ClinSphere Journals
International Peer-Reviewed Open Access Journal
Advancing Healthcare, Clinical Research & Innovation
DOI: 10.5281/zenodo.23792239

Review Article

AI-Driven Antimicrobial Stewardship and Prediction of Antimicrobial Resistance: Current Evidence, Clinical Applications, and Future Perspectives

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Acknowledgments: None.

ABSTRACT

Background: Antimicrobial resistance (AMR) threatens the effectiveness of antimicrobial therapy and increases the risk of treatment failure, prolonged hospitalization, and mortality. Antimicrobial stewardship programmes (ASPs) seek to optimize antimicrobial selection, dosing, route, and duration. Artificial intelligence (AI), including machine learning (ML) and natural language processing, may strengthen stewardship through resistance prediction, individualized empirical therapy, surveillance, and clinical decision support.

Objective: To review current evidence, clinical applications, limitations, and future directions for AI-driven antimicrobial stewardship and AMR prediction.

Methods: A narrative review approach was used to synthesize peer-reviewed studies, systematic reviews, clinical guidance, and authoritative surveillance resources on ML-based resistance prediction and stewardship. No formal systematic screening or quantitative synthesis was undertaken.

Results: Retrospective studies show that ML models can estimate resistance risk from clinical history, prior microbiology, antimicrobial exposure, and local epidemiology. Personalized antibiogram approaches have demonstrated potential to maintain predicted coverage while reducing broad-spectrum prescribing in retrospective datasets. However, external validation, calibration, workflow integration, and prospective evidence of patient-centred benefit remain essential.

Conclusion: AI can augment antimicrobial stewardship by providing timely, patient-specific risk estimates and helping prioritize treatment review. Predictions do not confirm susceptibility, and model performance does not by itself establish clinical benefit. Implementation should include prospective validation, multidisciplinary oversight, transparent uncertainty communication, and ongoing monitoring of clinical and microbiological outcomes.

Keywords: Artificial intelligence; antimicrobial stewardship; antimicrobial resistance; machine learning; antimicrobial susceptibility testing; clinical decision support; personalized antibiogram; precision medicine.

1. Introduction

Antimicrobial resistance (AMR) develops when microorganisms acquire or express mechanisms that reduce susceptibility to antimicrobial agents. It is associated with increased morbidity, mortality, healthcare expenditure, and pressure on health systems. In a global analysis, bacterial AMR was estimated to be directly attributable to 1.27 million deaths and associated with 4.95 million deaths in 2019.[1]

Antimicrobial stewardship programmes (ASPs) promote the appropriate selection, dose, route, and duration of antimicrobial treatment. Core interventions include prospective audit and feedback, preauthorization, guideline-directed empirical therapy, antimicrobial time-outs, dose optimization, and de-escalation when microbiological results become available.[2,3]

A persistent challenge is choosing empirical treatment before the causative organism and susceptibility profile are known. Clinicians must balance the need for prompt effective treatment against harms associated with unnecessarily broad-spectrum therapy. AI may help integrate patient-specific clinical information with microbiology and local epidemiology to estimate resistance risk and support more consistent decisions.[4–6]

This review examines the evidence and practical considerations for AI-enabled antimicrobial stewardship, with an emphasis on separating demonstrated predictive performance from evidence of improved clinical outcomes.

2. Methodology / Literature Search Strategy

This narrative review synthesizes literature on machine learning-based AMR prediction, personalized antibiograms, clinical decision support, antimicrobial susceptibility testing, stewardship implementation, and AMR surveillance. Relevant publications were identified from biomedical literature resources, including PubMed/MEDLINE, and authoritative sources from the World Health Organization (WHO), the US Centers for Disease Control and Prevention (CDC), and the US Food and Drug Administration (FDA).

The review prioritized peer-reviewed original studies, systematic reviews, professional guidance, and authoritative surveillance resources. Concepts included artificial intelligence, machine learning, antimicrobial resistance prediction, antimicrobial stewardship, electronic health records, personalized antibiograms, antimicrobial susceptibility testing, and clinical decision support. Studies were considered qualitatively for clinical relevance, population, data source, validation strategy, and applicability. This is not a systematic review. A complete reproducible database search, formal screening log, risk-of-bias assessment, and quantitative synthesis were not performed. Accordingly, no exhaustive study count or PRISMA flow diagram is claimed.

