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Prescribing Intelligence: How Machine Learning Can Help Combat Antimicrobial Resistance

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ABSTRACT

While Clinical Decision Support Systems (CDSS) are widely used in clinics and medical settings, machine learning (ML) based systems are only recently being explored, especially in the context of recommending treatments based on previous data. This literature review addresses this gap by comparing the impact of ML-based CDSS to clinician performance in antibiotic treatment in hopes of improving diagnostic accuracy and decreasing chances of antimicrobial resistance (AMR) development. PubMed and Google Scholar were used to identify 11 studies that were categorized based on their diagnostic accuracy, type of ML model used, and the difference in outcomes from physicians. The evidence shows that ML-based CDSS had an average of 16% increased accuracy compared to clinicians. Even though the studies used a variety of models and training sets, the findings indicate that ML can help clinicians in their treatment selection. However, due to the diversity in data sources, model design, and evaluation methods, generalizing these results is difficult. Overall, ML-based CDSS seems like a promising way to reduce overprescription of unnecessary antibiotics and improve diagnostic accuracy.

Keywords: Clinical Decision Support System; Machine Learning; Antibiotic Prescription; Antimicrobial Resistance

INTRODUCTION

Antimicrobial Resistance is a major global health crisis that involves bacteria becoming resistant to antibiotics. The World Health Organization (WHO) recognizes antimicrobial resistance (AMR) as one of the top ten global public health threats, stating that AMR could cause 10 million deaths per year by 2030 (1). This problem affects patients and healthcare systems worldwide. It has become vital to come up with solutions to combat AMR, especially in how antibiotics are prescribed.

One of the main causes of AMR is the overprescription of antibiotics. An increased amount of antibiotics in your body can greatly increase the likelihood of a mutation occurring in bacteria. Each time an antibiotic is used, bacteria have another chance to adapt and mutate their DNA to develop antibiotic resistant genes (ARGs). A prime example of these ARGs are the genes that code for antibiotic efflux pumps, which degrade and remove the antibiotics from the bacterial cells (2).

These ARGs are then transferred to other bacteria through horizontal gene transfer (HGT), a process where bacteria transfer genes directly to another bacterium,

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allowing them to become antibiotic-resistant (3). This process occurs in three different ways: 1) conjugation, where DNA is transferred from one bacterium to another through a pilus (hair-like structures on the exterior of cell membranes); 2) transformation, where a bacterium picks up pieces of DNA from a dead bacteria and incorporates them into its own DNA; and 3) transduction, where DNA is transferred through a virus (bacteriophage) between two bacteria (3).

HGT is a vital process because bacteria function in large groups and communities, so when different bacteria in the same group carry the same antibiotic resistance genes, they can work together to make the antibiotic less effective. By sharing the resistance, they decrease the danger of the antibiotic in the environment to a level that is too weak to kill them in a process called collective resistance (2). As a result, the spread of ARGs through HGT and collective resistance significantly accelerates the rate at which antibiotics lose their effectiveness. Thus, overprescription of antibiotics creates more opportunities for HGT, leading to these drugs becoming less effective for millions of infections worldwide.

Deaths from antimicrobial resistance have been increasing since the last decade, and are currently projected to double by 2050, reaching about 1.9 million per year (4). On the other hand, Figure 1 shows the prevalence of antibiotic use worldwide by year. We can see there is a clear correlation between the two.

Machine Learning is a type of artificial intelligence that adapts to a situation while making a decision. ML systems use massive volumes of data to understand the basic rules used by others in similar situations and then apply those rules to unknown situations without needing additional information. They are able to predict outcomes in unfamiliar problems based on previous learned data (6). Sometimes, ML systems are referred to as data-intensive systems, because the performance and ability of the algorithms to learn is driven by the volume and quality of data provided (7).

