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Review Article

Artificial Intelligence for Combating Antimicrobial Resistance: Recent Advances in Prediction, Surveillance, Drug Discovery, Antimicrobial Stewardship and Precision Therapy

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Abstract

Objective: To review the role of artificial intelligence (AI) in addressing antimicrobial resistance (AMR), with a focus on its applications in antimicrobial resistance prediction, surveillance, antimicrobial drug discovery, and personalized antimicrobial therapy. **Data Sources:** A comprehensive literature search was conducted using electronic databases, including PubMed, Scopus, Google Scholar, and Web of Science, to identify relevant peer-reviewed articles on AI-driven approaches to AMR management. The search primarily covered publications from 2018 to 2026, supplemented by landmark studies and international reports published before 2018 to provide essential background information. **Study Selection:** Relevant peer-reviewed studies investigating the application of artificial intelligence, machine learning, and deep learning in AMR prediction, surveillance, drug discovery, and personalized antimicrobial therapy were selected. Studies were critically assessed for their relevance to the objectives of the review and their contribution to understanding the potential and limitations of AI-based AMR management. **Summary of Content:** Antimicrobial resistance is a major global public health challenge that reduces the effectiveness of antimicrobial therapy and contributes to increased morbidity, mortality, and healthcare costs. AI-driven approaches have demonstrated considerable potential in predicting antimicrobial resistance using genomic and clinical data, strengthening AMR surveillance, accelerating antimicrobial drug discovery, and supporting personalized treatment decisions. Unlike previous reviews focusing on individual AI applications, this review presents an integrated multidisciplinary perspective on AI-based AMR management. It also highlights key challenges, including data quality, model interpretability, generalizability, and the need for rigorous clinical validation before widespread implementation. **Conclusion:** Artificial intelligence offers promising opportunities to improve antimicrobial resistance prediction, surveillance, drug discovery, and personalized antimicrobial therapy. Integrating AI into antimicrobial stewardship and clinical decision-making may contribute to more effective AMR management. However, further validation, high-quality data, interpretable models, and prospective clinical studies are essential to establish the reliability, safety, and practical applicability of these approaches.

Keywords: Artificial intelligence; antimicrobial resistance; machine learning; antimicrobial stewardship; deep learning; precision therapy

1. Introduction

The introduction of antimicrobial agents revolutionized modern medicine and transformed human life, contributing to effective management of infectious diseases and significant decline in mortality [1]. Nevertheless, accelerated spread of antimicrobial resistance (AMR) has emerged as a global health security crisis. Resistance mechanisms displayed by microbes render currently available therapies inefficient, thereby increasing the treatment challenges posed by community or hospital-acquired infections [4].

The problem of AMR has grown alarmingly over time. A significant systemic analysis estimated that 1.27 million deaths worldwide were caused by bacterial AMR across 204 nations in 2019 alone. This is predicted to worsen further in the coming future without implementation of proactive interventions [1]. Concurrently, due to several scientific, regulatory, and commercial obstacles, the development of new antimicrobial agents has declined, partly because of scientific, regulatory and commercial barriers often described as the 'valley of death'. [2]. While the World Health Organization global action plan on AMR called for collective action, execution varies across countries [2]. The most sophisticated computational technology AI has been proposed for a variety of challenges associated with disease management [5,7,15–17].

This artificial intelligence approach (which incorporates both machine learning and deep learning algorithms) can analyze enormous volumes of clinical and biologic data to identify elusive relationships, anticipate resistance patterns, expedite the discovery of antimicrobial agents and provide guidelines to individuals as per their need [5].

