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REVIEW ARTICLE

Role of Artificial Intelligence and Its Mechanistic Approach in Combating Antimicrobial Resistance

Mayank Raj[1], Rishu Raj[1], Shad Khan[1], Sushil Kumar Upadhyay[1], Manoj Singh[1]*, Nirmala Sehrawat[1], Mukesh yadav[1], Yogendra Prasad Pandey[2] and Deepak Yadav[3]
[1]Department of Bio-Sciences and Technology, MMEC, Maharishi Markandeshwar (Deemed to be University), Mullana-Ambala (Haryana)-133207, India
[2]Department of Zoology, Government Model Science College, Rewa (M.P.), India
[3]Department of Zoology, Miranda House (University of Delhi), New Delhi, India
***Corresponding author's Email:** manoj.singh@mmumullana.org

ABSTRACT
Antimicrobial resistance (AMR) is a significant worldwide health concern caused due to improper and excessive use of antibiotics, resulting in the development of microbes resistant to drugs. The origin of AMR can be traced back form discovery of penicillin, as the emergence of multidrug-resistant organisms has presented substantial obstacles to healthcare systems globally. The improper utilization of antibiotics in human and animal healthcare has lead to the dissemination of resistance genes, resulting in the emergence of a "Silent Pandemic" that has the potential to surpass and causes mortality. The unrestricted use of antimicrobials in animal feed has significantly contributed to the formation and spread of antimicrobial resistance. Antimicrobial resistance in humans and animals, as it presents difficulties in the treatment of diseases caused by resistant microorganisms. Artificial intelligence (AI), which encompasses machine learning (ML) and deep learning (DL), has shown great potential in various areas of medical research, particularly in combating antimicrobial resistance. AI applications in antimicrobial resistance (AMR) utilize advanced computational techniques to analyze gene expression and whole-genome sequencing data. This helps in identifying the root causes of infectious diseases and classifying different types of diseases. AI-driven systems offer numerous advantages compared to conventional ones, such as reduced reliance on human intervention, enhanced precision and decreased expenses. Thus, the current review have to used on evaluating antimicrobial resistance utilizing artificial intelligence (AI) on different datasets and compare the efficacy of different AI models.
Keywords: *antibiotics; antimicrobial resistance; artificial intelligence; machine learning*

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INTRODUCTION

Antibiotics are highly efficient weapons in the battle against bacteria and are widely regarded as the most significant medical breakthrough of the 20th century. The advent of antibiotics transformed the therapeutic approach and continues to rescue many lives from bacterial infections. According to the Centres for Disease Control and Prevention (CDC), it is estimated that in 2018, antimicrobial resistance (AMR) resulted in 35,900 deaths in the United States [1]. This number is expected to increase as the population becomes older. Based on statistical data, 700,000 individuals die annually worldwide [2-4]. Antibiotics have proven incredibly beneficial to humanity, serving not only therapeutic objectives but also being utilised in other ways such as animal husbandry and production as preventive measures in undeveloped and developing countries for many years [5]. Microorganisms have evolved antimicrobial resistance due to their growing utilization and improper handling. Antimicrobial resistance is the ability of microorganisms, such as bacteria, viruses, fungi, and parasites, to survive and multiply in the presence of treatments intended to eliminate them. Infections generated by antimicrobial-resistant organisms pose significant challenges in treatment and are associated with a heightened risk of severe disease and

mortality. Various categories of antimicrobial agents, such as antibiotics, antifungals, antivirals, disinfectants, and food preservatives, function by either inhibiting the development and reproduction of microorganisms or causing death. Antibiotics are a type of antimicrobial drugs that are specifically designed to fight against bacterial infections and the growing problem of antibiotic resistance. AMR, or antimicrobial resistance, is a natural process observed in all species. It occurs when genetic mutations occur to protect against the harmful effects of strong selection pressure. Bacteria endeavor to acquire resistance against antibacterial treatments in order to withstand environmental selection pressure, hence rendering these drugs ineffective [6]. The evolution and spread of antimicrobial resistance is influenced by a multitude of interconnected factors pertaining to healthcare and agriculture. Furthermore, AMR, which stands for antimicrobial resistance, can be influenced by other factors such as medications, improper waste management, trade, and finance. These aspects contribute to the complexity of AMR, making it a significant global public health issue [7]. According to the World Health Organization (WHO), AMR is among the top 10 threats to global health. AMR poses a hazard to the environment, food. The mortality rate caused by antimicrobial resistance is a significant global danger. The present mortality rate in AMR stands at 1.27 million in 2023 [8]. The World Health Organization predicts that the number of fatalities caused by AMR will reach 10 million by the year 2050. Figure 1 display the mortality rates attributed to AMR, cancer, and various other disorders, including traffic accidents. Developing novel techniques to detect strains that are vulnerable to immune system or particular antibiotics are essential in combating the rise of antibiotic-resistant diseases. The proliferation of artificial intelligence (AI) has profoundly transformed research methodologies in various fields, particularly biomedical research, in the twenty-first century [9].

