rapid epidemic intelligence from internet-based sources. This approach can use informal data via internet-based intelligence methods to enable more responsive epidemic monitoring [36, 40].

Comprehensive global surveillance has been facilitated by Natural Language Processing (NLP) which is a subfield of AI focused on enabling machines to interpret human language. This has been instrumental in extracting meaningful insights from multilingual data streams, including clinical notes. Large Language Models (LLMs) and other advanced AI systems can facilitate scalable human language processing. Integrated with real-time analysis of structured and unstructured data, they enable a comprehensive dynamic assessment of global disease threats [40]. Their ability to utilise signals from vast amounts of health and non-health data sources, including news reports, social media trends, and web searches, gives them a distinct advantage over traditional surveillance methods, which typically rely solely on health-related data [40, 41]. However, the combination of social media, news media, and web-based data streams into AI-supported AMR surveillance systems risks misinformation, signal duplication, and inclusion of unverified cases. To mitigate these risks, robust safeguards are required. These may include source credibility scoring, cross-platform triangulation, semantic de-duplication algorithms, and confidence tagging of suspected versus laboratory-confirmed events [42–44]. Temporal smoothing thresholds and anomaly persistence criteria should be applied to minimise amplification of transient media spikes. Detection of automated or coordinated messaging behaviour is also essential to reduce susceptibility to propaganda-driven distortion. AI-generated alerts should be reviewed by humans before escalation. Digital signals must also be periodically calibrated against laboratory-confirmed surveillance data to ensure fidelity [41]. Transparent documentation of data sources and validation procedures further strengthens trust and accountability in hybrid digital-AMR surveillance systems.

AI-powered clinical decision support systems (CDSS), which often use a Markov decision process, can review antimicrobial prescriptions. These systems provide feedback to healthcare professionals, helping them identify incorrect prescriptions and prevent adverse effects, including AMR. This can eventually reduce morbidity, mortality, and sepsis rates [45]. While AI-powered surveillance systems show great promise for AMR surveillance, they face significant limitations, particularly in low- and middle-income countries. A primary challenge is the fragmented nature of many AI models, which

hinders practical cross-source data synthesis and makes it difficult to combine and analyse information from various sources.

The lack of reliable data and the poor quality of electronic medical records (EMRs) in these regions further hinder integration. Limited-quality data is another significant obstacle that prevents AI algorithms from producing meaningful predictions and conclusions about AMR and from engaging in real-time surveillance [8]. In fragmented health systems, datasets are often inconsistent, incomplete, or poorly coded. However, AI can play a transformative role in generating and augmenting high-quality data necessary for model training and validation. Natural language processing (NLP) models can extract structured clinical variables from unstructured sources such as handwritten charts, discharge summaries, microbiology reports, pharmacy logs, and infection control notes. Machine learning algorithms can identify outliers, reconcile duplicate entries, impute missing values, and standardise terminology, for example, by mapping local drug names to WHO ATC codes or by harmonising laboratory breakpoints [37]. Such pre-processing increases data reliability and allows pooled analysis across hospitals.

2.3 Predictive modelling and outbreak forecasting

AI has accelerated predictive modelling across the AMR–HAI continuum. For example, AI has estimated future resistance prevalence through bedside risk scoring and real-time outbreak alerts. AI-based bedside risk-scoring models can integrate prior colonisation history, recent antibiotic exposure, healthcare contact intensity, patient comorbidities, and real-time local epidemiological indicators to estimate the probability of a resistant infection. For example, machine Learning algorithms have been trained to learn from longitudinal antibiograms and antibiotic consumption data across hospitals in England. These developments have demonstrated hospital-specific resistance levels that are relatively stable and predictable, enabling forward forecasting to guide stewardship and formulary planning [25]. These models have been applied, and can be applied, at different levels of the hierarchy of AMR spread. For example, at the population and meso-levels, such as in a hospital or a network, AMR forecasting models increasingly integrate surveillance, pharmacy, and laboratory information system data. A 2024 proof-of-concept study demonstrated an ML pipeline that predicts the probability of antimicrobial susceptibility across multiple pre-culture stages, including sampling, direct examination, and initial culture [46]. The results from these predictions offered actionable lead time before the antibiogram was finalised. By relying on routinely collected ecology data, this approach can be implemented with minimal privacy burden.