3. Background

3.1 Antimicrobial resistance and precision prescribing

Resistance mechanisms include enzymatic drug inactivation, target modification, reduced permeability, active efflux, and acquisition of resistance determinants. Clinical impact depends on the pathogen, resistance mechanism, infection site, drug exposure, source control, and patient characteristics. WHO identifies AMR as a major global health threat and supports standardized surveillance through the Global Antimicrobial Resistance and Use Surveillance System (GLASS).[7,8]

Phenotypic antimicrobial susceptibility testing (AST) remains central to definitive therapy, but results may not be available when empirical treatment is initiated. Molecular tests can detect selected organisms or resistance determinants rapidly, although gene detection does not always establish the complete phenotypic susceptibility profile. Predictive models may help estimate risk before definitive results, but their outputs remain probabilities rather than microbiological confirmation.

3.2 AI and machine learning

AI describes computational methods used for tasks such as pattern recognition and decision support. ML models learn relationships from data and may be used for classification, risk estimation, forecasting, or prioritization. Common approaches include logistic regression, decision trees, random forests, gradient boosting, neural networks, natural language processing, and time-series methods. Algorithm selection should reflect the clinical question, data quality, interpretability needs, and consequences of error.[5,6]

3.3 Data sources

Potential inputs include patient demographics and comorbidities; infection source and severity; previous culture and AST results; recent antimicrobial exposure; healthcare contact and invasive devices; current laboratory results; local antibiograms; and genomic information where available. Variables must be available at the intended decision point. Data leakage, in which information generated after the clinical decision is included during model development, can produce unrealistically high performance.

4. Current Evidence

4.1 Machine learning for AMR prediction

A systematic review and meta-analysis of ML for AMR prediction reported pooled discrimination in the moderate-to-good range, but also highlighted retrospective model development, non-standardized data processing, and limited validation in randomized or real-world settings.[5] These limitations mean that performance estimates should not be interpreted as proof of clinical effectiveness.

Yelin and colleagues demonstrated that ML models using electronic medical record data could predict antibiotic resistance in urinary tract infections caused by organisms including Escherichia coli and Klebsiella pneumoniae.[4] The study supports the feasibility of using prior clinical history and prescribing data to inform empirical treatment, while underscoring the importance of local validation.

4.2 Personalized antibiograms and empirical selection

Personalized antibiograms extend traditional population-level antibiograms by estimating susceptibility for an individual patient using clinical history and other available data. In a retrospective multicentre study, Corbin and colleagues developed ML-based personalized antibiograms using 8,342 infections from Stanford emergency departments and 15,806 uncomplicated urinary tract infections from two Boston hospitals. Model-based selection achieved coverage comparable to clinician selection in the Stanford dataset and higher coverage in the Boston dataset, while suggesting opportunities to narrow some broad-spectrum regimens.[9] These findings are promising but are not equivalent to evidence from a prospective trial demonstrating improved patient outcomes.

4.3 AST and genomic prediction

ML may support AST through automated interpretation of growth patterns, laboratory images, phenotypic data, and microbial genomic features. Genomic models may identify associations between genes or mutations and susceptibility phenotypes, but genotype-to-phenotype prediction can be complicated by novel resistance mechanisms, incomplete databases, gene expression, and interactions between determinants. Reviews of ML in clinical microbiology and AMR emphasize the need for validated methods and careful interpretation before routine clinical deployment.[6,10]

4.4 Stewardship workflow support

AI-enabled systems may flag broad-spectrum prescriptions for review, identify possible de-escalation opportunities after AST, highlight renal-dose concerns, detect prolonged treatment, and prioritize cases for prospective audit and feedback. These functions should be treated as decision-support mechanisms. The clinical benefit depends on timing, recommendation quality, clinician response, and integration into existing workflows. Established stewardship guidance supports structured interventions, but the effectiveness of a specific AI intervention must be evaluated directly.[2,3]

4.5 Evidence interpretation

Evidence should be considered across distinct stages: retrospective model development, internal validation, external validation, prospective implementation, and comparative

evaluation of patient outcomes. A model may discriminate between higher- and lower-risk patients yet remain poorly calibrated, generate excessive alerts, or fail to improve treatment decisions. Meaningful outcomes include time to effective therapy, broad-spectrum exposure, de-escalation, adverse drug events, treatment failure, length of stay, mortality, and antimicrobial consumption.