Machine Learning is being used to combat the AMR problem in a variety of ways including Clinical-Decision Support Systems. Clinical Decision Support Systems (CDSS) are computer-based tools that help

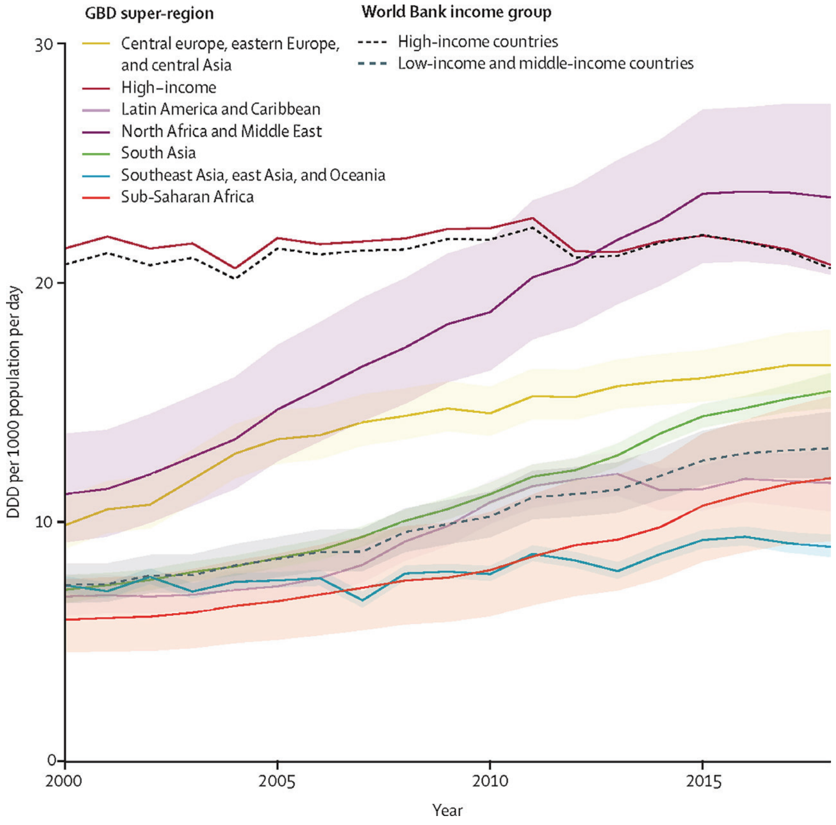

Figure 1. Temporal trends in the total antibiotic consumption rates for Global Burden of Disease super-regions and World Bank income groups (5).

doctors and clinicians make better medical decisions by giving them helpful information like reminders or recommendations based on patient data. Initially, they were used for information management, but they have evolved to provide patient-specific recommendations (7). More recently, CDSS use AI, ML, or statistical pattern recognition to provide its recommendation, rather than being programmed to follow expert medical knowledge (7).

These systems help physicians select appropriate antimicrobial prescriptions by evaluating patient data, past resistance patterns, and real-time diagnostic results. For example, studies by Liang *et al.* (2022) have shown that ML models can predict carbapenem-resistant bacterial infections in ICU patients, enabling faster isolation and treatment decisions (8). This research analyzes how the overprescription and overuse of antibiotics in humans contributes to antimicrobial resistance, and what role machine-learning algorithms can play in slowing down its rise. It specifically examines the integration of machine-learning algorithms into Clinical Decision Support Systems, and reviews the overall benefits and drawbacks.

METHODS AND MATERIALS

The methodology used was a search of peer-reviewed academic journals through PubMed and Google Scholar for articles published between 2010 and 2025. PubMed and Google Scholar were used because they are comprehensive databases that provide wide access to high-quality, peer-reviewed research essential for evaluating ML-CDSS effectiveness.

Search Strategy

The key words “clinical decision support system AND machine learning AND antibiotic prescription” were used to find articles relevant to the purpose of this antimicrobial resistance research paper. “English” and “Humans” filters were applied to limit the results to English-language articles and human clinical studies when applicable.

Inclusion and Exclusion Criteria

Articles were included if they discussed how machine learning was applied to antibiotic prescription practices, focused on clinical tools like CDSS and EHR integration, or provided original data of current applications of ML. Articles were excluded if they did not talk about machine learning, used ML for a different context, or were opinion pieces or literature reviews that conducted no original research.