Additionally, various strategic frameworks advocate antimicrobial learning systems that iteratively retain models trained on local data to reduce diagnostic latency. These models can also target high-risk settings and integrate outputs into stewardship workflows [47]. These strategic frameworks can consist of multiple algorithmic methods, such as classification algorithms based on logistic regression, decision trees, and support vector machines. These methods can explore different variables to predict antimicrobial susceptibility. For example, evidence shows that a simplified score-based model was developed among hospitals in Lower Saxony, Germany, to determine the transmission of Methicillin-Resistant *Staphylococcus aureus* using logistic regression. This model identified three major predictors with 75% sensitivity, 78.8% specificity, and an AUC of 0.8 [48]. These predictors could easily be transformed into clinical scores that can

forecast the MRSA spread. Other algorithmic methods include regression models that may employ clustering techniques, such as K-means, to identify and predict AMR across clusters [47]. The combined use of these frameworks can lead to better AMR identification and more effective stewardship. Further evidence indicates strong discrimination in HAI prediction tasks. In selected studies focusing on surgical site infections and urinary tract infections, some models achieved AUC values exceeding 0.80 [37]. However, these results are not directly comparable across studies due to heterogeneity in populations and outcome definitions [37]. Also, external and internal validation, as well as transportability, remain recurring gaps that must be addressed to ensure reliable deployment across sites.

At the point of care, ML models trained on EHRs identify patients at risk of resistant infections or adverse outcomes. Examples include XGBoost models that estimate resistance to multiple agents in *Enterobacterales* bloodstream infections, supporting empiric therapy choices [49]. “*Personalised antibiogram*” models using structured EHR features have achieved AUCs of approximately 0.74–0.78 across five commonly used antibiotics [49]. These findings demonstrate that compact, interpretable feature sets can rival larger, opaque models and are easier to implement in clinical systems [50]. Thus, temporal data is critical and should be enhanced using time-series deep learning. Such models should focus on routine clinical measures to improve individualised risk prediction for bloodstream infections, enabling earlier detection [50]. For transmission-sensitive HAIs, graph-based and network-aware models are emerging as early-warning tools. These have been widely used and offer an opportunity to further integrate them into healthcare to monitor and track these infections [51]. Such systems can prioritise screening, isolation, and environmental decontamination before clusters amplify. At the system level, hospital-wide resistance forecasting enables proactive inventory management. It also enables preemptive stewardship interventions when models signal impending rises in specific phenotypes, such as Extended-Spectrum Beta-Lactamases (ESBL) and Carbapenem-Resistant *Enterobacteriaceae* (CRE). Embedding these predictions into dashboards and alerting pipelines operationalises the “*sense-and-respond*” loop, thereby improving responses and actions [25, 47].

2.4 Intelligent antimicrobial stewardship and infection control automation

AI-supported systems have the potential to improve infection-detection sensitivity, detect outbreaks earlier, and enhance risk stratification for resistant pathogens. These systems can also improve harmony between empiric therapy and susceptibility patterns in selected hospital settings [37]. Recent findings demonstrate the effectiveness of automated antimicrobial stewardship programs (ASPs) as a cost-saving tool to improve patient care [52]. Adopting clinical decision support systems within electronic health records significantly improved adherence to *Staphylococcus aureus* bacteraemia management bundles and improved outcomes [52, 53]. The creation of antibiograms using custom Python code streamlined the process, as data generation was fast and customising antimicrobial sensitivity data was easy. For example, a five-year report on ASP implementation across four hospitals demonstrated decreased antimicrobial use, healthcare costs, and healthcare-related infections [54, 55]. These developments point to the use of smart automation to support antimicrobial stewardship strategies.