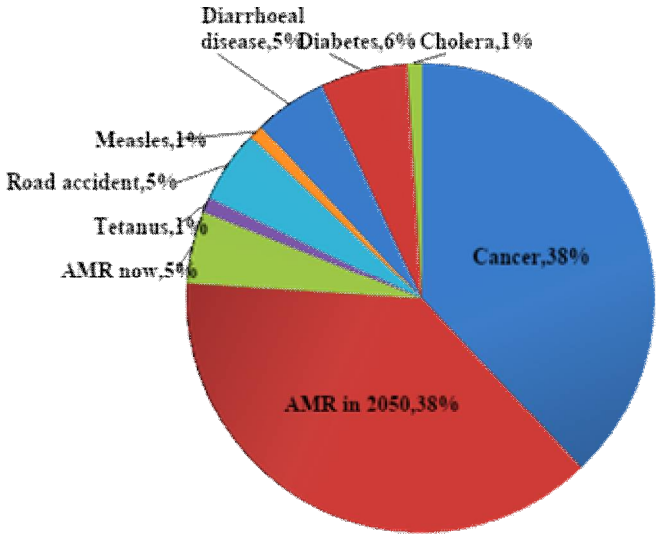

Figure 1: Deaths due to AMR compared to other common deaths in 2023.

The subfields of machine learning (ML) and deep learning (DL) within the science of AI have emerged as viable methods for addressing these intricate phenomena. Machine Learning primarily concentrates on developing algorithms that can construct predictive models using training data sets [10]. In the last decade, there has been a surge in the inclination towards utilizing machine learning (ML) and deep learning (DL) techniques to enhance the quality of healthcare. This phenomenon can be ascribed to the escalating accessibility of biological and medical data, in computing notable progress in algorithm development. Identifying and tracking the genes associated with antimicrobial resistance is a complex task due to its intricate nature [11]. The emergence of an antibiotic-resistant gene is influenced by both biological and environmental variables. The primary goal of this effort is to utilize artificial intelligence in different phases of investigation for antimicrobial resistance. Data availability and the accessibility of standard tools are currently constrained [12]. This work extensively investigates the new approaches of Artificial Intelligence; specifically machine learning and deep learning, to identify the crucial solution for antimicrobial resistance analysis. For this study, we specifically examined a limited number of research articles from our library that utilised machine learning or deep learning as the model to analyze antimicrobial resistance in infectious diseases.