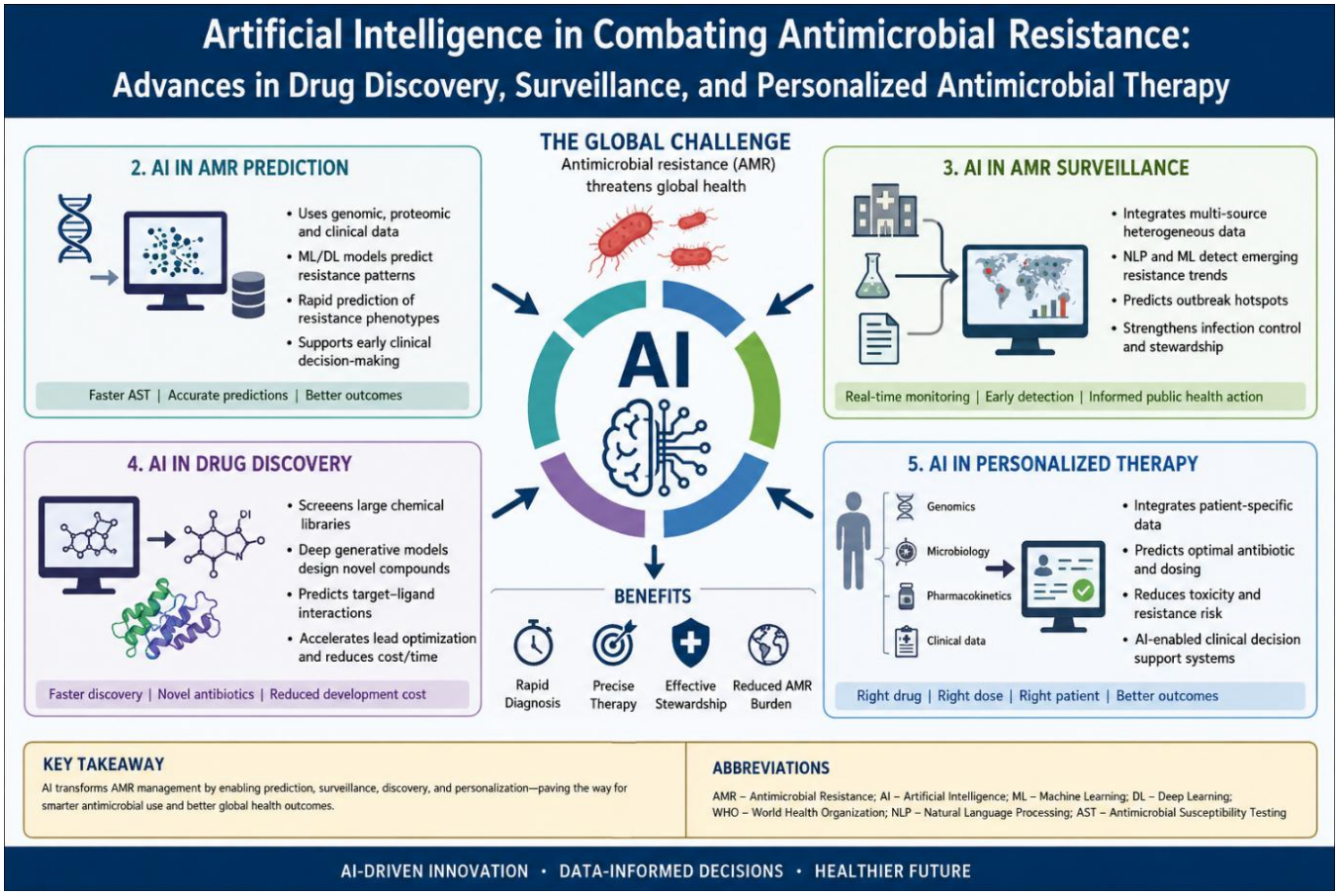


Figure 1. Graphical abstract Source: Created by the author using AI-assisted tools

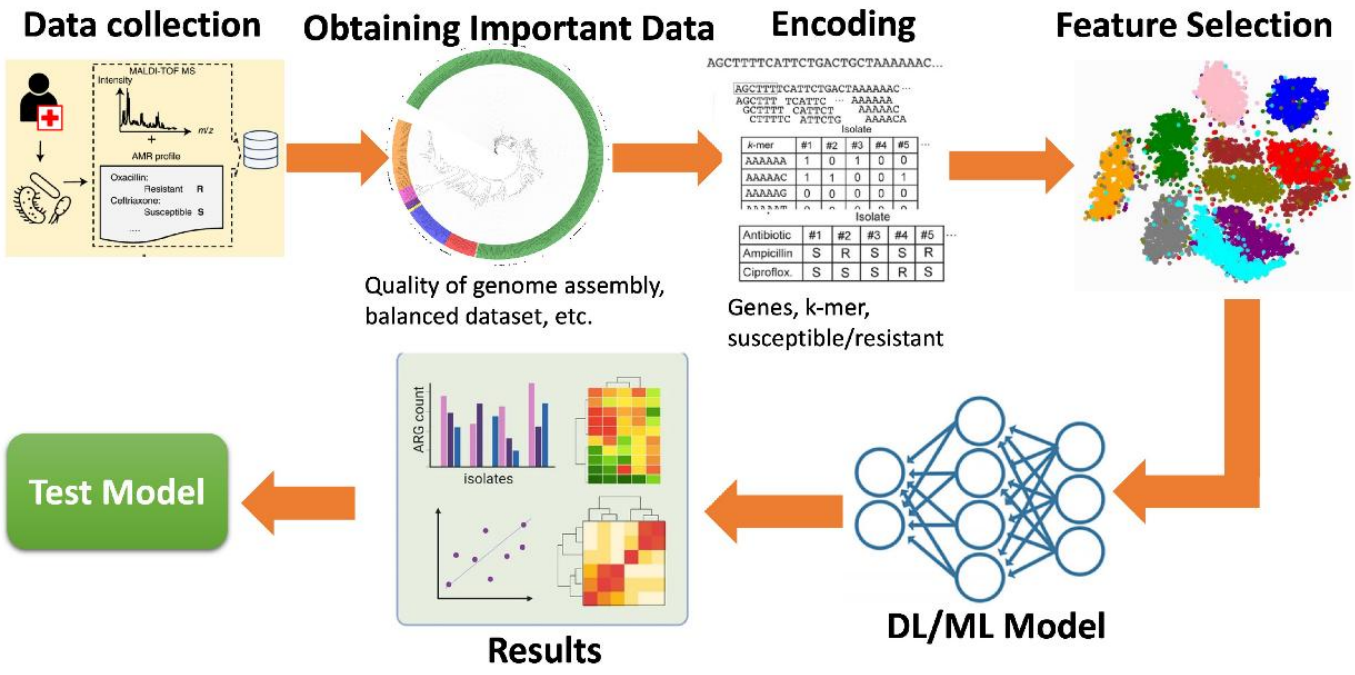


Figure 2. Machine-learning and deep-learning models for antimicrobial resistance identification.

Source: Reproduced from Ali T, Ahmed S, Aslam M. Artificial intelligence for antimicrobial resistance prediction: challenges and opportunities towards practical implementation. Antibiotics. 2023;12(3):523. https://doi.org/10.3390/antibiotics12030523. Reproduced under the Creative Commons Attribution 4.0 International (CC BY 4.0) licence.

Table 1. Applications of Artificial Intelligence in Antimicrobial Resistance (AMR)

Adapted from: Anahtar et al. (2021), Arango-Argoty et al. (2018), Miotto et al. (2018), Vamathevan et al. (2019), Stokes et al. (2020), and Peiffer-Smadja et al. (2020)

