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Journal Of Biological Research and Biotechnology

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REVIEW ARTICLE



Applications of Artificial Intelligence (AI) in Enhancing Laboratory Procedures and Antimicrobial Resistance Detection

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ARTICLE INFO

Received: 25th May 2026Revised: 16th August 2026Accepted: 28th August 2026Published online: 31st August 2026DOI: <https://dx.doi.org/10.4314/br.v24i2.21>

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e-ISSN: 2705-3822

print-ISSN: 1596-7409

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Biological Sciences
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ABSTRACT

The role of artificial intelligence (AI) in providing global solutions and public awareness in regards to antimicrobial resistance can never be overemphasized. This review aims at explaining key roles AI has demonstrated in creating global solutions and awareness of antibiotic resistance through media orientation, data integration, use of highly sophisticated Chabot and AI methods which can potentially augment the detection of antibiotic resistance genes and enhance the discovery of novel drugs by predicting the efficacy of new compounds and potential antimicrobial agents and modifying existing ones. It further explains how to employ AI technology against the rational use of antibiotics and its combinations, more so, commonly used AI algorithms for antibiotic resistance such as eXtreme Gradient Boosting (XGBoost), Random forest (RF), Decision tree (DT), Support vector machine (SVM), Naive Bayes (NB), Artificial neural network (ANN) Logistic Regression (LR) and more were discussed. It is therefore evident that AI renders a powerful toolkit for addressing global health challenges, particularly antimicrobial resistance by improving diagnostic capabilities, surveillance and public education. However, a holistic interdisciplinary approach to incorporate AI with technologies like synthetic biology and nano-medicine is recommended for promoting effective management and control of antimicrobial resistance and ensuring sustainability of antimicrobials for future generations.

Keywords: Microorganisms; Artificial Intelligence; Antibiotic resistance; Laboratory protocols; Public health awareness.

Cite this article: Shitu, T., Tomilayo, R.B., Lawal, A.N., Sa'ad, B.A., Ahmed, M.M. Bamidele, K.F., Abubakar, M.S., & Ahmad, N.D. (2026). Applications of Artificial Intelligence (AI) in enhancing laboratory procedures and antimicrobial resistance detection. *Journal of Biological Research and Biotechnology*, 24(2), 673-681

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DOI: <https://dx.doi.org/10.4314/br.v24i2.21>

1.0 INTRODUCTION

The emergence of antibiotic resistance all over the world have indicated the desperate need for remedies to rapidly arrest its widespread in other to safeguard global health and this would require a multifaceted approach that includes both clinical intervention and general public enlightenment, one of which is Artificial intelligence. Artificial intelligence is a rapid growing technology that scrutinize and build machines which learns and predicts outcomes given sets of human-defined objectives through understanding intelligent act (Rabaan et al., 2022). It is a transformative pedal to global health solutions as it is very auspicious and serves as a novel model to confront antibiotic resistance. Over the years, the menace antibiotic resistance poses to public health have tremendously reduced therapeutic efficacy, result to long hospital stays and have escalated persistent infections (Ezeanya-Bakpa & Martins, 2024). The vast interactions between microorganisms and their genetics alongside other external factors such as overuse and abuse of drugs tends to accelerate this threat of antibiotic resistance. Antibiotic resistance is a phenomenon where bacteria develop the ability to survive or grow despite being exposed to antibiotics that would normally kill them or inhibit their growth (Shitu, 2024). Antibiotics are medications used to treat infections caused by bacteria. They either kill the

bacteria (bactericidal antibiotics) or inhibit their growth and reproduction (bacteriostatic antibiotics). Murray et al. (2022) reported that globally, 1.27 million annual deaths results from antibiotic resistance and the cost of management are foreseen to exceed \$100 billion by 2050. Antibiotic resistant infections are most times difficult to treat resulting to increased healthcare cost and increased death rate. According to the Centers for Disease Control and Prevention (CDC) over 2 million people annually are diagnosed with antibiotic resistant infections accounting for 23,000 annual deaths globally. The use of AI in form of machine learning (ML) offers chances to accurately forecast and determine antibiotic resistance in microorganisms. AI enhances analysis of different variety of data, such as genomic sequences, images and spectra. The application of ML to these data sets enhances the identification of several features of microbes. Without AI, analyzing quality data would be cumbersome, requiring substantial expert and time-exhausting. More so, the merger of laboratory analysis and machine learning algorithms holds great influence to promote the identification of new antibiotics (Melo et al., 2021) thereby creating innovative solutions to combat antibiotic resistance and decreasing antibiotic misuse through accurate prescription practices. Recently, AI has proven to be an upcoming and reliable tool in the management of antibiotic

resistance. It has been used as a guide for clinicians in antibiotic therapy optimization and examining different patterns in resistance and enhancing antibiotics usage. AI algorithms have also been utilized to discover novel

antibiotics and to tackle antibiotic resistance and mechanisms. Some common AI algorithms include the following as presented in Table 1