Table 1. Major AI applications in antimicrobial stewardship

Application	Potential inputs	Potential value	Key limitation
AMR risk prediction	Prior cultures, medication history, patient factors, local epidemiology	Patient-specific resistance probability	Prediction is not confirmation of susceptibility
Empirical therapy support	Infection source, severity, prior resistance, guidelines	Supports choice of initial regimen	Must not replace clinical assessment
De-escalation support	AST, culture results, clinical response, treatment duration	Identifies review opportunities	Culture results require clinical context
Dose optimization	Renal function, weight, drug levels, pharmacokinetic variables	Supports individualized dosing	Requires validated dosing methods and monitoring
Treatment-failure alerts	Clinical trajectory, laboratory trends, microbiology	Prompts earlier reassessment	Deterioration is not specific to AMR
Surveillance dashboards	Laboratory data, prescribing, ward-level trends	Supports trend monitoring and resource allocation	Data delay and sampling bias may mislead

Abbreviations: AI, artificial intelligence; AMR, antimicrobial resistance; AST, antimicrobial susceptibility testing.

5. Clinical Applications

5.1 Individualized empirical therapy

A validated model may estimate resistance probability for relevant agents by combining infection source, severity, previous culture results, antimicrobial exposure, and local epidemiology. Clinicians can consider these estimates alongside allergies, organ function, source control, pharmacokinetics/pharmacodynamics, and treatment guidelines. A low predicted resistance probability does not prove susceptibility; a high probability does not confirm resistance.

5.2 Early recognition of possible treatment failure

Models may flag patients at risk of deterioration using physiological observations, laboratory trends, microbiology, and medication records. Alerts should prompt reassessment of diagnosis, source control, antimicrobial exposure, and resistance results rather than automatic escalation. Deterioration may have causes unrelated to AMR.

5.3 De-escalation and duration review

After microbiology results become available, AI may identify patients whose treatment could be narrowed, discontinued, converted to an appropriate oral regimen, or reviewed for duration. Decisions must consider specimen quality, infection site, polymicrobial disease, clinical stability, and guideline recommendations.

5.4 Hospital stewardship dashboards

Dashboards may consolidate antimicrobial consumption, guideline adherence, susceptibility trends, treatment duration, and intervention outcomes. Metrics should be interpreted in light of case mix, occupancy, infection burden, and prescribing indications to avoid misleading comparisons.

5.5 Proposed clinical workflow

- Clinical assessment and appropriate specimen collection.
- Integration of relevant clinical history, medication exposure, microbiology, and local resistance data.
- Generation of a validated, patient-specific resistance-risk estimate with uncertainty displayed.
- Review of options by the treating clinician and antimicrobial stewardship team.
- Empirical treatment based on the full clinical context.
- Reassessment when culture and AST results become available.
- De-escalation, dose optimization, or treatment modification where indicated.
- Monitoring of prescribing decisions, clinical outcomes, safety, and model performance.

6. Safety & Limitations

6.1 Data quality, leakage, and generalizability

Clinical datasets may contain missing medication histories, inconsistent coding, delayed results, and variable documentation. A model trained in one institution may perform poorly elsewhere because of differences in resistance prevalence, patient mix, prescribing practice, and laboratory methods. External validation and local recalibration may be necessary. Information unavailable at the intended decision point must not be used to estimate prospective performance.

6.2 Bias, interpretability, and automation bias

Unrepresentative datasets can produce uneven performance across patient groups or healthcare settings. Clinicians should be able to understand the basis and limitations of recommendations, and systems should communicate uncertainty. Automation bias may lead users to over-trust an algorithm or disregard contradictory clinical evidence.

6.3 False predictions and clinical consequences

False-negative predictions may contribute to ineffective initial therapy; false-positive predictions may promote unnecessary broad-spectrum treatment and avoidable toxicity. Model thresholds should be selected in relation to the clinical setting and the consequences of error. Performance evaluation should include calibration, sensitivity, specificity, predictive values,

discrimination, and decision-analytic utility rather than accuracy alone.