Data Extraction and Synthesis

Each study was reviewed for its objectives, ML techniques used, healthcare setting, outcome measures, and limitations. A semi-quantitative analysis was used to identify similar themes across studies, such as the use of ML in decision-making, customizing prescriptions, or improving accuracy. The themes were then contrasted to show how different ML models compare to clinician performance in antibiotic prescription.

RESULTS

Initially, 41 articles were found through PubMed, but 36 were excluded for irrelevant studies (n=20) and irrelevant outcomes (n=16), leaving only 4 studies to be included. A total of 1,220 articles came up through Google Scholar, but 1,180 were excluded without screening due to time constraints. The remaining top 40 results were full text screened, and only 7 studies were found that were included. This meant that 33 records were excluded because of irrelevant studies (n=17), irrelevant outcomes (n=10), duplicates (n=4), and lack of access (n=2). Across the two academic journals, 81 studies were screened in total, and finally 11 studies were used for assessment (Figure 2).

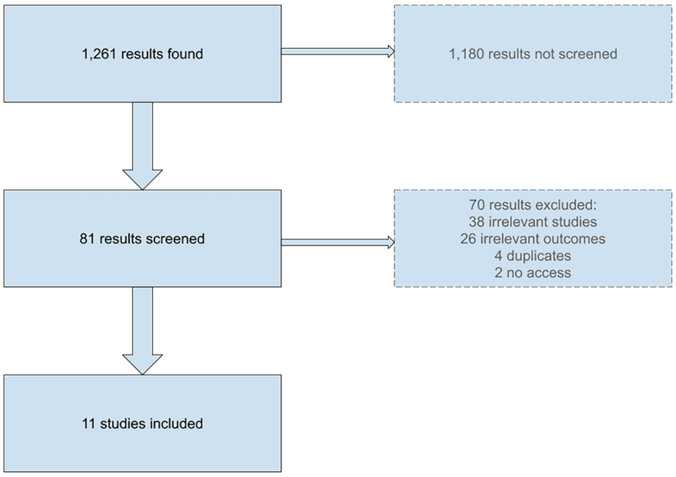

Figure 2. Screening Process of articles. A total of 1,261 records were identified (41 from PubMed and 1,220 from Google Scholar). After removing duplicates and excluding irrelevant or ineligible studies, 11 articles met the inclusion criteria and were analyzed following a PRISMA-style screening process.

Across both search engines, 11 studies were used for the final analysis. These studies applied various machine learning (ML) models to diagnose infectious diseases, mostly focusing on urinary tract infections (UTIs) and bloodstream infections (Table 1 and Table 2).

ML algorithms employed across the reviewed studies ranged from traditional classifiers, such as Lasso (9), Ridge (9), Random Forests (10), Gradient-Boosted Trees (9), Decision Trees (11), Logistic Regression (11), and Case-Based Reasoning (12), to more advanced approaches including WEKA (13), XGBoost (14), and large language models (15).

Similarly, the datasets used across the reviewed studies were highly diverse, encompassing electronic health records from multiple institutions (such as Stanford University and Massachusetts General Hospital), hospital laboratory data, and emergency department blood culture orders, among others.

Table 1. ML Model Performance vs Clinician Performance

Author (Year) - (Reference #)	Type of ML Used	Dataset Used	Infection Site	% of outcomes improved	Limitations
Corbin (2022) - (9)	Lasso, Ridge, Random forests, Gradient-boosted trees	Massachusetts General Hospital	UTIs	Yes by 2.3%	Study does not provide any downsides
Kanjilal *et al*. (2020) - (11)	Decision tree, Logistic regression, and Random forest	EHR data	UTIs	Yes, by 18%	25% of decisions were contraindications
Rawson (2020) - (12)	Case-based reasoning (CBR) algorithm	Details not provided	Blood stream infections	Yes by 7%, but not statistically significant	Observational study
Amrollahi (2025) - (15)	LLM models in EHR	Stanford Medicine Research Data Repository	Blood cultures	Yes by 10%	Low specificity
Boominathan (2020) - (17)	2 indirect and 1 direct Predictive Algorithms	Massachusetts General Hospital	Urinary tracts	Yes by 25%	Old dataset (from 2020)
Ari Frenkel *et al*., (2025) - (16)	K-fold, Subsampling, Holdout validation, and HITL	Lab-based infectious disease data	Not mentioned	Same as clinicians; 0%	Single-day data sample
Sergounioti (2025) - (10)	Random Forest, XGBoost, Extra Trees, Voting Classifier, and Stacking Classifier	Laboratory Medicine Department of the General Hospital	UTIs	Yes by 56%	Retrospective and limited data
Herter (2022) - (19)	Decision tree classifiers	Nivel Primary Care Database	UTIs	Yes by 8%	Laboratory Data not used