Table 1. Artificial Intelligence (AI) algorithms used for antibiotic resistance

Artificial Intelligence (AI) algorithms	Applications in antibiotic resistance
1. Machine Learning (ML)	Machine learning is a branch of AI that focuses on building systems capable of learning and improving from data without being explicitly programmed. It involves creating algorithms that can identify patterns in data and make decisions or predictions. ML is grouped into supervised learning and unsupervised learning (Figure 1).
a. Supervised Learning	This is also known as predictive learning. It is employed in antibiotic resistance to make future predictions from sets of training data. This aids in predicting diagnosis, to predict potential compounds with antimicrobial activity and also determine antibiotic resistance trends and outcomes (Figure 1). Supervised learning is also divided into classification and regression. Classification involves forecasting the group of given data points e.g. microbial or non-microbial groups. Regression is when the predicted output variable is a real value e.g. predicting drug capacity. Examples include: Naive Bayes (NB), Decision trees (DT), Random forests (RF), Support vector machines (SVM), eXtreme Gradient Boosting (XGBoost) and Logistic Regression (LR) (Reddy, 2023).
Naives bayes (NB)	Naive Bayes is a classification method based on Bayes' theorem with independent assumptions of each feature. Scientific investigations have successfully used it as a surveillance model for antibiotic resistance especially in estimating probabilities of ineffective treatment due to antibiotic resistance and also in identifying reasons for resistant patterns.
Decision tree (DT)	This is another classification AI model usually employed for effective distribution of medical resources by estimating the burden of antibiotic resistance. It was used by Reynolds et al. (2014) to provide an estimate healthcare utilization and cost for antibiotic resistance, and it indicated that the decrease in antibiotic resistance or enhancement of antibiotic selection could result to substantial savings and even resulted to rapid duration of treatment and reduced dosages. Decision tree involves three steps: feature selection, decision tree generation and decision tree pruning. In feature selection, it divides the dataset into two groups, either based on the value of an attribute or randomly. For decision tree generation the two groups are compared to know the best-split point and then decision tree pruning is done to categorize the data points.
Random Forest (RF)	This ML algorithm is a symbol of Leo Breiman and Adele Cutler. It put together outputs of multiple decision trees to achieve one result with high accuracy and reliability. RF models are also used to predict antibiotic combinations and to handle both classification and regression problems because they are flexible and user friendly. It was employed by Chandrasekaran et al. (2016) in which they use chemo-genomics data and orthology analysis to forecast the combination of antibiotic drugs which has a simple and definite pattern, require low computation and gives high generalization performance.
Support Vector Machines (SVM)	SVM models are mostly regarded as potential tools for antibiotic resistance surveillance and hospital diagnosis as they covered wide range datasets. SVM models have been used to predict antibiotic resistance phenotypes among bacterial strains and classify them as either 'resistant' or 'susceptible' to antibiotics based on their genetic sequences and metabolic pathway. Scientific investigations showed that SVM models have been used to examine resistance among antibiotics to predict whether bacteria such as <i>Escherichia coli</i> are resistant to antibiotics with about 90% accuracy (Her & Wu, 2018; Liu et al., 2020).
eXtreme Gradient Boosting (X GBoost)	XGBoost is an optimized implementation of gradient boosting designed to maximize computational efficiency and predictive performance. It is widely used in machine learning competitions and real-world applications due to its speed and accuracy. They are also employed to predict antibiotic resistance among bacterial strains by training models on labelled datasets of bacteria and their resistance profiles.
Logistic Regression (LR)	Logistic Regression is a classification AI algorithm used for binary classification tasks, where the goal is to predict one of two possible outcomes (e.g., "yes" or "no," "0" or "1"). It is also used to predict antibiotic resistance among bacterial strains by training models on labelled datasets of bacteria and their resistance profiles (Mohseni & Ghorbani, 2024).
b. Unsupervised learning	This is applied when detecting patterns in bacterial genomes without label data. They are mostly used to identify new resistance genes through gene clustering and most times algorithms for unsupervised ML are provided with a highly dimensional dataset in the form of a dissimilarity matrix. Examples include the clustering algorithms which include the hierarchical clustering and partitional clustering (K-Means clustering).
Hierarchical clustering	Builds a tree of clusters or dendrogram through divisive approaches. e.g nested clusters.
Partitional clustering	Divides data into K clusters by minimizing intra-cluster variance. e.g. un-nested clusters.
2. Deep Learning (DL)	One of the most recognized deep learning-based antibiotic resistance gene (ARG) identification system currently is DeepARG which is a manually curated database put together from ARG databases such as CARD (Arango-Argoty et al., 2018). In deep learning, AI model algorithm includes; Convolutional Neural Networks (CNN) and Artificial neural networks (ANN) which solves ordinal or temporal issues using past inputs to modify current inputs and outputs (Figure 1).
Convolutional Neural Networks (CNN)	This assesses large scale data of biological origin such as organisms' genome sequences in other to identify origin and patterns associated to antibiotic resistance mechanisms. It is also used in antibiotic discovery to identify compounds with antimicrobial activities.
Artificial neural networks (ANN)	Artificial neural networks are computing systems inspired by biological neural networks that make up the brain of animals. Using this DL approach, many new antibiotics have been discovered without any prior assumptions. In an experiment using mouse, ANN was used to detect molecules which have antimicrobial activities against a wide range of pathogens (Stokes et al., 2020). Currently, DL approaches are been applied to effectively design new antibiotics and enhance existing molecules or compounds.
3. Natural Language Processing (NLP)	This is another AI algorithm used in detecting antibiotic resistance among microorganisms. It uses Text Mining Algorithm (TMA) to acquire information from a pool of already established medical notes and other scientific literatures in other to identify potential resistance genes.

4. **Reinforcement Learning (RL)** This is mostly employed to enhance antibiotic treatments in other to improve therapeutic efficacies and avoid resistance problems. RL algorithms are applied in the discovering novel antibiotics, here, the AI model is taught and modify to search through chemical compounds so as to identify potential antibiotics that could be effective against antibiotic resistant organisms.
5. **Bayesian Networks** This type of AI model is used in probabilistic modelling to ascertain the possibility of an emerging antibiotic resistance among group of microorganisms subjected to different antibiotic treatments. It enables scientists to predict uncertainties especially while using antibiotics.

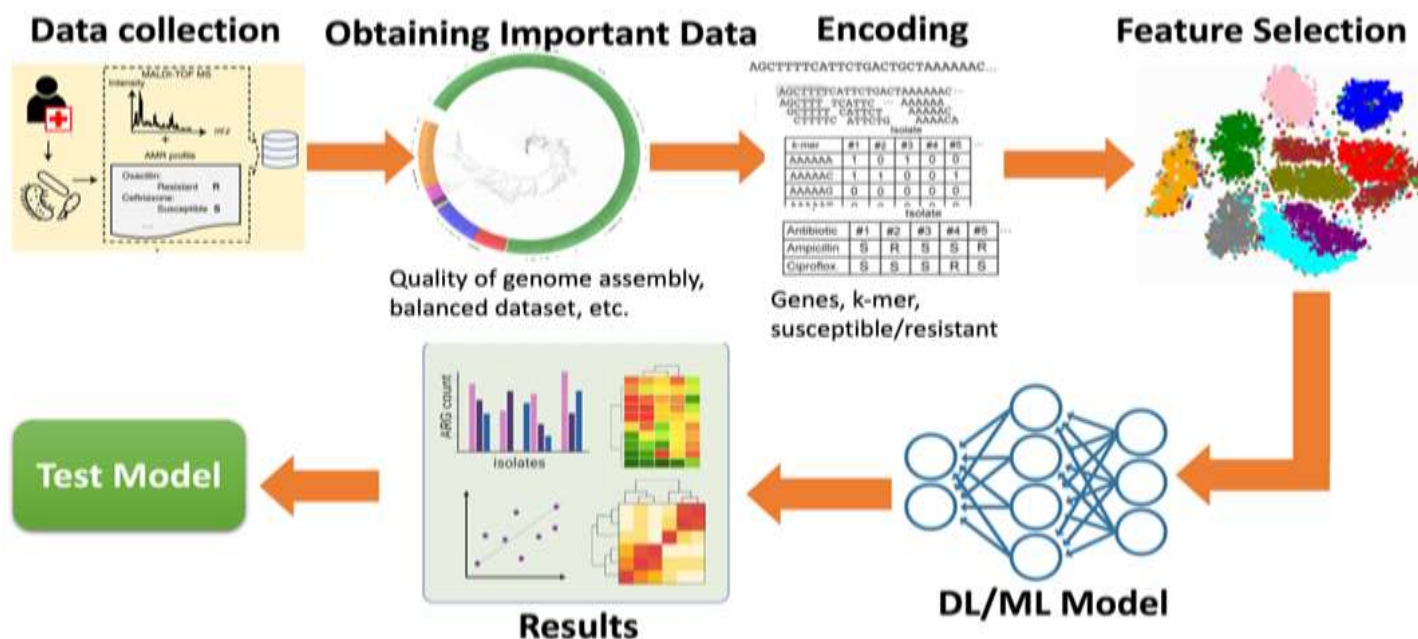


Figure 1. General AI workflow in the detection of antimicrobial resistance (Ali et al., 2023)