S. No.	AI Application Area	Description	Common AI Methods	Impact on AMR Management
1	Resistance Prediction	Predicts antimicrobial resistance patterns from genomic and clinical data	Random Forest, SVM, Deep Neural Networks	Faster diagnosis, early targeted therapy
2	AMR Surveillance	Real-time monitoring of resistant pathogens	NLP, ML, Predictive Analytics	Early outbreak detection
3	Drug Discovery	Identifies new antimicrobial compounds	Deep Learning, GANs	Reduced development cost
4	Personalized Therapy	Tailored treatment	Predictive ML	Optimized dosing
5	Genomic Analysis	Detects resistance genes	Deep Learning	Better mechanism understanding
6	Clinical Decision Support	Assists clinicians	AI-based CDS	Improved stewardship
7	Literature Mining	Extracts evidence	NLP	Faster evidence synthesis
8.	Graph-based Resistance Prediction	Predicts antimicrobial activity and resistance using molecular graph representations	Graph Neural Networks (GNNs), Directed Message Passing Neural Networks (D-MPNNs)	Improved prediction accuracy, identification of novel antimicrobial compounds, enhanced molecular feature learning
9	Explainable Clinical Decision Support	Improves transparency and interpretability of AI-assisted treatment recommendations	Explainable AI (SHAP, LIME, Attention Mechanisms)	Greater clinician confidence, regulatory acceptance, and safer clinical implementation
10	Foundation Models & Self-supervised Learning	Learns molecular and genomic representations from large unlabeled datasets	Foundation Models, Self-supervised Learning, Transfer Learning	Better generalization, improved prediction for rare pathogens, reduced dependence on labelled datasets
11	Privacy-preserving AMR Surveillance	Enables collaborative AI model development without sharing sensitive patient data	Federated Learning	Secure multi-centre surveillance, improved data privacy, enhanced global AMR monitoring
12	Next-generation Antimicrobial Discovery	Generates and optimizes novel antimicrobial molecules with desired biological properties		Accelerated drug discovery, reduced development time and cost, improved lead optimization

2. Research Gap and Novelty

Most review articles have been published to overview artificial intelligence (AI) application in antimicrobial resistance (AMR), with each reviewing different parts including AMR prediction, discovery of antimicrobials, clinical decision-making support or antimicrobial stewardship alone. Many of the previously published reviews only summarized conventional machine learning, without focusing on newly emerging advanced AI, such as graph neural networks (GNNs), directed message passing neural networks (D-MPNNs), foundation models, generative AI, explainable artificial intelligence (XAI), federated learning and multimodal AI. However, very few attentions have been given to the integration of the new AI technologies into a comprehensive antimicrobial resistance management framework covering prediction, surveillance, rapid diagnostics, antimicrobial stewardship, precision therapy and One Health strategy.

In the current review, we updated a more systematic and an integrative review of AI applications across the entire scope of antimicrobial resistance management.

Specifically, instead of a summary of traditional knowledge, the present review critically highlights advances made from 2024 to 2026 and points out a new generation of AI technologies which could promote antimicrobial resistance prediction, accelerate

antimicrobial drug discovery, improve clinical decision making, enhance antimicrobial stewardship programs, and enable precision antimicrobial therapy. Furthermore, this review discusses current implementation challenges, ethical and regulatory implications, and potential future directions of research to foster effective translation of AI-based AMR solutions into clinical practice. We integrated the state-of-art AI technologies with today's antimicrobial stewardship strategies and One Health concept to create a timely and clinically relevant overview for researchers, clinicians and health policymakers. AI in Antimicrobial Resistance Prediction Artificial intelligence (AI) has become a crucial player in facilitating rapid analysis of complex genomic, proteomic, microbiological and clinical data to advance the prediction of antimicrobial resistance (AMR).

To further clarify the scope and novelty of the present review, a structured comparison with previously published reviews was undertaken (Table 2). Previous reviews have addressed specific or overlapping applications of AI in AMR, including resistance prediction, antimicrobial discovery, clinical decision support, diagnostics, surveillance, and antimicrobial stewardship. The present review brings these domains together and additionally considers precision antimicrobial therapy and emerging AI approaches, including graph-based learning, explainable AI, foundation and self-supervised models, federated learning, multimodal AI, and generative AI. The comparison also highlights the broader integration of these technologies across the AMR management continuum.

Table 2. Comparison of the thematic scope of previous AI–AMR reviews and the present review

Review	AMR Prediction	Surveillance	Diagnostics / CDSS	Drug Discovery	Stewardship	Precision Therapy	Emerging AI Approaches
Anahtar et al., 2021 [5]	✓	–	–	✓	✓	–	Limited
Peiffer-Smadja et al., 2020 [13]	✓	–	✓	–	✓	Limited	–
Alkhanbouli et al., 2025 [16]	✓	–	✓	–	–	✓	✓
Salama et al., 2026 [18]	✓	✓	✓	✓	✓	✓	✓
Present review	**✓**	**✓**	**✓**	**✓**	**✓**	**✓**	**✓**

✓ indicates that the application area is substantially addressed; "Limited" indicates that the topic is discussed but is not a major focus; "–" indicates that the topic is not a principal component of the review.

To further clarify the scope and novelty of the present review, a structured comparison with selected previous reviews was undertaken (Table 2). Previous reviews have addressed important but varying aspects of AI applications in AMR. Anahtar et al. [5], for example, focused primarily on genomic AMR prediction, antimicrobial mechanisms and drug development, and antimicrobial stewardship, whereas Peiffer-Smadja et al. [13] examined machine-learning applications for clinical decision support in infectious diseases, including antimicrobial management. More recent reviews have expanded the scope toward AI-enabled antimicrobial discovery [19], explainable AI and clinical prediction [16], and broader AI applications across AMR management, including surveillance, diagnostics, stewardship and drug discovery [18].

The present review brings these application domains together within a single framework encompassing AMR prediction, surveillance, rapid diagnostics and clinical decision support, antimicrobial drug discovery, antimicrobial stewardship, and personalized/precision antimicrobial therapy. In addition, it considers emerging approaches such as graph-based learning, explainable AI, foundation and self-supervised models, federated learning, multimodal AI, and generative AI. These approaches are discussed not only in terms of their potential applications but also with respect to current evidence, implementation challenges, ethical considerations, and requirements for clinical translation.

Thus, the contribution of the present review is its integrated and updated perspective across multiple stages of AMR management, with particular attention to the convergence of established AI methods and emerging AI technologies and their potential translation into clinically relevant and One Health-oriented AMR strategies. Typical antimicrobial susceptibility testing (AST) approaches usually take 24–72 hours to yield results, potentially delaying selection of appropriate antimicrobial agents. In contrast, predictive AI models can integrate genomic information, clinical data including electronic health records, and microbiological laboratory results to predict antimicrobial susceptibility outcomes more rapidly and thereby support clinical decision-making [5,6,15].