BIOCHEMICAL APPROACHES IN REDUCING RESISTANCE AND INCREASING SUSCEPTIBILITY TO AVAILABLE ANTIBIOTICS

Lately, scientists have shifted their research efforts towards exploring alternative methods to eradicate antibiotic-resistant bacteria, without solely relying on the development of new antibiotics. This strategy is intriguing due to the financial and logistical difficulties associated with the exploration and creation of novel antibiotics. The primary concept behind this technique is to counteract the inherent defense mechanisms of microbes, enhancing the efficacy and lethality of existing antibiotics [13]. This is intriguing because we aim to enhance the effectiveness of existing antibiotics with proven safety records, making them more powerful. This would result in greater availability of highly effective antibiotics for treating infectious diseases, potentially at a lower cost. A thorough comprehension of the mode of action of antibiotics and the mechanisms of resistance in bacteria is essential in order to create successful alternative medicines. Each bactericidal antibiotic class possesses a distinct mode of action that specifically targets a separate component of the bacterial cell, ultimately resulting in the demise of the pathogen [5, 14, 15]. It is widely believed that different kinds of antibiotics function by affecting bacteria in distinct ways, such as causing a loss of membrane permeability, changing cell shape, or inhibiting critical metabolic pathways. However, the precise effects of microbial molecular networks resulting from antibiotic exposure and their direct role in causing bacterial cell death are not yet fully understood. The process of bacterial killing by antibiotics is an intricate one, initiated by the direct interaction between the medication and its specific target in the bacteria. This interaction triggers a series of biochemical, molecular, and ultra structural alterations in the affected bacterium [16]. The continuous evolution and dissemination of drug-resistant bacteria highlights the need for a deeper comprehension of the intricate mechanisms via which existing antibiotics eradicate bacteria, in order to discover novel antibacterial treatments. Calhoun et al. [17] and Hong et al. [18] have documented that all antibiotic medicines have a shared secondary impact once they have successfully reached to their main targets. The report states that they compel the targeted bacterium to generate "reactive oxygen species (ROS)," commonly referred to as free radicals. These free radicals have the potential to cause significant harm to the bacterium's DNA and proteins if not promptly neutralized. Regardless of their modes of action, all bactericidal antibiotics have a common secondary impact on the bacterial cell, leading to the death of the organism. This concept was supported by previous research conducted by Kohanski et al. [19], which showed that bactericidal antibiotics targeting specific cellular components caused the production of reactive oxygen species in both Gram-negative and Gram-positive bacteria. Nevertheless, bacteriostatic antibiotics did not induce the generation of hydroxyl radicals [20]. Subsequent investigations have revealed that hydroxyl radicals are generated through a Fenton-like reaction, wherein ferrous iron is oxidized to ferric iron by peroxide, leading to the production of hydroxyl radicals. The main process by which peroxide causes the death of bacteria is by the creation of double-strand DNA breaks [21]. These breaks are a product of the Fenton reaction, which can also be triggered by antibiotics. Additionally, there is a small amount of evidence suggesting that when bacteria are exposed to antibiotics, a DNA repair pathway called the SOS response is activated. This pathway responds to oxidative stress and DNA damage. It has been observed that bacterial species that cannot form iron-sulfur clusters, which are a source of iron, are less vulnerable to drugs that kill bacteria [22]. Administration of large doses of bactericidal antibiotics leads to the generation of harmful hydroxyl radicals via a shared physiological mechanism that involves changes in the central tricarboxylic acid (TCA) cycle and iron metabolisms [23, 24]. Additionally, following exposure to antibiotics that kill bacteria, there was a noticeable decrease in the levels of nicotinamide adenine dinucleotide (NAD) + hydrogen (H) (NADH), which resulted in the production of ferrous iron. Conversely, a decrease in the TCA cycle impairs the amount of NADH, which reduces the vulnerability of bacteria to bactericidal medicines [25]. The augmentation in the generation of hydroxyl radicals causes harm to DNA and proteins. This phenomenon was consistently recognized as a prevalent adverse effect of all antibiotics included in the study, as well as a recurring factor in bacterial mortality. In order to successfully address the growing problem of antibiotic resistance, it is crucial that we utilize our advanced knowledge of antibiotic mechanisms in the development of new clinical treatments and methods. Two primary targets for the development of alternative antibiotic therapy will be examined: the SOS response and the function of hydrogen sulphide in generalized antibiotic resistance in bacteria.

SOS RESPONSE: A KEY STEP IN THE DEVELOPMENT OF ANTIBIOTIC RESISTANCE

The Save our souls response is a DNA repair mechanism that is activated in response to DNA damage and oxidative stress [26, 27]. The SOS pathway plays a crucial role in bacterial adaptation, pathogenicity, and diversification. It is also significant in the formation of persister cells, prolonged tolerance, and stress resistance, including antibiotic resistance as shown in figure 2. Kohanski et al. 2017 [19] conducted a

study which found that antibiotic exposure caused the SOS response, leading to reduced susceptibility to bactericidal drugs in bacterial mutants that cannot form iron-sulfur clusters. Moreover, this study reinforces prior findings that antibiotics, such as ciprofloxacin, can induce the SOS response, which may play a crucial role in the emergence of drug resistance [5, 28]. Proteins responsible for repairing DNA damage, such as RecA (an activator), LexA (a suppressor), and chaperones, are synthesized as components of the SOS response [29]. The process of repairing damaged DNA usually requires the ability to tolerate small genetic alterations, which might lead to the emergence of antibiotic resistance and persistence. Antibiotics can elevate the levels of reactive oxygen species (ROS) inside the cell, leading to damage in DNA, proteins, and lipids, and triggering the SOS response. Oxidative stress occurs when there is an excess of ROS being produced in the cell compared to the amount that is eliminated [30]. The generation of hydroxyl radicals may be linked to bacterial death and antibiotic resistance, based on extensive understanding. The RecA protein is commonly recognized as the primary initiator of the SOS response through its interaction with single-stranded DNA [31]. The growing data connecting the action of antibiotics with the cellular response to damage caused by hydroxyl radicals can now be utilised to create novel antibacterial drugs. Compounds that inhibit the SOS response have the ability to both hinder the emergence of antibiotic resistance, especially when the medicine is administered in low doses, and improve the effectiveness of antibiotics that kill bacteria [32]. Currently, there are ongoing efforts to produce RecA inhibitors for clinical uses. Initially, the SOS response was identified as a key regulator of DNA damage repair. However, its role has been observed to extend beyond expectations. Similar to a biologist's perspective, the SOS response induces an increased mutation rate, leading to genetic variation and microbial adjustment, which encompasses the development of antibiotic persistence and resistance [31, 33, 34].