6.4 Privacy, governance, and regulation

Clinical and genomic data require appropriate access controls, secure handling, audit trails, and compliance with applicable privacy rules. Governance should define responsibility for model approval, maintenance, incident review, and updates. Regulatory obligations depend on intended use and jurisdiction. The FDA issued updated Clinical Decision Support Software guidance in January 2026; developers and institutions should consult the current official guidance when determining applicable requirements.[11]

6.5 Workflow and resource considerations

Poorly integrated tools can increase alert fatigue, documentation burden, or delays. Implementation requires staff training, interoperable systems, maintenance, and evaluation of costs and benefits. Resource-constrained settings may need simpler approaches based on reliable clinical history and local surveillance rather than data-intensive models.

7. Emerging Advances

7.1 Genomic and multimodal prediction

Integration of genomic data with clinical history, laboratory findings, and antimicrobial exposure may improve resistance prediction in selected settings. Its value should be assessed against conventional AST and rapid diagnostics, accounting for incomplete genomic databases and complex genotype-phenotype relationships.[6,10]

7.2 Federated learning

Federated learning may allow institutions to collaboratively develop models without centralizing all patient-level records. It does not automatically remove privacy risks or bias, and differences in coding, laboratory methods, and patient populations still require careful harmonization.

7.3 Explainable and uncertainty-aware systems

Explainable models may identify variables contributing to a prediction, while uncertainty-aware systems may flag cases outside the model's validated range. In some cases, the safest recommendation may be additional testing or specialist review rather than a treatment directive.

7.4 Generative AI and documentation

Generative AI may help summarize microbiology reports, extract relevant information from clinical notes, and draft stewardship documentation. These outputs can omit important details or generate unsupported statements and must be verified against the clinical record. Generative AI should not serve as an independent source of susceptibility results.

7.5 Real-time surveillance

Combining laboratory surveillance, antimicrobial consumption, and epidemiological information may help identify changing resistance patterns. Such systems require timely data, defined alert thresholds, and prospective evaluation before being described as real-time outbreak detection.

8. Pharmacist's Role

Clinical pharmacists are essential to translating AI predictions into safe and appropriate antimicrobial use. Their role includes interpreting resistance estimates in the context of previous cultures and local epidemiology; assessing agent, dose, route, duration, allergy, interaction, and organ-function considerations; and participating in de-escalation and prospective audit and feedback.

Pharmacists can also review therapeutic drug monitoring, validate dose recommendations, evaluate toxicity alerts, educate prescribers about model uncertainty, and monitor whether AI recommendations improve stewardship outcomes. Multidisciplinary governance should include pharmacy, infectious diseases, microbiology, clinical teams, epidemiology, and information technology.

Table 2. Pharmacist-led checks when using AI-supported AMR prediction

Check	Practical question	Action if concern identified
Clinical fit	Does the prediction match infection source, severity, and likely pathogens?	Reassess diagnosis and seek clinical review
Microbiology	Are prior culture results relevant and are current specimens adequate?	Confirm result context and obtain appropriate testing
Patient safety	Are allergy, renal function, interactions, and dosing addressed?	Adjust or clarify regimen using validated guidance
Stewardship	Is broad-spectrum treatment still necessary after new results?	Review de-escalation, discontinuation, or duration
Model reliability	Is the tool validated locally and is uncertainty visible?	Avoid unsupported reliance and escalate uncertain cases
Outcome monitoring	Did the recommendation change care and was it appropriate?	Document outcome and report errors or drift

9. Research Gaps

- Prospective validation: Many models remain retrospectively evaluated; prospective implementation studies are needed.
- Patient-centred outcomes: Predictive accuracy alone does not establish reductions in mortality, treatment failure, toxicity, or length of stay.
- External validation: Multicentre studies should test transportability across regions, hospitals, and resistance prevalence levels.

- Equity and resource constraints: Research should include settings with incomplete electronic records and limited microbiology capacity.
- Standardized reporting: Studies should clearly report intended use, prediction time point, data sources, missing-data handling, calibration, and external validation.
- Cost-effectiveness: Implementation costs should be compared with measurable clinical and stewardship benefits.
- Human factors: Research should assess alert burden, clinician trust, recommendation acceptance, and unintended effects.
- Long-term AMR impact: Longitudinal studies should determine whether AI-supported prescribing changes sustained resistance trends.

10. Future Perspectives

Future systems should be developed for clearly defined clinical decisions and validated in the populations in which they will be used. Local epidemiology should be updated appropriately, and recommendations should be delivered at the point where they can influence prescribing without creating excessive alerts.