Early predictive modelling largely relied on conventional machine-learning approaches such as random forest (RF), support vector machines (SVM), and gradient-

boosting methods. More recently, these approaches have been extended to graph-based deep-learning methods, in which molecular and genomic information can be represented as graphs and learned using graph neural networks (GNNs) and directed message-passing neural networks (D-MPNNs). Graph-based representations can capture structural relationships within molecular and genomic data and have shown potential for improving prediction and identifying candidate compounds with anti-AMR activity [42,43].

Recent developments in graph-based self-supervised learning and foundation models have further expanded AMR prediction by enabling models to learn useful representations from large datasets, including situations in which labelled antimicrobial datasets are limited. Pretrained molecular representations can subsequently be transferred to smaller target-specific datasets and fine-tuned for antimicrobial activity prediction [45,46]. AI-based prediction pipelines may also be combined with molecular docking and ADME/PK approaches to support downstream evaluation of promising antimicrobial candidates.

Explainable artificial intelligence (XAI) provides an additional layer of interpretability by identifying features that contribute to model predictions. Methods such as Shapley additive explanations (SHAP) and attention mechanisms can provide feature-level attribution and facilitate biological interpretation of model outputs[18,42]. However, reliable AMR prediction requires external and multicentre validation because models developed using random train/test splits from single-centre datasets may overestimate real-world generalizability. Differences in pathogen prevalence, clinical populations, laboratory practices, and dataset characteristics may further affect model performance.

Future development should therefore emphasize multicentre validation, federated learning, multimodal AI, and interpretable models capable of integrating clinical, microbiological, genomic, and other relevant data sources. Such approaches may improve the robustness and clinical applicability of AI-assisted AMR prediction and support more precise antimicrobial decision-making and stewardship[18,38–45].

3. Literature Search Methodology

A narrative literature search was conducted to identify peer-reviewed publications on the application of artificial intelligence (AI), machine learning (ML), and deep learning (DL) in antimicrobial resistance (AMR) management. Electronic searches were performed using PubMed, Google Scholar, Scopus, and Web of Science. The primary search period covered publications from 2018 to 2026, while selected landmark studies and international reports published before 2018 were included to provide essential background information.

The main search concepts included combinations of the terms “artificial intelligence,” “machine learning,” “deep learning,” “antimicrobial resistance,” “antibiotic resistance,” “AMR prediction,” “AMR surveillance,” “antimicrobial drug discovery,” “antimicrobial stewardship,” “clinical decision support,” and “personalized antimicrobial therapy.” Peer-reviewed studies addressing the application of AI, ML, or DL in AMR prediction, surveillance, antimicrobial drug discovery, stewardship, clinical decision support, or personalized antimicrobial therapy were considered eligible. Publications unrelated to AMR or without a relevant AI-based application were excluded.

Approximately 55 publications were identified through the literature search. Following screening of titles and abstracts and assessment of relevant full-text articles, 40 publications were considered relevant and included in the final narrative synthesis. The selected literature was thematically analyzed according to the major areas of AI application in AMR management: prediction, surveillance, antimicrobial drug discovery, antimicrobial stewardship, and personalized antimicrobial therapy.

4. AI in AMR Prediction

Artificial intelligence (AI) has increasingly been applied to antimicrobial resistance (AMR) prediction by integrating clinical, laboratory, microbiological, genomic, and molecular data. Earlier machine-learning approaches commonly included logistic regression, decision trees, random forest, support vector machines (SVM), and gradient-boosting methods, which were used to identify patterns associated with antimicrobial resistance and predict resistance phenotypes from clinical and microbiological datasets [5,6,15]. More recent predictive frameworks increasingly employ advanced ensemble methods such as XGBoost, LightGBM, and CatBoost, which can model nonlinear relationships among clinical and laboratory variables and provide efficient risk prediction.

Clinical predictors used in AMR-related models may include C-reactive protein (CRP), procalcitonin, white blood cell (WBC) count, vital signs, presenting symptoms, previous antimicrobial exposure, microbiological findings, and other electronic health-record variables. Integration of these features can facilitate earlier identification of patients at increased risk of resistant infection and support more informed empirical antimicrobial selection [5,13,30–35]. In parallel, genomic and molecular approaches have expanded AMR prediction beyond conventional clinical variables. Deep-learning and graph-based models, including graph neural networks (GNNs) and directed message-passing neural networks (D-MPNNs), can learn representations directly from molecular and genomic structures and have demonstrated potential for resistance prediction and antimicrobial discovery [42–44].

A further emerging approach involves host transcriptomic neural-network classifiers, in which expression signatures containing a defined set of messenger RNAs (for example, 29-mRNA signatures) are investigated for distinguishing infection phenotypes and supporting rapid clinical classification. Such host-response approaches may complement pathogen-based resistance prediction by providing information derived from the patient's biological response. Recent developments in self-supervised learning and foundation models are also enabling the extraction of

useful representations from large datasets, including settings where labelled AMR data are limited [45,46].

Future AMR prediction systems are expected to increasingly incorporate multimodal Transformer architectures and hybrid explainable artificial intelligence (XAI) approaches that integrate clinical, laboratory, genomic, transcriptomic, and microbiological information. Explainability methods such as SHAP and attention-based mechanisms may further assist in identifying the features contributing to individual predictions and improve the interpretability of AI-assisted clinical decision-making [18,42]. However, external and multicentre validation remains essential because model performance can be affected by dataset composition, pathogen prevalence, local laboratory practices, and differences between healthcare settings.