2. Applications of AI in global health solutions for antibiotic resistance

2.1.1 Advanced diagnostics

Regrettably, accurately diagnosing diseases and monitoring infectious diseases still pose challenges, particularly in low- and middle-income countries (LMIC) (Anekpo et al., 2024). AI technologies can enhance the speed and accuracy of diagnosing antibiotic resistance bacterial infections by using algorithms to analyze clinical samples, (Table 2) these tools can identify pathogens and their susceptibility to antibiotics ensuring that patients receive the most effective treatments and reducing unnecessary antibiotic use (Figure 2). For example, there are two standard techniques used in diagnosing antibiotic resistance such as antimicrobial susceptibility testing (AST) which is a conventional method but does not explain the mechanisms of antibiotic resistance and it requires over 24 hours. Another is the whole genome sequencing for antimicrobial susceptibility testing (WGS-AST) which is more rapid, consistent and gives accurate diagnosis but requires the knowledge of bioinformatics and large dataset is been processed to extract information. However, with flow cytometer

antimicrobial susceptibility testing (FAST) and supervised machine learning the time of analysis reduced to less than 3 hours. With advancement, infrared (IR) spectroscopy with AI artificial neural networks (ANN) was seen to achieve the analysis in just 30 minutes as described in Figure 3. Matrix-Assisted Laser Desorption/Ionization coupled to Time-Of-Flight Mass Spectrometry (MALDI-TOF MS) is widely recognized as a reference method for the rapid and inexpensive identification of microorganisms in routine laboratories, little attention has been paid to its ability to determine antimicrobial resistance (AMR). Some recent studies have evaluated its potential use in conjunction with machine learning to detect AMR in clinical pathogens (Feucherolles et al., 2022). MALDI-TOF mass spectra analyzed with ML have achieved sensitivities around 91.8%, specificities of 83.3%, and accuracies of approximately 87.6% for methicillin resistant *Staphylococcus aureus* (MRSA) classification in some cohorts, illustrating the potential of such approaches in routine microbiology laboratories (Baddal et al., 2024).

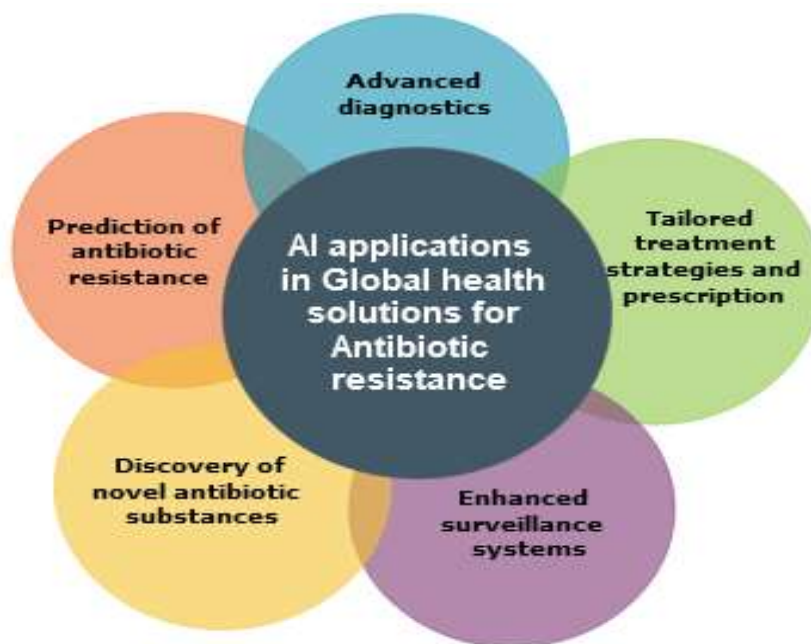


Figure 2. Applications of AI in Global health solutions for antibiotic resistance

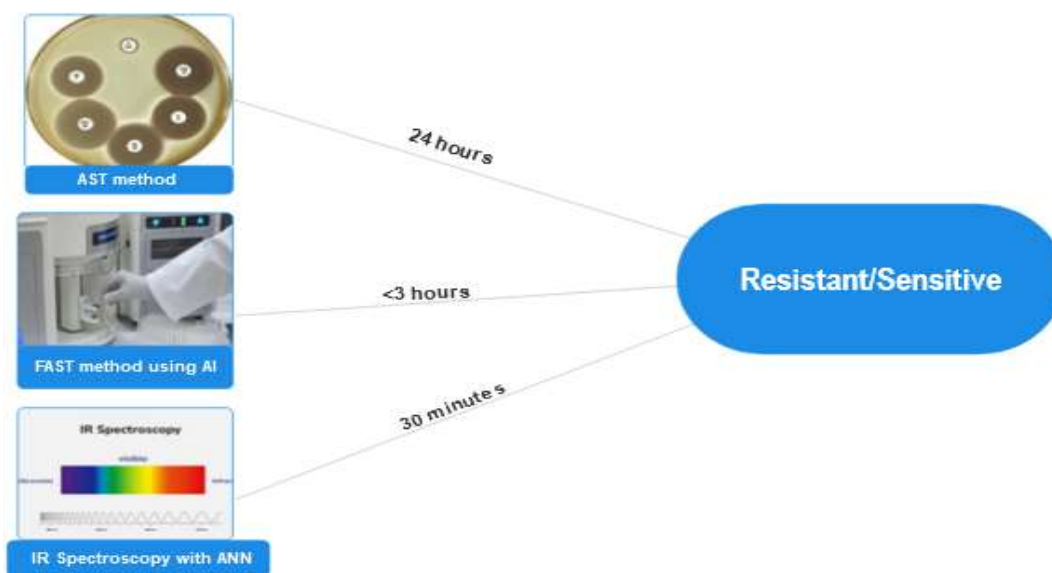


Figure 3. Conventional AST methods versus AI based AST methods (Lv et al., 2021)