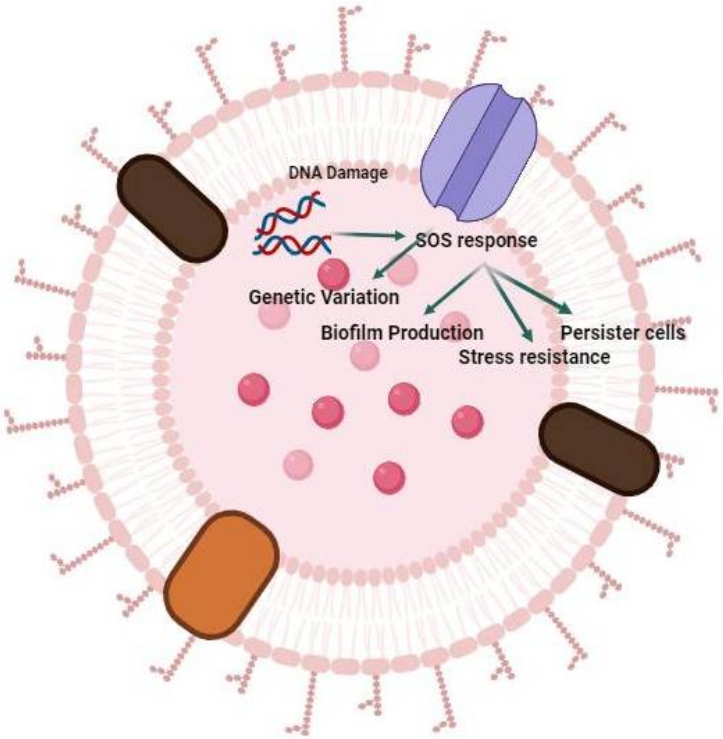

Figure 2: Bacterial SOS response: a schematic view.

This approach has the potential to be utilised for other essential proteins that play a role in the response to hydroxyl radicals. They may have been overlooked in previous attempts to discover new antibiotic targets because they are not crucial for cell growth. AMR poses a significant risk to both human health and food production as it allows for the transmission of resistant zoonotic pathogens from animals to humans [35]. Excessive use of antibiotics in livestock for medical treatment and to enhance livestock growth has resulted in the emergence of resistance. This increases the chances of MDR bacteria such as *Salmonella* and *Campylobacter* being transmitted through the food chain or by animal handlers. Bacterial strains that are resistant can easily spread between different species. Wildlife also acquires AMR through

indirect environmental exposures, which leads to increased transmission of pathogens. Microbes that are resistant to antibiotics can spread beyond their original habitat and infiltrate the surrounding environment. This occurs when fertilizers, which are derived from animal waste, are used. As a result, water sources and the food we consume can become contaminated with these resistant microbes. They also share AMR genes with regular environmental and human commensal micro-flora. With limited treatment options available for animal infections caused by resistance, the escalation of outbreaks among cattle, poultry, and sheep becomes a serious concern. This often leads to the difficult decision of animals, resulting in substantial economic losses and posing a threat to food supplies. Estimates suggest that AMR could result in a significant financial burden of $3-4 billion in the livestock industry in the coming decades [36]. The negative effects of resistance have far-reaching consequences for agriculture, economic systems, national security, and trade. Therefore, it is crucial to adopt a comprehensive One Health approach that includes monitoring and interventions for human, animal, and environmental health. This is essential in order to effectively tackle the significant current and future negative effects of antimicrobial resistance on animals, which in turn increases the risks of human exposure even more [37–40].