Table 3. Representative AI and machine-learning studies for antimicrobial resistance prediction

Study	Organism / clinical setting	Data type	Resistance phenotype / genotype predicted	AI/ML model	Key performance
Lewin-Epstein et al., 2021 [47]	Hospitalized patients with bacterial infections	Electronic health records, clinical variables and (where available) bacterial species information	Resistance to ceftazidime, gentamicin, imipenem, ofloxacin, and sulfamethoxazole-trimethoprim	Ensemble of machine-learning models	AUROC 0.73–0.79 without bacterial species; 0.80–0.88 when bacterial species was included
Valavarasu et al., 2025 [48]	917,049 bacterial isolates; multiple species (Pfizer ATLAS surveillance dataset)	Demographic, specimen, susceptibility, phenotype, and genotype data	Antibiotic resistance phenotype	XGBoost and other ML models	AUC 0.96 for phenotype-only data; 0.95 for phenotype-plus-genotype data
E. coli WGS study, 2024 [49]	Escherichia coli clinical isolates (256 genomes)	Whole-genome sequencing combined with AMRFinderPlus features and k-mer frequencies	Phenotypic susceptibility to ciprofloxacin	Random Forest and XGBoost (five-fold cross-validation)	>90% accuracy achieved with XGBoost using the combined feature approach
Wang et al., 2024 [50]	Staphylococcus aureus clinical isolates (DRIAMS and Taiwan datasets)	MALDI-TOF mass spectra	Resistance to multiple antibiotics, including oxacillin-associated resistance and mecA	MLP, LightGBM, AdaBoost, and other classifiers	DRIAMS dataset: MLP AUROC 0.81–0.87, AUPR 0.90–0.97; LightGBM strong across several phenotypes
Yuan et al., 2025 [51]	Enterobacterales bloodstream infections (hospital and community)	Hospital and community clinical data	Resistance to seven antibiotics	XGBoost	AUC 0.680–0.737 without species information; 0.723–0.827 with species identification included

These studies (summarized in Table 3) illustrate the diversity of data sources and prediction targets currently used in AI-based AMR prediction. Clinical and electronic health-record data can be used to estimate the probability of antibiotic resistance before definitive microbiological results are available. For example, Lewin-Epstein et al. used electronic medical records and antibiotic susceptibility results from hospitalized patients to predict resistance to ceftazidime, gentamicin, imipenem, ofloxacin, and sulfamethoxazole-trimethoprim using an ensemble of machine-learning models. The ensemble achieved AUROC values of 0.73–0.79 when bacterial species information was unavailable, which increased to 0.80–0.88 when bacterial species was incorporated [47]. At a larger scale, Valavarasu et al. analyzed 917,049 bacterial isolates from the Pfizer ATLAS dataset using demographic, specimen, susceptibility, phenotype, and genotype information. XGBoost achieved AUC values of 0.96 for the phenotype-only dataset and 0.95 for the phenotype-plus-genotype dataset [48].

Genomic and microbiological data provide additional opportunities for predicting specific resistance phenotypes. In *Escherichia coli*, whole-genome sequencing data from 256 bacterial genomes were combined with AMRFinderPlus features and k-mer frequencies to predict phenotypic susceptibility to

ciprofloxacin. Random Forest and XGBoost models were evaluated using five-fold cross-validation, with the combined feature approach achieving greater than 90% accuracy with XGBoost [49]. Similarly, MALDI-TOF mass spectra have been investigated for predicting antimicrobial resistance in *Staphylococcus aureus*. Wang et al. evaluated multiple machine-learning classifiers using DRIAMS and Taiwan datasets, with MLP, LightGBM, and AdaBoost demonstrating useful discrimination for several resistance phenotypes. In the DRIAMS dataset, MLP achieved AUROC values of 0.81–0.87 for selected antibiotics, with AUPR values of 0.90–0.97; spectral features were also associated with *mecA* and oxacillin resistance[50]. In Enterobacterales bloodstream infections, Yuan et al. developed XGBoost models using hospital and community clinical data to predict resistance to seven antibiotics. In held-out test data, AUC values ranged from 0.680 to 0.737 without species information and from 0.723 to 0.827 when species identification was incorporated [51].

Collectively, these examples demonstrate that AI-based AMR prediction can operate across clinical, phenotypic, genomic, and microbiological data modalities and can target either resistance phenotypes or underlying genetic markers. However, reported performance varies according to the organism, antimicrobial agent, dataset composition, prevalence of resistance, and validation strategy. A systematic review and meta-analysis of ML-based AMR prediction studies reported a pooled AUC of 0.82 (95% CI, 0.78–0.85), while also highlighting limitations related to retrospective study designs, non-standardized data processing, and limited external or real-world validation[36]. Therefore, high internal performance should not be interpreted as evidence of immediate clinical applicability, and multicentre external validation remains essential.

5. AI in Antimicrobial Surveillance

Antimicrobial resistance (AMR) surveillance has a key role in monitoring the emergence, distribution, and spread of resistant organisms and in guiding appropriate public-health and infection-control interventions [2]. Artificial intelligence can complement traditional surveillance by integrating large and heterogeneous datasets from hospitals, clinical microbiology laboratories, electronic health records, antimicrobial prescribing systems, genomic databases and public-health organizations. [5,8]. Machine learning (ML) and natural language processing (NLP) can be used to analyse structured and unstructured clinical and microbiological data and identify temporal or geographical changes in resistance patterns that may be difficult to detect through conventional manual surveillance [13].

Microbiological results, antimicrobial susceptibility testing (AST), patient characteristics, admission data, antimicrobial exposure and clinical records at the hospital level can be incorporated into AI-based surveillance to identify patients or hospital units at higher risk of infections caused by multidrug-resistant organisms. Machine-learning approaches have also been explored to predict multidrug-resistant infections and identify patients at higher risk that could allow earlier infection-control and antimicrobial-stewardship interventions. [13,33]. Such systems may facilitate continuous monitoring of resistance patterns and assist infection-prevention teams in prioritizing further investigation of unusual clusters or changes in resistance.

Genomic surveillance provides another important area in which AI can contribute to AMR monitoring. Whole-genome sequencing (WGS) generates extensive information on antimicrobial resistance genes, mutations, plasmids, and genetic relatedness between bacterial isolates. Computational and machine-learning approaches can assist in identifying resistance determinants and analysing genetic relationships among isolates, thereby supporting the detection and investigation of transmission of resistant organisms [6,7]. Integration of genomic information with clinical and epidemiological data may further improve surveillance of emerging resistant clones and transmission networks. However, the performance and generalizability of AI-based genomic surveillance models may be impacted by differences in sequencing platforms, genomic pipelines, data quality, and the availability of reference datasets.

At the population level, AI is able to combine information from hospitals, diagnostic laboratories, surveillance networks and public-health databases to identify temporal and geographical trends in AMR. Predictive analytics could potentially identify areas or populations at increased risk of emerging resistance, and help prioritize surveillance and preventive interventions.[5,13]. NLP may additionally facilitate extraction of AMR-related information from large volumes of clinical documentation and other unstructured data sources. Such approaches are particularly relevant for integrating heterogeneous data streams that are generated continuously across healthcare systems.