Evaluation should move beyond retrospective accuracy to prospective, controlled assessment of time to effective therapy, broad-spectrum exposure, de-escalation, adverse events, treatment failure, length of stay, mortality, antimicrobial consumption, and equity. Multidisciplinary governance and practical implementation research will be essential.

AI should be treated as one component of a broader AMR strategy that includes infection prevention, vaccination, diagnostic stewardship, microbiological surveillance, and equitable access to effective treatment. The most valuable systems will be those that provide reliable, actionable information and demonstrate measurable clinical benefit.

11. Conclusion

AI offers promising methods to strengthen antimicrobial stewardship by integrating clinical, microbiological, medication, and epidemiological data to estimate resistance risk and identify opportunities for treatment review. Personalized antibiogram research illustrates the potential to support narrower empirical treatment while maintaining predicted coverage, but current evidence does not justify assuming that all AI interventions improve patient outcomes. Robust external validation, prospective evaluation, clear communication of uncertainty, data governance, and ongoing monitoring are essential. Pharmacists and multidisciplinary stewardship teams remain central to interpreting predictions and ensuring that treatment decisions reflect the patient's complete clinical context. AI should augment, not replace, clinical judgment.

12. Declarations

Funding: No specific external funding was declared for preparation of this manuscript; authors should confirm before submission.

Conflicts of interest: The authors should disclose all relevant financial and non-financial conflicts. If none exist, state: "The authors declare no conflicts of interest."

Ethics approval: Not applicable to this narrative review; no new participant recruitment or identifiable patient data collection was undertaken.

Informed consent: Not applicable.

Data availability: No original dataset was generated or analysed for this review.

Author contributions: To be completed according to the actual contributions of each author.

Acknowledgements: To be completed if applicable.

Use of artificial intelligence: Disclose AI-assisted writing or editing in accordance with the target journal's policy and the authors' actual use.

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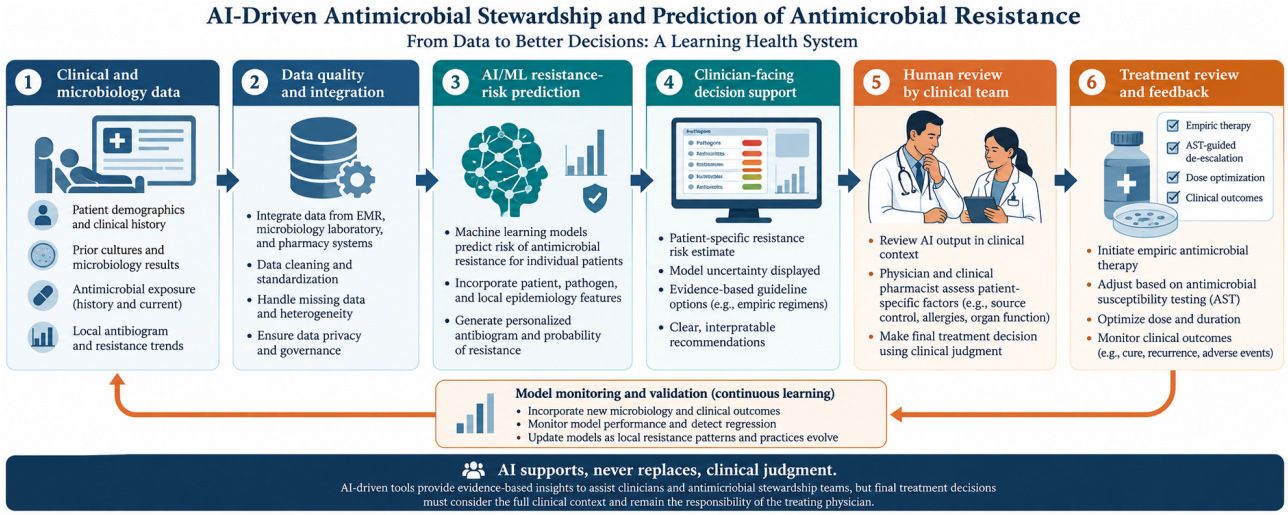
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14. Figures

Figure 1. Conceptual workflow for AI-driven antimicrobial stewardship and resistance prediction.



Note: The figure is a proposed conceptual workflow, not a validated clinical algorithm. AI outputs should support, not replace, clinician judgment.