ROLE OF ARTIFICIAL INTELLIGENCE IN DETECTING OF ANTIMICROBIAL RESISTANCE

Antimicrobial resistance is typically studied by employing antimicrobial susceptibility testing (AST), a method that depends on phenotypic testing [41]. Phenotypes refer to specific characteristics of microorganisms that pertain to their physical properties, such as their shape, size, and coloration. However, carrying out this type of testing necessitates a substantial amount of time [42]. As an illustration, the testing procedure for certain bacterial pathogens takes 2 days, whereas it can take several weeks for microbial species that grow slowly [43, 44]. Genome sequences provide further data that can be analyzed to investigate antimicrobial resistance. Thanks to technological developments and reduced costs, the process of obtaining genomic sequences has become more readily available [45]. Furthermore, later studies have employed environmental data, such as temperature, humidity, and other variables, to predict the probability of antimicrobial resistance [46]. Multiple methodologies employ genetic data to forecast the occurrence of antimicrobial resistance. Deep learning and machine learning models are sophisticated instruments capable of precisely forecasting and interpreting antimicrobial resistance. These models build a connection between the input features and the goal labels by means of non-linear correlations [47]. The objective is to do regression or classification, and in specific cases, analyze and understand the outcomes [48]. These models have exhibited a notable level of precision in forecasting antimicrobial susceptibility when an adequate amount of data is accessible. The following sections offer a thorough overview of the overall techniques used in Machine Learning and Deep Learning for predicting antibiotic resistance.

MECHANISM OF MACHINE LEARNING AND DEEP LEARNING AS MODEL FOR THE DETECTION OF ANTIMICROBIAL RESISTANCE

Supervised learning issues often encompass prediction and classification tasks. During these tasks, models undergo training utilizing given input data in order to make an estimation of a specific target, sometimes referred to as a "label". The first phase entails collecting and organizing the data. The dataset primarily consists of whole-genome sequences (WGS) and single-nucleotide polymorphisms (SNPs) along with their corresponding phenotypes [49]. A particular investigation, cited as, employed whole-genome sequencing (WGS) to analyze different strains of *E. coli* bacteria collected from both animal and human clinical samples. This data was acquired using proprietary means and is also accessible online as a publicly accessible dataset. The study aimed to examine the impacts of antibiotics, including CIP (ciprofloxacin), CTX (cefotaxime), CTZ (ceftazidime), and GEN (gentamicin). The dataset consists of isolates that exhibit resistance and susceptibility. Sequences can be segmented into k-mers, which are subsequences of length k, in order to construct features [50]. This method is beneficial when dealing with incomplete genome strains, and using short k-mers can offer vital information about the precise regions that are responsible for resistance [51–53]. Afterward, the procedure of pre-processing and feature extraction becomes essential. This In addition, the machine-learning models can be trained using label encoding and one-shot encoding techniques [54]. K-mers are labeled according to their phenotypes and perform the encoding procedure. Various Python libraries can be used to easily implement data pre-processing, encoding, and feature extraction. Diverse machine learning and statistical technologies can also be utilized to create meaningful characteristics. A convolutional neural network has been utilized to employ machine-learning techniques in order to build effective features for predicting AMRs. Previous research have utilized various machine-learning models, including logistic regression (LR), support vector machine (SVM), random forest (RF) for the prediction and classification of AMRs, in addition to

data management [31, 55-57]. Similarly, the researchers in utilized a deep-learning model consisting of artificial neurons organized in layers to replicate the operations of the human brain [58]. The scikit-learn Python library is employed for constructing LR, RF, and SVMs, whereas Tensor Flow and Python are utilized for implementing CNN and other deep-learning architectures. The core principle of all these models is to construct a mathematical relationship between input qualities and target labels using the available data. Therefore, the meticulous selection and organization of relevant data is highly important. By iteratively training the models with the provided training data, they acquire the ability to establish a mapping and understand a concealed non-linear connection [59]. Once the models have completed their training, they are subjected to testing using new and unseen data, commonly known as test data, in order to assess their performance before being applied in actual scenarios. Multiple evaluation metrics, including as root mean square error (RMSE), mean absolute error (MSE), accuracy, precision, recall, and confusion matrix, can be used to analyze the models [51, 60, 61]. After reaching the necessary level of precision, it can then be used to real-world applications.