AI based AMR surveillance should complement, not replace, established microbiological and epidemiological surveillance systems. The reliability of the models depends on the completeness, representativeness and standardization of the underlying data. Differences in antimicrobial susceptibility testing practices and resistance breakpoints, absence of clinical information, limited capacity for genome sequencing, and lack of external validation may decrease transferability of models between institutions and geographical settings. Therefore, multicentre validation, standardized data collection, interoperable surveillance systems, transparent reporting and appropriate oversight by humans are required for implementation of AI-supported AMR surveillance in a reliable manner.

6. AI in Antimicrobial Drug Discovery

Artificial intelligence (AI) is increasingly being used to accelerate antimicrobial drug discovery by enabling rapid screening and prediction of promising compounds from large chemical and biological datasets. Deep-learning approaches, including graph neural networks (GNNs) and directed message-passing neural networks

(D-MPNNs), can learn molecular representations and predict antimicrobial activity more efficiently than conventional descriptor-based approaches [11,42,43]. AI-assisted screening has contributed to the identification of novel antimicrobial candidates, including halicin and abaucin, while integration with molecular docking and ADME/PK prediction can further support lead optimization [11,42–44]. More recently, self-supervised learning and foundation models have enabled the use of large unlabelled chemical datasets to improve prediction when target-specific labelled data are limited [45,46]. Thus, AI provides a promising computational framework for accelerating antimicrobial discovery and reducing the time and resources required for conventional drug-development workflows.

Antimicrobial Stewardship and AI in Antimicrobial Stewardship

Antimicrobial stewardship (AMS) involves a coordinated and evidence-based approach aimed at promoting the responsible use of antibiotics. It seeks to optimize patient outcomes while minimizing adverse effects, toxicity, unnecessary antimicrobial exposure, healthcare costs, and the development and spread of antimicrobial resistance (AMR). The concept emerged in the mid-1990s with increasing recognition of antibiotics as valuable and limited resources that require careful and appropriate use [20,21]. Initially focused primarily on hospital-based antibiotic use, AMS has subsequently evolved into a broader framework encompassing human health, veterinary medicine, agriculture, and the One Health perspective [22,23].

Modern AMS programs focus on appropriate antimicrobial selection, correct dosing and route of administration, optimal duration of therapy, microbiology-guided de-escalation, and continuous monitoring of antimicrobial prescribing patterns [24,25]. These interventions are intended to improve the quality and safety of patient care while reducing unnecessary antimicrobial exposure and limiting the selection and transmission of multidrug-resistant microorganisms. Effective AMS programs require multidisciplinary collaboration involving physicians, pharmacists, microbiologists, infection-control specialists, nurses, policymakers, and patients [26,27]. Accordingly, AMS has become an important component of global strategies for preserving antimicrobial effectiveness and addressing the continuing AMR crisis [28,29].

The increasing availability of electronic medical records, microbiological data, laboratory results, and other clinical information has created opportunities for the integration of artificial intelligence (AI) and machine learning (ML) into AMS. AI-based approaches can analyze large and complex datasets to identify patterns associated with inappropriate antimicrobial prescribing, predict the risk of antimicrobial resistance, and support selection of empirical antimicrobial therapy [30–35,38]. By integrating patient characteristics, previous antimicrobial exposure, microbiological findings, clinical history, and other relevant parameters, ML models can provide risk estimates that may assist clinicians in making more informed prescribing decisions.

AI-assisted clinical decision-support systems may also support antimicrobial audits, surveillance, prescribing review, and AMS program activities. Such systems have the potential to identify patients who may be receiving unnecessary or inappropriate antimicrobial therapy and facilitate earlier review of treatment decisions [31,32,35]. Similarly, AI-based risk-prediction models can help identify patients at increased risk of resistant infections, allowing clinicians and AMS teams to consider microbiological testing, antimicrobial optimization, or modification of empirical treatment at an earlier stage [33,34,38]. In this context, AI can complement conventional stewardship approaches by processing information rapidly and consistently across large patient populations.

However, the clinical value of AI-based AMS depends not only on predictive performance but also on the quality, completeness, and representativeness of the underlying data. Concerns regarding data quality, algorithmic transparency, bias, external validation, ethical considerations, and integration into routine clinical workflows remain important barriers to widespread implementation [39–44]. Models developed using data from a single institution or limited patient populations may have reduced generalizability when applied to different hospitals, geographical regions, patient populations, or prescribing environments. Therefore, external and multicentre validation is essential before AI-supported recommendations are incorporated into routine antimicrobial decision-making.

AI should consequently be considered an adjunct to, rather than a replacement for, multidisciplinary AMS teams and clinical judgement [39–44]. Future implementation should emphasize robust and interpretable models, appropriate validation, ethical use of patient data, and seamless integration with existing clinical workflows. When appropriately developed and validated, AI-based approaches may support precision antimicrobial therapy, improve the efficiency of stewardship activities, and contribute to reducing unnecessary antimicrobial exposure and the development and transmission of AMR [38–44].

Future research should focus on explainable AI, integration of multi-omics and longitudinal clinical data, and development of hybrid computational approaches for antimicrobial research and decision support. Emerging technologies, including advanced computational methods and AI-assisted experimental platforms, may also contribute to reducing dependence on conventional approaches in early-stage pharmaceutical research and improving translational efficiency [17]. Sustained government support, interdisciplinary collaboration, appropriate regulatory frameworks, and investment in digital and computational infrastructure will be important for the safe and effective implementation of AI-enabled approaches within pharmaceutical and healthcare systems.

Despite the promising applications of artificial intelligence in antimicrobial resistance management, several challenges limit its widespread clinical

implementation. These include data quality and availability, algorithmic bias, limited model interpretability, inadequate external validation, data privacy concerns, and difficulties in integrating AI systems into routine clinical practice. Addressing these challenges is essential for the safe, reliable, and effective implementation of AI-driven AMR solutions.