2.1.2 Tailored treatment strategies and prescription

AI has the ability to analyze patient-specific data, AI can support personalized medicine by recommending targeted antibiotic therapies. This customization minimizes the risk of developing resistance by avoiding inappropriate antibiotic prescriptions, as unnecessary broad-spectrum antibiotics can be avoided (Table 3). Most times, appropriate prescription of antibiotics is a serious problem, as it involves choosing appropriate therapy for the suspected pathogen, regulating the drug concentration, frequency of administration, and identifying the appropriate route to ensure that the actual drug levels reach the site of infection. One of the difficulties in prescribing antibiotics is the need to sequentially adjust a patient's treatment as new clinical data become available. Most medical facilities are increasingly relying on automated decision support systems for the review of antibiotic prescriptions as inadequate specialized healthcare resources and large amount of information to be processed makes manual surveillance unsustainable. Most prescription monitoring systems use a rule base acquired from published and expert guidelines to

identify inappropriate prescriptions and prevent potential adverse events. These systems are often poorly defined and therefore generate a high rate of clinically unhelpful alerts. AI was critically used to address this problem using systems based on machine learning which was developed by Beaudoin et al. (2014). They described Antimicrobial Prescription Surveillance System (APSS), an antimicrobial monitoring system that, unlike the previous systems, was able to learn new rules for prescription surveillance. This feature, combined with user feedback supervision was designed to enable APSS to self-improve its knowledge base in the long term. APSS showed an indication learning capability that enabled an appropriate and clinically significant transition from intravenous to oral antibiotic therapy. The APSS system was also used in a subsequent study to identify inappropriate prescribing practices not supported by local antimicrobial stewardship experts. The learning module was able to extract clinically relevant rules by identifying inappropriate prescriptions not recognized by the baseline system (Umberto et al., 2020). Multiple logistic regression (MLR) was applied by Gibot et al. (2012) using three (3) set of

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biomarkers such as Soluble triggering receptor, Procalcitonin and Polymorphonuclear to estimate the probability of infections and this significantly increased, implying that AI algorithms could reduce the rate of misdiagnosis and improve the current methods guiding the judicious use of antibiotics. Also, using multiple biomarkers are better than a single one in identifying antibiotic resistant infections and ensuring judicious use of antibiotics.

2.1.3 Enhanced surveillance systems

AI can enhance disease surveillance by integrating data from various sources such as hospitals, laboratories and pharmacies. These would assist public health officials respond swiftly to emerging threats and also monitor antibiotic use and resistance patterns. AI can also provide comprehensive insights into local and global trends, informing policy decisions. Another AI reinforcement learning based tool in which a virtual agent learns a set of rules from a trial and error system to optimize them and maximize the expected performance was used to extract an amount of patient information that exceeded the life experience of human physicians by many folds and learned the optimal treatment of sepsis by analyzing multiple decisions by clinicians. Its application resulted in lower mortality in patients for whom the doctors' actual decisions matched those of AI, showing the clinically reliable ability of this tool to customize sepsis treatment and assist doctors in making real-time decisions (Komorowski et al., 2018).

2.1.4 Discovery of novel antibiotic substance

AI in drug synergism and combination therapy and in silico discovery of new antibiotic molecules has been widely utilized. As a matter of fact, between year 2014 and 2019, only 14 new antibiotics were developed and

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approved, the implementation of AI algorithms could accelerate the discovery and production of more novel antibiotics within a short period of time. In year 2020, some researchers developed a deep neural network model to predict growth inhibition of a bacteria known as *Escherichia coli* using a collection of 2335 molecules. The AI model was applied to over 107 million molecules to identify active compounds against *Escherichia coli*, and a molecule called c-Jun N-terminal kinase inhibitor known as halicin was discovered alongside with eight antibacterial compounds structurally variant from known antibiotics. Halicin showed potent therapeutic activity against *Escherichia coli*, *Clostridium difficile* and pan-resistant *Acinetobacter baumannii* in mouse models with mechanisms that differ from conventional antibiotics (Stokes et al., 2020). It is therefore evident that the use of AI can both reduce the expenses in identifying guide molecules and accelerate the process of identifying structurally novel compounds with the desired bioactivity.

2.1.5 Prediction of Antibiotic resistance

AI in predicting antibiotic resistance and could be of a great benefit to physicians especially when diagnostic tests and antibiotic resistance assays takes prolong period of time and resources. Antibiotic resistant gene-sequencing models such as DeepARG can predict antibiotic resistance categories with excellent precision according to the results of assessment of the deep and machine learning models (Arango-agorty et al., 2018). Predictive analytics can help forecast future resistance trends, enabling healthcare systems to implement proactive measures. With deep and machine learning prediction the identification of risk factors associated with antibiotic misuse would be guided (Table 4). Figure 4 below describes the process involved in the prediction of antibiotic resistance by AI.

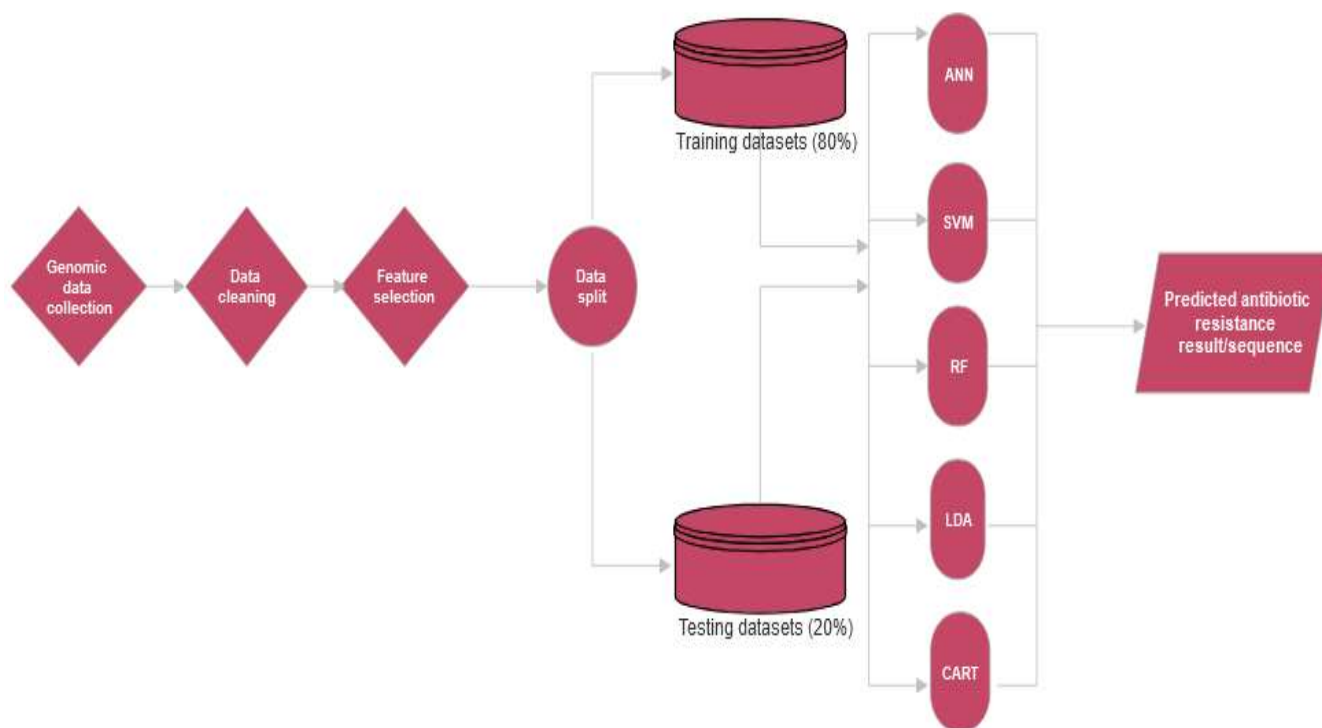


Figure 4. Steps involved in AI prediction of antibiotic resistance (Chowdhury et al., 2020)

3. Performance metrics of common AI algorithms used in antimicrobial resistance detection

AI used in detecting and predicting antimicrobial resistance (AMR) depends on certain computerized models to assess genomic and clinical data, and they are mainly evaluated using performance metrics such as Area Under the Receiver Operating Characteristic Curve (AUROC), Recall (sensitivity), Precision and F1 score (Sakagianni et al., 2023).