PREDICTION OF ANTIMICROBIAL RESISTANCE THROUGH ARTIFICIAL INTELLIGENCE

Antibiotics are little compounds that possess the ability to impede or exterminate microorganisms, and are frequently employed in medical settings to combat bacterial diseases [62]. Regrettably, the misuse of antibiotics leads to antimicrobial resistance (AMR). Given that AMR substantially diminishes the effectiveness of antibiotics as a treatment, it is crucial for us to monitor its development and dissemination. Presently, there are two commonly employed approaches for diagnosing antimicrobial resistance (AMR) [63]. There are two methods used for antibiotic susceptibility testing (AST). The first method is called antimicrobial susceptibility testing (AST) [43], and the second method is called whole-genome sequencing for antimicrobial susceptibility testing (WGSAST) [64]. Antibiotic susceptibility testing (AST) is a traditional approach for measuring levels of antibiotic resistance [65, 66]. However, it is not efficient and does not provide an explanation for the mechanism of antimicrobial resistance [67]. Whole-genome sequencing and antimicrobial susceptibility testing (WGS-AST) offers a fast, reliable, and precise method for diagnosing antimicrobial resistance (AMR). However, it necessitates the use of extensive and complex datasets in order to properly extract information. Artificial intelligence technologies are utilized to enhance existing methodologies [68–70] in the following manner. In order to enhance AST approaches, Inglis *et al*. employed a hybrid approach that involved utilizing flow cytometer antimicrobial susceptibility testing (FAST) [71] in conjunction with supervised machine learning [72] to conduct antimicrobial susceptibility testing. This particular artificial intelligence technique produces a dependable outcome in less than 3 hours [73]. In addition, Lechowicz et al. [74] achieved a significant reduction in the duration of AST, from 24 hours to just 30 minutes, by creating a method that integrates infrared (IR) spectroscopy [80] with artificial neural network using an IR-spectrometer. According to Figure 4, AI-based IR-spectrometry and the FAST approach are significantly quicker than traditional AST methods. Current research using WGS-AST primarily rely on k-mer analysis, which involves analyzing specific sequences of nucleotides derived from the entire genome of samples. Nevertheless, k-mer datasets are excessively voluminous and repetitive to be directly employed for AI applications. In order to determine the presence of a specific k-mer in the genome, Davis *et al.* [75] utilized rapid annotation using subsystem technology (RAST) [37, 76] to transform the k-mer into a binary matrix. In addition, Mahé et al. employed the stability selection method to create a concise and predictive subset of k-mers from a vast number of redundant and correlated ones [77], as opposed to using a binary matrix. This strategy enhances the efficiency and interpretability of the predictive model. Figure 3 demonstrates that a binary matrix or a limited subset of k-mer, in combination with AST results, can be utilized to construct a classifier model capable of predicting antimicrobial resistance and exploring the connections between genotype and phenotype [78].

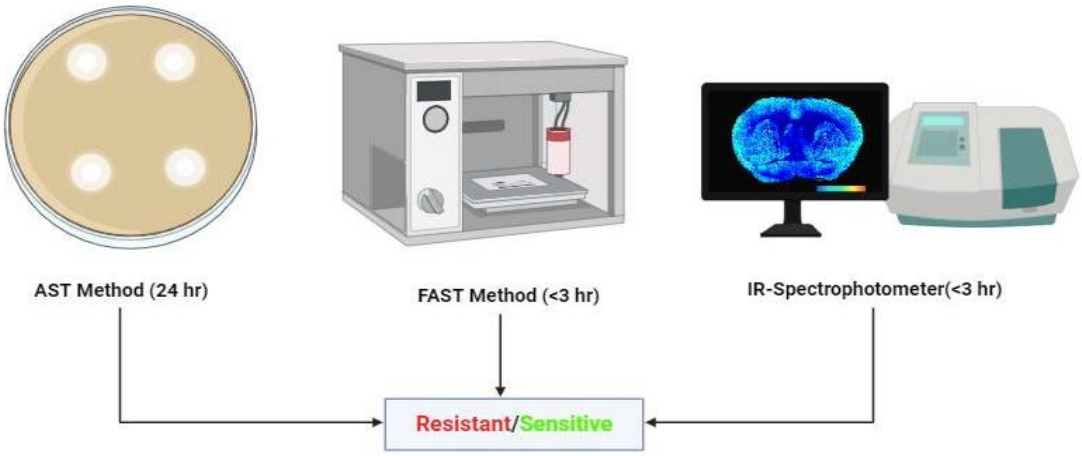

Figure 3: A comparison between classic AST methods and AI-based AST methods.