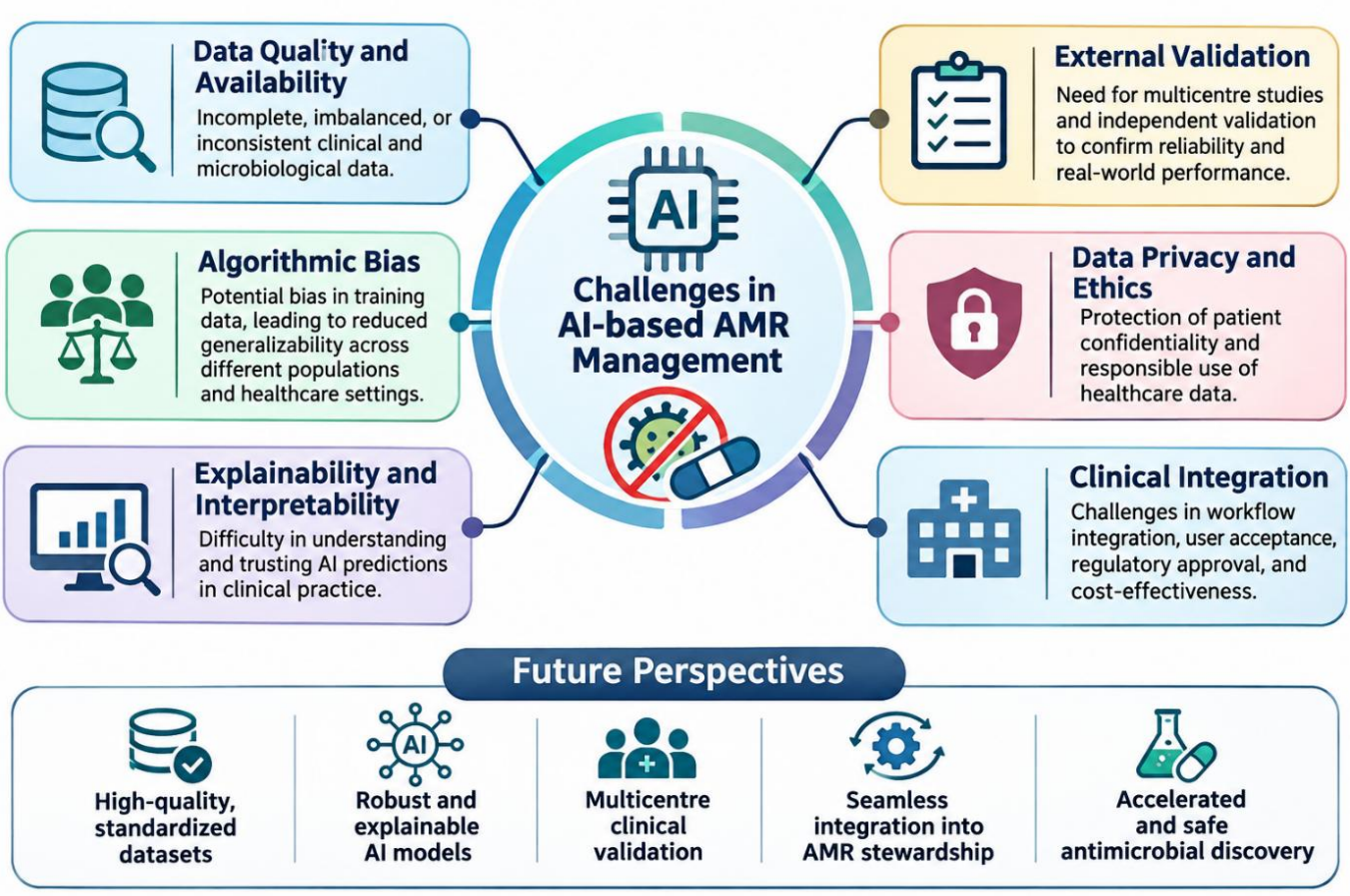


Figure 3. Challenges and future perspectives of artificial intelligence in antimicrobial resistance management. Source: Created by the author using AI-assisted tools.

7. AI in Personalized Antimicrobial Therapy

Artificial intelligence (AI) can support personalized antimicrobial therapy by integrating patient-specific clinical, laboratory, microbiological, and other health-record data to guide antimicrobial selection and dosing. Predictive machine-learning models can help identify patients at higher risk of resistant infections and support more targeted empirical therapy, while AI-based clinical decision-support systems may assist clinicians in optimizing antimicrobial choice and treatment duration [13,15,30–35]. Integration of pharmacokinetic, pharmacodynamic, and patient-specific characteristics may further facilitate individualized dosing and reduce unnecessary antimicrobial exposure. However, prospective multicentre validation is required before widespread clinical implementation because model performance may vary across patient populations and healthcare settings.

8. AI in Rapid Diagnostics and Clinical Decision Support

Traditional microbiological diagnostic procedures may be time-consuming and can postpone the start of timely appropriate antimicrobial therapy. To address this, artificial intelligence (AI) models, often utilizing deep learning algorithms, medical image processing and genomic data analysis techniques, have demonstrated the potential for speeding up the detection of pathogens and their resistance. AI models have achieved considerable success in analyzing microscopic imaging, Matrix-Assisted Laser Desorption/Ionization-Time of Flight (MALDI-TOF) mass spectrometry and whole-genome sequencing (WGS) datasets, providing for accelerated and more accurate clinical diagnostics.

AI can augment existing Clinical Decision Support Systems (CDSSs) and generate individualized treatment options considering patient's intrinsic features, prior antimicrobial treatment, microbiology results and local epidemiology of resistance.

In this context, AI can support antimicrobial stewardship by prompting more rational antibiotic prescribing and promoting more favourable clinical outcome, limiting the empirical use of unnecessary antimicrobial agents. Nevertheless, a number of barriers continue to hinder its adoption into daily clinical practice, the current literature being predominantly from retrospective single-institution studies, with a scarcity of prospective multicentre clinical studies. AI-related predictions depend on the pathogen prevalence,

protocol of the local microbiology lab and quality of the training dataset. Other limitations include transparency issues, need for clinical interpretability of results, need for full integration in clinical workflow, and regulatory approval, with specific emphasis on issues applicable in limited resource settings[18].