AUROC: This parameter helps determines an AI model's ability to identify either resistant or susceptible classes, which usually highly efficient models exceeds value of 0.85 – 0.90.

Recall/Sensitivity: This aids in measuring the proportion of actual antimicrobial resistant cases correctly identified by a model and this is paramount to avoid undertreating dangerous infections.

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Precision/Specificity: This measures the proportion of positive predictions that are truly antimicrobial resistant and this is essential in reducing unnecessary or overtreatment with the use of antimicrobial agents.

F1 Score: This put in account the mean value of the precision and recall of an AI model which is used in balancing model evaluation when imbalanced datasets occur.

Table 2. Performance metrics of machine learning AI models in clinical decision support systems

S/N	ML Algorithms	Bacterial species	Performance evaluation	Reference
1.	XGBoost, Multiple logistic regression, Random forest (RF) and Decision tree (DT)	Gram negative bacteria	A = 0.78 -0.91 R = 90% P = 91%	Liang et al., 2022.
2.	Support vector machine (SVM) and Neural network (NN)	<i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> and <i>Proteus mirabilis</i>	A = 0.761 R = 90% P = 95%	Lee et al., 2021.
3.	Decision tree (DT)	Extended spectrum Beta-lactamase (ESBL) Bacteria	A = 0.77 R = 93% P = 90%	Goodman et al., 2019.
4.	Support vector machine (SVM), Random forest (RF), Decision tree (DT) and Logistic regression (LR)	Bacterial isolates from blood cultures	A = 0.74 – 0.85 R = 85% P = 89%	Oonsivilai et al., 2018.
5.	Recursive partitioning and Decision tree (DT)	Gram negative bacteria	A = 0.70 R = 95% P = 86%	Sick-Samuels et al., 2020.

Key: A = AUROC, R = Recall, P = Precision

Table 3. Performance metrics of machine learning AI models in antibiotic prescription

S/N	ML Algorithms	Bacterial species	Performance evaluation	Reference
1.	Decision tree (DT)	Bacterial isolates from urine cultures	A = 0.57 - 0.66 R = 70% P = 80%	Rich et al., 2022.
2.	Logistic regression (LR) and Neural network (NN)	Bacterial isolates from urine and blood cultures	A = 0.80 – 0.88 R = 92% P = 95%	Lewin-Epstein et al., 2021.
3.	Penalized logistic regression (PLR)	Bacterial isolates from urine cultures	A = 0.65 – 0.69 R = 81% P = 80%	Hebert et al., 2020.
4.	Gradient boosting decision tree (GBDT)	<i>Escherichia coli</i> , <i>Klebsiella pneumoniae</i> and <i>Proteus mirabilis</i>	A = 0.83 R = 95% P = 99%	Yelin et al., 2019.
5.	Random forest (RF)	Bacterial isolates from urine and blood cultures	A = 0.64 - 0.74 R = 91% P = 86%	Corbin et al., 2022.

Key: A = AUROC, R = Recall, P = Precision

Table 4. Performance metrics of machine learning AI models in predicting antibiotic susceptibility patterns

S/N	ML Algorithms	Bacterial species	Performance evaluation	Reference
1.	Random forest (RF), Naïve Bayes, Gradient boosting, Support vector machine (SVM) and Penalized logistic regression (PLR)	Multi-drug resistant Enterobacterales	A = 0.70 R = 90% P = 94%	Henderson et al., 2022.
2.	Gradient boosting machine (GBM), Random forest (RF), XGBoost and Generalized linear model (GLM)	Multi-drug resistant <i>Pseudomonas aeruginosa</i> and Extended-spectrum Beta-lactamase <i>Escherichia coli</i> (ESBL-E)	A = 0.79 R = 94% P = 95%	Sakagianni et al., 2023.
3.	XGBoost	Carbapenem resistant bacteria	A = 0.846 R = 98% P = 95%	Kollef et al., 2021.
4.	Multiple Logistic regression (MLR)	All bacterial species	A = 0.758 R = 89% P = 95%	Feretakis et al., 2020.
5.	Decision tree (DT)	Gram negative bacteria	A = 0.61 – 0.80 R = 95% P = 86%	Vazquez-Guillamet et al., 2017.
6.	Random forest (RF)	<i>Pseudomonas aeruginosa</i> , <i>Acinetobacter baumannii</i> and <i>Klebsiella pneumoniae</i>	A = 0.933 R = 98% P = 97%	Feretakis et al., 2021.

Key: A = AUROC, R = Recall, P = Precision

4. How AI could promote public awareness on antibiotic resistance

4.1.1 Educational campaign initiatives

Through AI certain educative platforms for campaigns can be designed for sensitization to raise awareness and enlighten the populace about the risks of antibiotic misuse and resistance. By analyzing demographics, these campaigns can effectively communicate with specific audiences and promote better understanding and responsible behaviors. For example, Chatbots and other interactive apps can provide essential information on the appropriate use of antibiotics and the dangers of self-medication.

4.1.2 Engagement through gamification

AI gamified tools can stimulate learning about antibiotic resistance reaching vast audiences. Most times games stimulate real-world consequences and are more captivating, this can be used to mimic that of antibiotic abuse, thereby enhancing retention of information and encouraging responsible practices.

4.1.3 Community engagement programs

AI can facilitate the design and implementation of community-based initiatives focused on antibiotic stewardship. By assessing local health data, programs can be customized to meet community-specific needs, driving higher engagement and understanding.

4.1.4 Social media monitoring

AI tools can be used to assess and analyze social media conversations to gauge the public's perception of antibiotics and its resistance, as understanding this perception is pertinent and key to allowing health and pharmaceutical organizations to craft more effective messaging strategies to address misconceptions, change narratives and promote responsible antibiotic use.

4.1.5 Advertisements

AI tools can also be tailored into advertisements portraying antibiotic abuse and the resultant havoc of antibiotic resistance through the use of animations, short video skits, frequently asked questions (FAQ) and search tools that could be incorporated on street sign posts, Television and Radio programs etc. As this would further disperse the awareness and enlightenment of antibiotic resistance.