Table 2. ML Model Accuracy without comparison to Clinician Performance

Author (Year)	Type of ML Used	Dataset Used	Infection Site	Accuracy	Limitations
Dai *et al*. (2025) - (14)	XGBoost model	EHR dataset from UK	Urinary tract infections	High	% value not determined by ML model
Feretzakis (2020) - (13)	WEKA—Data Mining Software in Java Workbench	Microbiology Laboratory dataset in Greece	Blood + Urine + tissue	76% accurate	Old dataset (from 2020) + clinical stats not used
Shen (2018) - (21)	Infectious Disease Diagnosis and Antibiotic Prescription (IDDAP)	Details not provided	332 infection sites	89.91% accurate	No comparison against traditional clinician decision-making

Studies that compared ML performance with that of clinicians reported outcome improvements ranging from 2.3% to 56% (9, 10). For instance, Sergounioti *et al*. (2025) observed a 56% reduction in overtreatment of UTIs, whereas Ari Frenkel *et al*. (2025) found that ML achieved accuracy comparable to clinicians in diagnosing UTIs (10, 16) (Figure 3).

DISCUSSION

This review shows evidence that machine learning (ML) based clinical decision support systems (CDSS) can perform better than clinicians in selecting the correct antibiotic prescriptions. When machine learning model performance was compared with clinician performance, every study except one had higher accuracy than clinicians (16). This means that 86% of the studies favored the ML model, and the average improvement performance across the studies was ~16%.

Across the reviewed studies, no single machine learning model consistently outperformed clinicians in all infection sites that were included (UTIs and blood cultures), but some patterns can still be seen. Logistic regression and decision tree-based models (including random forests and gradient-boosted trees) were the most used models, and several studies reported that these models improved outcomes compared to clinicians (10, 11). Similarly, XGBoost was used in both Dai *et al*. (2025) and Sergounioti (2025), and it demonstrated positive results in both studies, although its effectiveness depended heavily on the dataset quality. Simpler case-based reasoning and predictive algorithms showed slight improvements, although Rawson (2020)'s results were not statistically significant (12, 17).

Interestingly, more traditional regression models showed mixed outcomes. Some performed well with some datasets but not others, suggesting that accuracy strongly relies on the datasets used. These results indicate that ensemble tree-based methods (random forest, XGBoost, gradient boosting) and logistic regression appear to show the most improvements compared to clinicians, while simpler algorithms/models (Lasso and Ridge) show less improvement. The diversity of the ML models used allows flexibility, and different ML techniques can be implemented for every unique environment. This also implies that certain ML models can be substituted for one another, like a logistic regression model being used in place of a random forest model, without degrading the output. This allows clinicians to test which ML model works best for their environment and purposes, showcasing how versatile and adaptable ML-based CDSS can be. Ari Frenkel *et al*. (2025) yielded unexpected results with its model having 0% improvement. This suggests that not all ML