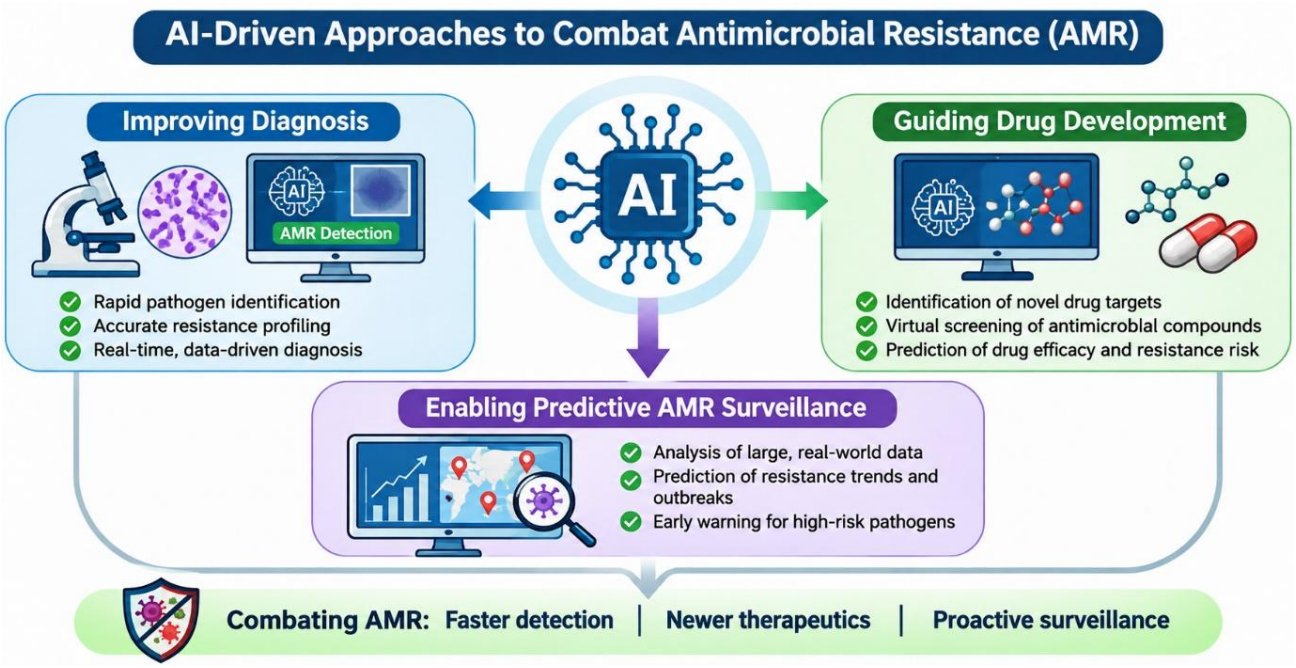


Figure 4: Application of AI

Source: AI-generated infographic created by ChatGPT (Open AI, 2026). AI, artificial intelligence; AMR, antimicrobial resistance.

9. Latest AI applications (2025–2026)

Artificial intelligence is extending beyond traditional machine learning models, such as foundation models, large language models, multimodal AI, and generative AI for anti-microbial resistance (AMR). AI models are now capable of quickly predicting AMR, discovering antimicrobial drugs with AI assistance, designing personalized antimicrobial therapies, automatically analyzing genomic and microbiologic data, and implementing antimicrobial stewardship at real-time. In addition, AI-based explainable artificial intelligence (XAI) makes AI-driven decision-making more transparent and clinically relevant, and federated learning enables secure sharing of data from multiple institutions without patients' anonymity. Taken together, these new forms of artificial intelligence will speed up the application of precision medicine and augment global AMR mitigation efforts[19].

9. Practice Points:

- AI provides efficient predictions of AMR, guiding targeted timely treatment with antibiotics. - AI-based clinical decision support programs enhance antibiotic prescribing practices and improve antibiotic stewardship.

- New AI tools such as generative AI, Foundation Models, and explainable AI are fast-tracking antibiotic drug discovery and precision medicine.

- Valid external verification, transparency of AI models, and the use of quality data are imperative for safe clinical deployment.

- Cross-specialty teamwork and effective regulations will ensure that the application of AI for AMR control is successful.

10. Conclusion

Antimicrobial resistance (AMR) has emerged as a major global public health concern, as the increasing resistance of microorganisms to antimicrobial agents reduces the effectiveness of standard treatments and contributes to the growing burden of infectious diseases worldwide[1], [4]. Conventional approaches to antimicrobial drug development and diagnostic procedures face considerable challenges in addressing the rapidly evolving nature of antimicrobial resistance[15]. Artificial intelligence (AI) offers promising opportunities to support various aspects of AMR management, including resistance prediction, antimicrobial drug discovery, personalized antimicrobial therapy, and surveillance[5]. By analysing large and complex datasets, machine learning and deep learning approaches can contribute to improved diagnostic accuracy and more informed clinical decision-making.

Furthermore, AI-driven drug discovery technologies have the potential to accelerate the identification and optimization of novel antimicrobial compounds, thereby supporting the development of more effective therapeutic strategies[11], [13]. These advancements may also contribute to precision medicine and strengthen antimicrobial stewardship practices. However, limitations related to data availability and quality, insufficient external validation, model interpretability, and clinical implementation remain significant challenges. Addressing these issues requires

interdisciplinary collaboration among clinicians, data scientists, policymakers, and microbiologists. Recent developments in generative AI and machine learning have further demonstrated the potential of AI to accelerate antimicrobial drug development and strengthen AMR monitoring[16]. Overall, AI represents a valuable complementary tool for improving AMR management and reducing the global burden of antimicrobial resistance, provided that its implementation is supported by rigorous validation, appropriate regulatory frameworks, and ethical oversight.

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Abbreviations

AMR – Antimicrobial Resistance
AI – Artificial Intelligence
ML – Machine Learning
DL – Deep Learning
WHO – World Health Organization
NLP – Natural Language Processing
AST – Antimicrobial Susceptibility Testing

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