5 Ethical dilemmas in AI for global health and in combating antibiotic resistance

Ethical challenges are inherent in the use of AI, particularly in healthcare contexts where decisions can directly impact lives. Despite the potential of AI in addressing global health issues, the following challenges must be properly attended to:

5.1.1 Algorithm bias and fairness

AI systems, especially those that use ML algorithms, learn from data that may reflect existing societal biases. For instance, if an AI model is trained primarily on data from high-income countries or certain demographic groups, it may perform poorly or unfairly for populations that are underrepresented in the dataset. This could lead to biased medical recommendations or diagnoses, exacerbating health disparities rather than mitigating them. AI systems can inadvertently perpetuate existing bias if not controlled and monitored carefully. Continuous evaluation and refinement of AI algorithms are essential to avoid misrepresentation of data and to maintain accuracy and fairness.

5.1.2 Issue of interpretability and explaining ability

Breaches in the transparencies of AI models like the DL algorithms makes it hard to understand the decision-making process of AI models and to give clear explanations for AI-generated results particularly in healthcare, where accountability for decisions such as medical diagnoses is crucial. More so, there are mostly cases of mistranslation and misinterpretation by AI models as they are trained to just pool knowledge from any existing data or information without querying its authenticity especially in AI algorithms such as Natural language processing.

5.1.3 Generalization and dynamics in microbial systems

There is also difficulty in generalizing AI models across diverse microbial species as models for one set of conditions might not be transferred to other environments due to disparity in environmental conditions. Changes occur in microbial ecosystems naturally, and changes in antibiotic resistant patterns poses challenges in developing a constant or fixed model especially with microbial populations that experiences mutations.

5.1.4 Funds

availability of funds serves as a major challenge, the high cost of computation involved in the maintenance and training of AI models in the field of antibiotic resistance has slow down the advancement and distribution of sophisticated AI models. More so, there are limited access to computational resources.

5.1.5 Human-AI collaboration and integration into conventional methods

Resistance occurs among scientists on the reliability and acceptability of AI systems as a result of dependence on conventional methods and difficulties in aligning AI techniques with already established laboratory standard operating procedures. There are ethical concerns about the extent to which it should influence or replace human decision-making. Overreliance on AI might also undermine the role of healthcare providers, leading to reduced autonomy in clinical practice and potentially compromising patient care. However, assessing the prospects AI innovations upon humanity and balancing of efficiencies between human and AI becomes paramount.

6 Data governance in AI for global health

Data governance refers to the policies, standards, and regulations that determine how health data is managed, shared, and protected. In global health, data governance faces several unique challenges:

6.1.1 Equity in access and Data sharing

Disparities in access to technology can widen the gap between high and low resource settings and this can hinder the effectiveness of AI solutions. Different countries have varying regulations regarding health data collection and sharing. This raises concerns about how to ensure equitable access to data for AI development, particularly in low- and middle-income countries, where data may be scarce or poorly organized. Effective data sharing must balance the need for broad datasets to improve AI models with respect for privacy laws and regulations. Therefore, ensuring that all communities benefit from AI advancements is essential for equitable health improvements.

6.1.2 Data privacy and consent

AI systems require vast amounts of data to function effectively, often involving sensitive personal health information. The ethical dilemma arises in how this data is collected, shared, and protected. Many countries have different regulations for data privacy, and healthcare providers must navigate how to balance the need for large datasets with individuals' rights to privacy and informed consent. The utilization of private health data in AI-driven diagnostics therefore raises privacy and security issues. It becomes very paramount to ensure compliance with regulations and safeguard sensitive patient information.

6.1.3 Data Sovereignty

Countries have different laws around data sovereignty, meaning that the data generated within a country should remain under its control. This can complicate international collaborations in health AI, where datasets might need to be shared across borders to develop more comprehensive AI systems. Striking the right balance between cross-border data flow and local control is a critical governance issue.

6.1.4 Data quality and standardization

In global health, data quality is essential for AI applications to be effective. Variations in data quality (e.g., missing information, poor labeling, and inconsistent measurement) across countries and healthcare systems could

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impact the accuracy and effectiveness of AI models. Governance frameworks must ensure that health data is accurate, standardized, and up-to-date.

6.1.5 Security and cyber threats

Health data is a valuable target for cyber-attacks. As AI systems rely on large, centralized datasets, they could become attractive targets for malicious actors. Proper data governance frameworks must incorporate robust cyber-security measures to protect against breaches and unauthorized access.

7 Role of policy-making in ensuring equitable AI applications in global health

Policymakers play a critical role in shaping the landscape for equitable AI applications in global health. Effective policy-making is essential to ensure that AI technologies benefit all populations, particularly marginalized groups, and reduce health inequities. Key aspects of policy-making include:

7.1.1 Regulation and standards

Governments need to establish and enforce clear regulations that guide the development and deployment of AI in health systems. This includes creating standards for data privacy, security, and transparency, as well as setting performance benchmarks for AI models to ensure fairness and effectiveness across different populations. Regulatory frameworks must also include accountability mechanisms to address any harms caused by AI applications.

7.1.2 Inclusive Policy Development

Policies should be developed with a focus on inclusion, ensuring that AI applications do not disproportionately benefit only certain populations (e.g., wealthy nations or certain ethnic groups). Policymakers should engage diverse stakeholders, including healthcare providers, ethicists, AI developers, and vulnerable communities, in the policy-making process to ensure AI systems are equitable and meet the needs of all populations.

7.1.3 Global collaboration and governance

Given that AI in global health often requires cross-border cooperation, there needs to be a global governance framework to guide the ethical development and use of AI. This could involve international organizations such as the World Health Organization (WHO) and the United Nations (UN) working with governments to establish shared ethical guidelines, data sharing agreements, and standards for AI applications in healthcare.

7.1.4 Monitoring and evaluation

Policymakers should establish mechanisms to continuously monitor and evaluate the impact of AI technologies on healthcare systems. This includes assessing the effectiveness of AI applications, tracking the reduction or exacerbation of health disparities, and making necessary adjustments to policies and regulations to promote fairness.

7.1.5 Public trust and engagement

Policymakers must prioritize building public trust in AI technologies by ensuring that AI systems are developed in a way that aligns with societal values. This includes fostering transparency, educating the public about AI, and ensuring that citizens have a say in the use of their health data. Policymakers must ensure that AI technologies are developed and deployed in a way that promotes equitable access to healthcare and minimizes the risk of exacerbating existing health disparities. Only by carefully navigating these ethical dilemmas and governance challenges can we harness the full potential of AI to improve global health outcomes.

Conclusion

AI gives rapid and more accurate predictions and discoveries of drugs. It is therefore evident that AI renders a powerful toolkit for addressing global health challenges, particularly antimicrobial resistance. By improving diagnostic capabilities, surveillance and public education, AI can significantly tackle the threat of antimicrobial resistance thus, speeding up laboratory protocols. However, careful consideration of ethical issues and access equity is paramount to ensure that the benefits of AI are widely

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shared. A collaborative effort among healthcare providers, policymakers and technology developers will be essential to maximize the potential of AI in safeguarding global health. Future interdisciplinary research should also focus on addressing the inherent challenges of AI using extensive validation with high quality datasets in other to make sure that it is reliable and transferable.