Automated systems have shown promise through infection-control alert systems. Such systems analyse microbiological and patient data and predict potential clusters of pathogens, providing comprehensive surveillance compared to conventional manual surveillance [56, 57]. These systems can identify sporadic and endemic outbreaks of pathogens with detection rates of 33–100%, depending on the pathogen and outbreak definition, algorithm design, and evaluation methodology [57, 58]. Therefore, attention should be directed to ensuring alignment between algorithm design and the diverse population characteristics in which these systems are used. Future trends in automated infection detection could include the use of emerging technologies, such as natural language processing and machine learning, to further improve outbreak identification and response [24, 29, 59]. For example, during the COVID-19 pandemic, AI was helpful in environmental disinfection and contact tracing. Mobile robots enabled by artificial intelligence can help plan efficient disinfection coverage patterns to reduce costs more quickly [60]. Furthermore, AI demonstrated competitive performance compared with human capabilities in rapid screening, diagnosis, and treatment monitoring [61, 62].

Topological data analysis (TDA), a set of algorithms that derive features from a dataset's global properties, also shows promise in both molecular modelling of outbreak risk within microbial populations and in predicting disease spread within human populations [63–65]. TDA combines spatial and temporal datasets into a single TDA summary, which is typically a barcode. This then tracks changes across time points with a time-series machine-learning algorithm, providing a robust initial analysis of trends and simplified risk tracking, as in the COVID-19 outbreak [64]. TDA, using persistent homology, has been applied in evaluating resistosomes from approximately 146 bacterial isolates at Johns Hopkins [66]. This methodology uncovered distinct clinical patterns among the bacterial isolates, enhancing understanding of resistance patterns. Merging this TDA-based time-series analysis approach can improve AMR tracking by coupling gene or molecular analyses with TDA methods. These can then be forecasted to future time points using deep learning or standard time-series algorithms. Integration of molecular or genetic TDA models of microbial evolution with TDA models of hospital-acquired infection datasets can improve forecasting within hospital systems and track the likelihood of major HAI outbreaks or the emergence of multidrug-resistant strains. The application of TDA could follow the workflow is shown in Fig. 1.

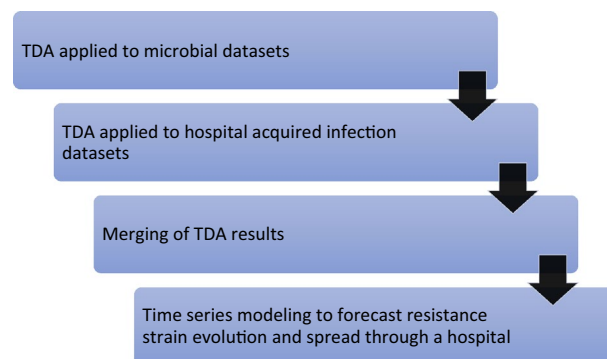


Fig. 1 The potential workflow of Topological data analysis algorithms and their application in AMR surveillance. This workflow can be applied to the different hospital datasets involving data relevant to AMR

2.5 Roadmap for sustainable AI integration into AMR programs

Integrating AI sustainably into AMR programs requires both technical expertise and pragmatic governance. Lessons from recent successes indicate that AI performs best when models are locally validated, explainable, and embedded in clinical workflows rather than run as isolated pilots [38, 39, 46]. For example, hospital-level resistance forecasting that leverages local antibiograms and prescribing data improved forward forecasts and stewardship planning [25]. Also, AI-enabled, interpretable decision support for common infections increased clinician trust and actionability in several proof-of-concept studies [67, 68]. A summary of the different lessons from the previous evidence to enhance AI integration into AMR programs is provided in the Table 3 below.

Other strategies for effectively integrating AI into HAIs and AMR programs include multi-stakeholder collaboration. Various co-design teams, such as clinicians, microbiologists, Infection Prevention and Control committees, Information Technology, data scientists, pharmacists, pharmacologists, and policymakers, can collaborate to develop these strategies [67]. These can work together through user-centred design and workshops, ward-based pilot dashboards, and continuous feedback loops to refine the models and decision thresholds [25]. A prospective roadmap for integrating AI to detect and manage HAIs over several months to years is shown in Fig. 2.