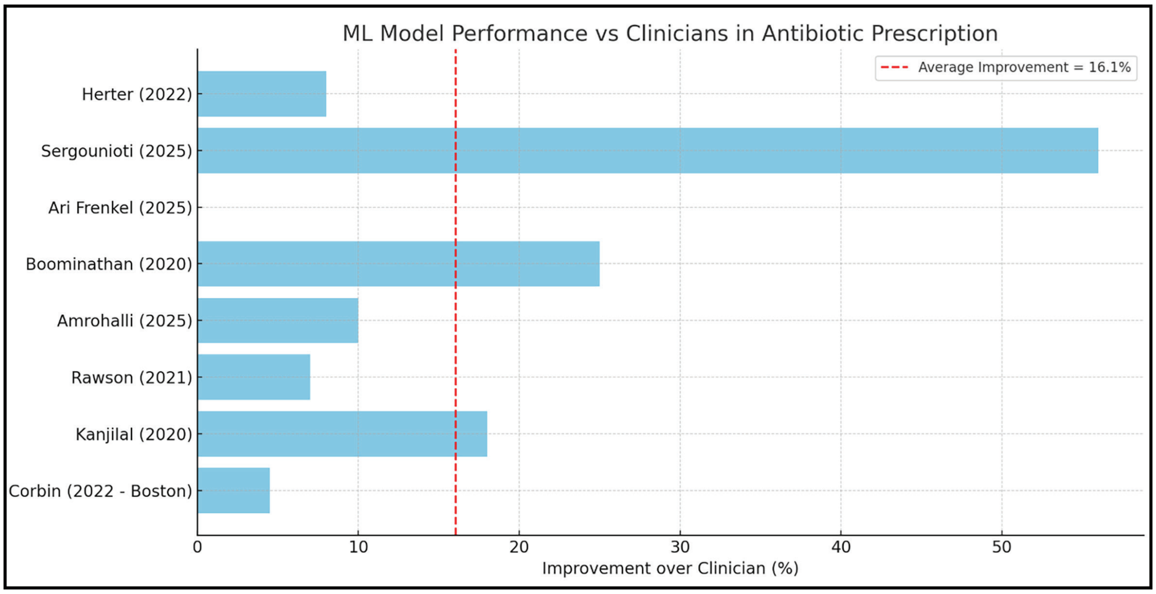

Figure 3. **Comparison of machine learning model performance and clinician accuracy in antibiotic prescribing.** The bar graph illustrates the relative performance of various ML models compared with clinicians in antibiotic prescription tasks.

systems perform better than humans, and this may be due to dataset limitations, model overfitting, or the complexity of the clinical cases that were included in this study. This also indicates that ML models are not guaranteed to perform better, and further testing is needed.

Limitations

Most studies used retrospective or observational datasets, which aren't the same as making decisions in real-time. Many models were also trained on outdated or narrow datasets, signifying that the results are very specific to one environment, and cannot be generalized to broader populations. Additionally, all the studies focused on urinary tract infections (UTIs) or bloodstream infections. While antibiotics are commonly prescribed to address these infections, the results from these studies cannot be generalized to other types of infections.

No studies looked at the impact of ML-CDSS when actually used by clinicians during live clinical workflows. Hence, future investigations should look at usability, workflow integration, and clinician & patient trust in ML outputs. Such studies will be important for studying how clinicians adapt to these new scenarios. Only a limited number of studies (40 out of 1,220 identified through the Google Scholar search) were reviewed due to time constraints. This restriction reduced the breadth of the dataset and limited the strength of the conclusions drawn. Inclusion of additional studies may have revealed clearer patterns or even challenged some of the findings presented in this review.

In the reviewed studies, ML models almost always outperformed clinicians in prescribing the correct antibiotic treatment, being up to 56% better when compared head-to-head. Even in studies that did not compare models to clinicians, the ML models still had impressive accuracy. This evidence suggests that integrating ML into CDSS could improve antibiotic prescriptions and reduce overprescription. This is vital because antimicrobial resistance stems from over prescription, so this technology could help address the development of AMR by eliminating it early on.

CONCLUSION

This literature review looked at the effectiveness of integrating machine learning in clinical decision support systems to limit overprescription of antibiotics. As seen in the studies with different models, ML models were almost always more accurate than clinicians and had accuracy levels that averaged 16% better (range 0-56%). This shows machine learning can play a potential role in improving treatment selection.

However, it is important to note that this study is a secondary analysis of existing literature, and not a direct experimental investigation. It was a simple scoping review and excluded many articles simply due to time constraints. Additionally, factors such as data quality, infection-specific variability, and clinical adaptation challenges must be addressed before implementing ML-CDSS in real-world settings. While current evidence is encouraging, future research should examine clinician responses to ML-CDSS integration, workflow compatibility, and trust in algorithmic recommendations.

CONFLICT OF INTERESTS

The author declares that there are no conflicts of interest related to this work.

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