The effectiveness of these procedures relies heavily on the thoroughness and excellence of the databases, which often contain precise information on antibiotic resistance genes (ARGs) and antimicrobial susceptibility testing (AST) results. For instance, Davis *et al.* have gathered bacterial genomes containing antimicrobial resistance (AMR) information, encompassing genomics, transcriptomics, and protein-protein interactions [79, 80]. While AI technology is increasingly utilized for AMR forecasts, there remains significant potential for further enhancement. Regarding AST, while the AI-powered FAST or IR spectrometer approach can enhance the pace of antimicrobial susceptibility testing, their procedures are excessively intricate for non-experts to utilize. Hence, our future research will focus on incorporating AI algorithms into the analytic software of FAST or IR spectrometers to achieve automated analysis.

DEVELOPMENT OF AI BASED ANTIMICROBIAL PEPTIDES MODELS

Through advancements in microbiology, biochemistry, and organic chemistry, scientists have identified around 100 different forms of antibiotics that effectively combat infectious infections [81]. As a result of opposition, the most of them have experienced a slow decline in utilization. It is worth mentioning that the number of newly approved antibiotics by the FDA has been steadily declining since the 1980s. This drop is attributed to the high level of risk discovered in the studies of these new antibiotics. Antimicrobial peptides are being considered as potential alternatives to traditional antibiotics. AMPs are essential elements of the innate immune system and have a wide range of activities that can defend the host against various pathogenic microorganisms, such as viruses, bacteria, parasites, and fungi [82]. However, the process of identifying and extracting AMPs is both costly and time-consuming. The utilization of drug combinations has garnered growing interest due to its ability to improve therapeutic effectiveness and minimize adverse effects. Due to the challenge of exploring effective medicine combinations from a vast number of possibilities, we must utilize artificial intelligence technology to address the afore mentioned issues. It utilized quantitative structure–activity relationship (QSAR) descriptors and artificial intelligence (AI) algorithms to discover 50 new antimicrobial peptides (AMPs) from a pool of 100,000 randomly generated peptides [83]. The in vitro bacteriostasis assay demonstrated that this model has a 94% accuracy rate in finding active peptides. In addition, several physical and chemical characteristics such as charge, hydrophobicity, isoelectric point, and aggregation propensity, as well as peptide sequence, can be employed as features to train artificial intelligence (AI) models [84-88]. Utilizing AI-based technology has the potential to greatly decrease the expenses and time required for conducting research [77, 89] aimed at identifying and validating viable candidates in vitro [90]. Moreover, due to the need for large training data to improve crucial parameters, current AI-based AMP models need the establishment of numerous public AI-based AMP databases. Artificial intelligence techniques can expedite the exploration of favorable antibiotic combinations in the antibiotic combination approach. The databases contain physical parameters such as lipophilicity [91], chemo genomics data, and molecular fingerprints. While AI demonstrates effectiveness in AMPs and antibiotic combination predictions, there remains sample opportunity for enhancement. Regarding AMPs, their limitations stem from the quantity and accuracy of the database [92]. Most AI-based AMP approaches are binary classification models that do not take into account continuous activity information [93]. Hence, our next work will focus on comprehending the utilization of AMPs continuous activity data to construct an AI model capable of precisely forecasting the activity of AMPs against certain bacteria. Existing widely used public databases for antibiotic

combinations need sufficient data to thoroughly investigate several characteristics for artificial intelligence (AI) models. Nevertheless, the inclusion of many characteristics, such as lipophilicity [94], chemo genomics data, and molecular fingerprints, greatly influences antibiotic combinations [81, 95]. Consequently, routinely employed AI models exhibit very low accuracy. In the future, we aim to combine antibiotic data with various attributes using AI approaches to identify more effective antibiotic combinations for certain diseases. This will be possible due to advancements in data collection, making the process faster and easier.

DEVELOPMENT OF AI PHAGE THERAPY

Phage treatment, along with small-molecule drugs and AMPs, has been an important approach in combating antibiotic resistance [96, 97]. Bacteriophages, which are natural predators of bacteria, have undergone co-evolution with their bacterial hosts for a staggering 3.8 billion years. They are an essential component of the human micro biome [98]. Phage treatment, in contrast to antibiotics, has significantly greater specificity, hence reducing disruptions to the microbiota and limiting the spread of antibiotic-resistant bacteria caused by antibiotics [99]. Multiple instances of clinical success have already been documented [100]. This section outlines the systematic process of designing phage therapy, which consists of four sequential steps: phage identification, prediction of phage virion proteins (PVPs), analysis of phage lifestyle, and research of phage-host interactions. It also discusses the role of artificial intelligence (AI) in each stage. Recent advancements in metagenomic sequencing have brought attention to the crucial significance of viruses in many ecosystems [101, 102]. In order to tackle this increasing importance, cutting-edge AI-powered methods have been created for the identification, labeling, and examination of viral sequences in intricate metagenomic datasets [103,104]. Seeker is a deep learning-based program that quickly identifies various bacteriophages, even when they have very little similarity in their genetic sequences to recognized phage families [105]. It utilizes a combination of machine learning and protein similarity methods to independently retrieve, annotate, and evaluate the metabolic effects of viruses in metagenomic assemblies. This surpasses the capabilities of conventional virus identification algorithms [106]. Furthermore, VirSorter greatly improves the precision and scope of virus sequence identification in metagenomic datasets by employing multiple classifiers to accurately detect a diverse array of viruses [107]. Furthermore, Phage Boost, an innovative machine learning technique that focuses on feature space and is specifically developed for rapid and comprehensive detection of prophages, greatly improves the process of identifying bacteriophages [108].