Governments must invest in data infrastructure at the hospital level through training local data stewards and adopting modular, low-cost pilots within hospital and ward settings. At the technical level, hospitals may require electronic health records capable of structured data extraction, such as organism identification, susceptibility testing results, and Minimum Inhibitory Concentration (MIC) values. Other information for extraction can include antibiotic prescribing records, such as drug class, duration, and days of therapy, as well as admission–discharge–transfer data to enable real-time epidemiological modelling [37]. A robust laboratory information system must permit automated, time-stamped export of culture and antibiogram data into a secure clinical unit. On-premises servers or compliant cloud environments must be in place and support real-time data streaming and model version control [37]. These servers could also support audit logging, explainability modules, cybersecurity safeguards, and mechanisms for recalibration as resistance patterns shift. Governance structures, including antimicrobial stewardship (AMS) oversight committees, local validation frameworks prior to scale-up, transparent documentation of model performance, and safeguards, are also relevant for this AI integration [28]. Also, AI tools must be embedded directly into prescribing workflows, for example, computerised provider order entry systems or stewardship dashboards, to influence decisions rather than remain parallel analytics tools.

Table 3 The different lessons and why they matter for integrating AI into AMR programs

Lesson (short)	Evidence/why it matters
Local data with continuous retraining	Hospital forecasts and local antibiogram models outperform one-size-fits-all models [25]
Interpretability builds uptake	Explainable models increased clinician acceptance in stewardship pilots [67, 68]
Network models detect transmission earlier	Graph-based approaches flagged vancomycin-resistant enterococci (VRE) carriers before clusters expanded [34]
Integrate into workflows (not silo)	Embedding predictions into dashboards/AMS workflows enabled action [25]
Link discovery to surveillance	AI in antibiotic discovery complements surveillance to reduce long-term burden [69]