Acknowledgements

We are grateful to the University of Ilorin, Nigeria for creating an enabling environment that supports research, innovation and development. This facilitated this review.

Funding declaration

There was no funding received for this work.

Conflict of interest

None declare

REFERENCES

- Anekpo, C.C., Okpara, T.C., and Nnadi, C.G. (2024). Application of genomic studies in epidemiological surveillance: A minioverview. *Journal of Biological Research and Biotechnology*, 22(1), 2292-2301. <https://dx.doi.org/10.4314/br.v22i1.7>
- Arango-Argoty, G., Garner, E., Pruden, A., Heath, L., Vikesland, P., and Zhang, L. (2018). DeepARG: A deep learning approach for predicting antibiotic resistance genes from metagenomic data. *Microbiome* 6:23. <https://doi.org/10.1186/s40168-018-0401-z>
- Ali, T., Ahmed, S., and Aslam, M. (2023). Artificial Intelligence for Antimicrobial Resistance Prediction: Challenges and Opportunities towards Practical Implementation. *Antibiotics*, 12:523. <https://doi.org/10.3390/antibiotics12030523>
- Baddal, B., Taner, F. and Uzun Ozsahin D. (2024). Harnessing of artificial intelligence for the diagnosis and prevention of hospital-acquired infections: a systematic review. *Diagnostics*, 14(5):484. <https://doi.org/10.3390/diagnostics14050484>
- Beaudoin, M., Kabanza, F., Nault, V. and Valiquette, L. (2014). An antimicrobial prescription surveillance system that learns from experience. *AI Mag.* 35:15–25. <https://doi.org/10.1609/aimag.v35i1.2500>
- Chandrasekaran, S., Cokol-Cakmak, M., Sahin, N., Yilancioglu, K., Kazan, H. and Collins, J.J (2016). Chemogenomics and orthology-based design of antibiotic combination therapies. *Mol. Syst. Biol.* 12:872. <https://doi.org/10.15252/msb.20156777>
- Chowdhury, A.S., Call, D.R. and Broschat, S.L. (2020). PARGT: a software tool for predicting antimicrobial resistance in bacteria. *Sci Rep* 10, 11033. <https://doi.org/10.1038/s41598-020-67949-9>
- Corbin, C.K., Sung, L., Chattopadhyay, A., Noshad, M., Chang, A., Deresinski, S., Baiocchi, M. and Chen, J.H. (2022). Personalized antibiograms for machine learning driven antibiotic selection. *Commun. Med.*, 2, 38. <https://doi.org/10.1038/s43856-022-00094-8>
- Ezeanya-Bakpa. C.C., and Martins, J.B. (2024). Transmission of antibiotic-resistant bacteria through laptop keyboard among students of a tertiary institution in Lagos, Nigeria and the associated risk factors. *Journal of Biological Research and Biotechnology*, 22(2), 2362. <https://dx.doi.org/10.4314/br.v22i2.5>
- Feretakis, G., Loupelis, E., Sakagianni, A., Kalles, D., Lada, M., Christopoulos, C., Dimitrellos, E., Martsoukou, M., Skarmoutsou, N. and Petropoulou, S. (2020). Using Machine Learning Algorithms to Predict Antimicrobial Resistance and Assist Empirical Treatment. *Stud. Health Technol. Inform.*, 272, 75–78. <https://doi.org/10.3233/SHTI200497>
- Feretakis, G., Sakagianni, A., Loupelis, E., Kalles, D., Martsoukou, M., Skarmoutsou, N., Christopoulos, C., Lada, M., Velentza, A., and Petropoulou, S. (2021). Using Machine Learning to Predict Antimicrobial Resistance of Acinetobacter Baumannii, Klebsiella Pneumoniae and Pseudomonas Aeruginosa Strains. *Stud. Health Technol. Inform.*, 281, 43–47.

Shitu et al..