CHALLENGES

This paper provides a concise and methodical overview of applications based on artificial intelligence. Initially, we provided a concise overview of classical approaches and their inherent constraints. Subsequently, we employed illustrative examples to demonstrate the enhancements that AI technologies bring to these conventional methodologies. Ultimately, we put out potential avenues for future research regarding various AI applications. AI-based AST and WGS-AST approaches have recently been used to quickly and accurately identify and describe antimicrobial resistance (AMR). WGS-AST approaches specifically assist physicians in achieving personalized treatment for chronic and complex antibiotic resistant illnesses [109]. Nonetheless, the effectiveness of these approaches relies on the thoroughness and excellence of the database housing the extensive clinical data [52, 110]. Despite the existence of numerous public databases for antimicrobial resistance, the absence of a consistent standardization and irregular updates to the data hinder the efficient training of AI-based AMR predictive models [37, 111]. At present, the collection of AMR data has become rapid and affordable due to advancements in AI-based AST approaches and sequencing techniques. Our objective is to develop a comprehensive AMR database capable of integrating advanced AI algorithms to enhance the accuracy of AMR prediction. While it is well acknowledged that the comprehensive collection and dissemination of AMR-related information might enhance our understanding of AMR development patterns and improve antibiotic usage strategies [66, 112] only a limited number of scientists are now prepared to volunteer their data. Therefore, our main objective is to concentrate on the creation of AI algorithms that possess exceptional predictive precision while utilizing a limited training dataset. However, current AI-based algorithms do not utilize multiple biomarkers to enhance predictive accuracy [113] and prevent misdiagnosis. Therefore, we are interested in utilizing AI to investigate the most effective combinations of multiple biomarkers. These combinations can then be integrated into CDSSs to provide guidance for making informed clinical decisions.

CONCLUSIONS

This article has examined the latest advancements in artificial intelligence for addressing obstacles and exploring potential linked to antimicrobial issues. Artificial intelligence is making remarkable advancements in various fields of human endeavor. Deep learning and machine learning are specialized branches of artificial intelligence that address complex problems through the utilization of vast quantities of data. Currently, a vast quantity of data pertaining to antimicrobials may be acquired from several sources. In addition, highly efficient computers equipped with huge storage devices can rapidly interpret this data, providing valuable insights. Researchers in the field of antibiotics have turned to artificial intelligence (AI) methods to address various issues. Currently, significant research is being conducted on the implementation of artificial intelligence (AI) in antibiotics, which has created new opportunities. By implementing AI, the time required for diagnostics is significantly decreased, going from days to hours. In addition, artificial intelligence is aiding in the discovery of new antimicrobial resistance (AMR) and mutations. The amount of antimicrobial substances present in water supplies can be accurately predicted. Nevertheless, there exist significant obstacles when it comes to implementing AI in the context of AMR. For instance, many applications just classify the output as either resistant or susceptible, without taking into account an intermediate category that falls between the susceptible and resistant categories. This can result in an inaccurate diagnosis. In addition, often single-variable characteristics are examined and linked to antibiotic genes. Nevertheless, it is widely acknowledged that numerous characteristics have a role in creating or recognizing AMR. Hence, it is necessary to develop multivariate/interactive models. The reliability of results acquired from training imbalanced data is questionable. Models are mostly trained on sequences from specific geographical regions, which may not yield universally applicable results. Data management is a significant issue of concern. The ongoing study on the integration of AI into AMR is still under progress, and further exploration is required before contemplating its widespread implementation in clinical and healthcare settings.

CONFLICT OF INTEREST

The authors claim no conflicts of interest because none financial support was received from any government, non-government agency or organization to conduct this research work.

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