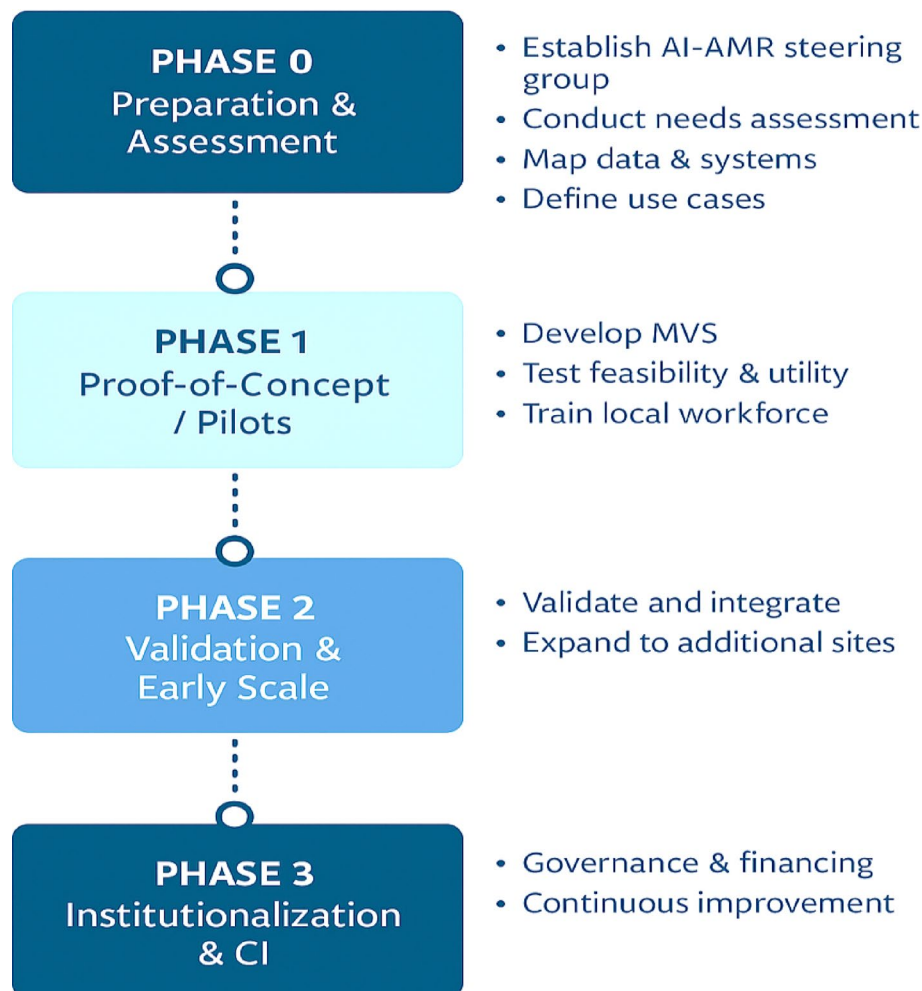


Fig. 2 A proposed roadmap that can be adopted to integrate AI for AMR from HAIs: MVS: Minimum Viable System

The impact of this adoption can be evaluated using clinical endpoints at the patient or hospital level [25, 70]. Patient-level endpoints can include improvement in appropriate empiric therapy rates, reduction in time to active antibiotic therapy, and decreases in unnecessary broad-spectrum antibiotic exposure, such as carbapenem days of therapy. Other endpoints can include safe de-escalation rates after susceptibility results and clinician adherence to AI-supported recommendations. Hospital-level endpoints may include reductions in incidence density of multidrug-resistant organism infections per 1,000 patient-days and earlier outbreak detection intervals. Stabilisation or decline in resistance prevalence for targeted pathogen–antibiotic pairs and improved compliance with infection prevention measures can also be captured [28]. Safety endpoints, such as rates of missed resistant infections, adverse drug reactions, and frequency of clinician override, are also essential to ensure that AI integration does not introduce unintended harm.

3 Conclusion

AMR in HAIs represents a growing crisis that threatens patient outcomes and health system resilience worldwide. Traditional surveillance approaches, while foundational, are reactive, fragmented, and insufficient to keep pace with the rapid emergence and spread

of resistance. AI integration can shift this paradigm from delayed response to proactive prediction, early detection, and timely intervention. Studies that have used machine learning models have demonstrated their potential to forecast resistance trends, identify high-risk patients, and issue early-warning alerts with increasing accuracy. However, sustainable AI adoption depends on more than technical innovation. It requires robust multi-stakeholder collaboration, regulatory alignment, ethical safeguards, and investments in capacity building, particularly in low- and middle-income countries. Embedding AI tools into clinical workflows, strengthening electronic health record systems, and ensuring continuous model retraining are essential steps toward meaningful impact. By combining these strategies, AI-driven surveillance can reinforce infection control and mitigate the growing threat of AMR in hospital settings.

4 Limitations

This narrative review is subject to selection bias and does not provide a quantitative synthesis of effect sizes or pooled outcomes, unlike systematic reviews and meta-analyses. The included literature may reflect thematic emphasis rather than a comprehensive coverage of all available evidence. Also, there is heterogeneity across the selected studies in study design, AI methodologies, models, clinical settings, and reported endpoints. This limits direct comparability across the different studies. Future studies can expand this topic through systematic literature reviews to ensure consistent comparisons across studies. Also, much of the current evidence base consists of proof-of-concept or retrospective validation studies, with relatively few prospective, implementation trials. Future studies can focus on prospective experimental evaluations of AI applications for AMR monitoring in hospital settings.

Abbreviations

AI	Artificial intelligence
AMR	Antimicrobial resistance
ASP	Antimicrobial stewardship programs
BERT	Bidirectional encoder representations from transformers
CDSS	Clinical decision support systems
CI	Continuous improvement
CNN	Convolutional neural networks
CRE	Carbapenem-resistant enterobacteriaceae
HAIs	Hospital-acquired infections
EHR	Electronic health records
ESBL	Extended-spectrum beta-lactamases
FNN	Feedforward neural networks
GANs	Generative adversarial networks
GRU	Gated recurrent unit
LLMs	Large language models
LSTM	Long short-term memory
MDR	Multi-drug resistance
ML	Machine learning
NLP	Natural language processing
RNN	Recurrent neural networks
SSIs	Surgical site infections
TDA	Topological data analysis
UTIs	Urinary tract infections
VAEs	Variational autoencoders
VRE	Vancomycin-resistant enterococci

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Competing interests

The authors declare no competing interests.

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