<https://doi.org/10.3233/SHTI210117>

- Feucherolles, M., Nennig, M., Becker, S.L., Martiny, D., Losch, S., Penny, C., Cauchie, H.-M. and Ragimbeau, C. (2022). Combination of MALDI-TOF Mass Spectrometry and Machine Learning for Rapid Antimicrobial Resistance Screening: The Case of *Campylobacter* spp. *Front. Microbiol.* 12, 804484. <https://doi.org/10.3389/fmicb.2021.804484>
- Goodman, K.E., Lessler, J., Harris, A.D., Milstone, A.M. and Tamma, P.D. (2019). A methodological comparison of risk scores versus decision trees for predicting drug-resistant infections: A case study using extended-spectrum beta-lactamase (ESBL) bacteremia. *Infect. Control Hosp. Epidemiol.*, 40, 400–407. <https://doi.org/10.1017/ice.2019.17>
- Gibot, S., Béné, M.C., Noel, R., Massin, F., Guy, J. and Cravoisy, A. (2012). Combination biomarkers to diagnose sepsis in the critically ill patient. *Am. J. Respir. Crit. Care Med.* 186: 65–71. <https://doi.org/10.1164/rccm.201201-0037OC>
- Hebert, C., Gao, Y., Rahman, P., Dewart, C., Lustberg, M., Pancholi, P., Stevenson, K., Shah, N.S. and Hade, E.M. (2020). Prediction of Antibiotic Susceptibility for Urinary Tract Infection in a Hospital Setting. *Antimicrob. Agents Chemother.*, 64, e02236-19. <https://doi.org/10.1128/aac.02236-19>
- Henderson, H.I., Napravnik, S., Kosorok, M.R., Gower, E.W., Kinlaw, A.C., Aiello, A.E., Williams, B., Wohl, D.A., and van Duin, D. (2022). Predicting Risk of Multidrug-Resistant Enterobacterales Infections Among People with HIV. *Open Forum. Infect. Dis.*, 9, ofac487. <https://doi.org/10.1093/ofid/ofac487>
- Her, H.L. and Wu, Y.W. (2018). A pan-genome-based machine learning approach for predicting antimicrobial resistance activities of the *Escherichia coli* strains. *Bioinformatics* 34: 89–95. <https://doi.org/10.1093/bioinformatics/bty276>
- Kollef, M.H., Shorr, A.F., Bassetti, M., Timsit, J.F., Micek, S.T., Michelson, A.P. and Garnacho-Montero, J. (2021). Timing of antibiotic therapy in the ICU. *Crit. Care*, 25, 360. <https://doi.org/10.1186/s13054-021-03787-z>
- Komorowski, M., Celi, L.A., Badawi, O., Gordon, A.C. and Faisal, A.A. (2018). The Artificial Intelligence Clinician learns optimal treatment strategies for sepsis in intensive care. *Nat. Med.* 24: 1716–1720. <https://doi.org/10.1038/s41591-018-0213-5>
- Lee, A.L.H., To, C.C.K., Lee, A.L.S., Chan, R.C.K., Wong, J.S.H., Wong, C.W., Chow, V.C.Y. and Lai, R.W.M. (2021). Deep learning model for prediction of extended-spectrum beta-lactamase (ESBL) production in community-onset Enterobacteriaceae bacteremia from a high ESBL prevalence multi-centre cohort. *Eur. J. Clin. Microbiol. Infect. Dis.*, 40, 1049–1061. <https://doi.org/10.1007/s10096-020-04120-2>
- Lewin-Epstein, O., Baruch, S., Hadany, L., Stein, G.Y., and Obolski, U. (2021). Predicting Antibiotic Resistance in Hospitalized Patients by Applying Machine Learning to Electronic Medical Records. *Clin. Infect. Dis.*, 72, e848–e855. <https://doi.org/10.1093/cid/ciaa1576>
- Liang, Q., Zhao, Q., Xu, X., Zhou, Y. and Huang, M. (2022). Early prediction of carbapenem-resistant Gram-negative bacterial carriage in intensive care units using machine learning. *J. Glob. Antimicrob. Resist.*, 29, 225–231. <https://doi.org/10.21203/rs.3.rs-129356/v1>
- Liu, Z., Deng, D., Lu, H., Sun, J., Lv, L. and Li, S. (2020). Evaluation of machine learning models for predicting antimicrobial resistance of *Actinobacillus pleuropneumoniae* from whole genome sequences. *Front. Microbiol.* 11:48. <https://doi.org/10.3389/fmicb.2020.00048>
- Lv, J., Deng, S., and Zhang, L. (2021). A review of artificial intelligence applications for antimicrobial resistance. *Biosafety and Health*, 3(01), 22-31. <https://doi.org/10.1016/j.bsheal.2020.08.003>
- Melo, M.C., Maasch, J.R., and de la Fuente-Nunez, C. (2021). Accelerating antibiotic discovery through artificial intelligence. *Commun. Biol.* 4:1050. <https://doi.org/10.1038/s42003-021-02586-0>
- Mohseni, P. and Ghorbani, A. (2024). Exploring the synergy of artificial intelligence in microbiology: Advancements, challenges, and future prospects. *Computational and Structural Biotechnology Reports* 1:100005. <https://doi.org/10.1016/j.csbr.2024.100005>
- Murray, C.J.L., Ikuta, K.S., Sharara, F., Swetschinski, L., Robles Aguilar, G., Gray, A., Han, C., Bisignano, C., Rao, P. and Wool, E. (2022). Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *Lancet*, 399:629–655. [https://doi.org/10.1016/S0140-6736\(21\)02724-0](https://doi.org/10.1016/S0140-6736(21)02724-0)
- Oonsivilai, M., Mo, Y., Luangsanatip, N., Lubell, Y., Miliya, T., Tan, P., Loeuk, L., Turner, P. and Cooper, B.S. (2018). Using machine learning to guide targeted and locally-tailored empiric antibiotic prescribing in a children's hospital in Cambodia. *Wellcome Open Res.*, 3, 131. <https://doi.org/10.12688/wellcomeopenres.14847.1>
- Rabaan, A.A., Alhumaid, S., Al Mutair, A., Garout, M., Abulhamayel, Y., Halwani, M.A., Alestad, J.H., Al-Bshabshe, A., Sulaiman, T. and Al-Fonaison, M.K. (2022). Application of Artificial Intelligence in Combating High Antimicrobial Resistance Rates. *Antibiotics*, 11:784. <https://doi.org/10.3390/antibiotics11060784>
- Reddy, B.M. (2023). Machine learning for drug discovery and manufacturing. *AI and Blockchain in Healthcare*. Springer, p. 3–30. https://doi.org/10.1007/978-981-99-0377-1_1
- Reynolds, C.A., Finkelstein, J.A., Ray, G.T., Moore, M.R. and Huang, S.S. (2014). Attributable healthcare utilization and cost of pneumoniae due to drug-resistant *Streptococcus pneumoniae*: a cost analysis. *Antimicrob. Resist. Infect. Control* 3:16. <https://doi.org/10.1186/2047-2994-3-16>
- Rich, S.N., Jun, I., Bian, J., Boucher, C., Cherabuddi, K., Morris, J.G., Jr. and Prosperi, M. (2022). Development of a Prediction Model for Antibiotic-Resistant Urinary Tract Infections Using Integrated Electronic Health Records from Multiple Clinics in North-Central Florida. *Infect. Dis. Ther.*, 11, 1869–1882. <https://doi.org/10.1007/s40121-022-00677-x>
- Sakagianni, A., Koufopoulou, C., Feretzakis, G., Kalles, D., Verykios, V.S., Myrianthefs, P., Fildisis, G. (2023). Using Machine Learning to Predict Antimicrobial Resistance, A Literature Review. *Antibiotics*, 12, 452. <https://doi.org/10.3390/antibiotics1203045>
- Shitu, T. (2024). Occurrence of Antibiotic Resistant *Salmonella* and *Shigella* in Diarrheal cases Resulting from a Common Source Consumption of Contaminated Water, UMYU Journal of Microbiology Research, 9 (3): 40 – 47. <https://doi.org/10.47430/ujmr.2493.006>
- Sick-Samuels, A.C., Goodman, K.E., Rapsinski, G., Colantouni, E., Milstone, A.M., Nowalk, A.J. and Tamma, P.D. (2020). A Decision Tree Using Patient Characteristics to Predict Resistance to Commonly Used Broad-Spectrum Antibiotics in Children with Gram-Negative Bloodstream Infections. *J. Pediatr. Infect. Dis. Soc.*, 9, 142–149. <https://doi.org/10.1093/jpids/piy137>
- Stokes, J.M., Yang, K., Swanson, K., Jin, W., Cubillos-Ruiz, A. and Donghia, N.M. (2020). A Deep learning approach to antibiotic discovery. *Cell* 180 (13): 688–702. <https://doi.org/10.1016/j.cell.2020.01.021>
- Umberto, F., Marco P., Vincenzo, C., Pierpacifico, G., Cosimo, N., Alberto, A., Adriana, C., Andrea, P. and Susanna, E. (2020). Role of Artificial Intelligence in Fighting Antimicrobial Resistance in Pediatrics. *Antibiotics*, 9: 767. <https://doi.org/10.3390/antibiotics9110767>
- Vazquez-Guillamet, M.C., Vazquez, R., Micek, S.T., and Kollef, M.H. (2017). Predicting Resistance to Piperacillin-Tazobactam, Cefepime and Meropenem in Septic Patients with Bloodstream Infection Due to Gram-Negative Bacteria. *Clin. Infect. Dis.*, 65, 1607–1614. <https://doi.org/10.1093/cid/cix612>
- Yelin, I., Snitser, O., Novich, G., Katz, R., Tal, O., Parizade, M., Chodick, G., Koren, G., Shalev, V. and Kishony, R. (2019). Personal clinical history predicts antibiotic resistance of urinary tract infections. *Nat. Med.* 25, 1143–1152. <https://doi.org/10.1038/s41591-019-0503-6>

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