

## The use of A.I. to Identify Drug Resistance in Bacteria: A Systematic Review

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### Abstract:

Artificial intelligence (A.I.) is revolutionizing the diagnosis of infections, offering faster and more accurate methods. By rapidly detecting pathogens and identifying antibiotic resistance, A.I. enhances diagnostic capabilities. It plays a crucial role in early disease detection, drug development, personalized treatments, and timely outbreak detection, leading to significant improvements in public health and healthcare. However, as A.I. becomes integral to medical decision-making, ethical considerations must be addressed. Ensuring patient data privacy, fair A.I. practices, data security, transparency in A.I. operations, equitable access to A.I. tools and human oversight of A.I. decisions are essential. Continued advancements in A.I. for infection diagnosis promise even more effective disease treatments and prevention strategies in the future, all while ensuring that healthcare practices remain ethical and equitable.

**Keywords:** Artificial intelligence, Antimicrobial, Antibiotic resistance, Drug development, Global health.

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### Introduction

The development of resistance in microorganisms to medications meant to destroy them is known as antimicrobial resistance (AMR). Overuse of antibiotics in humans, animals, and the environment contributes to the development of antimicrobial resistance (AMR). This implies that treatments that were effective in the past may no longer be effective, which will result in diseases lasting longer, an increase in the number of fatalities, and an increase in the expense of medical care. A significant issue requires prompt attention on a global scale. The World Health Organization (WHO) initiated the Global Antimicrobial Resistance and Use Surveillance System. According to the findings, antimicrobial resistance (AMR) is becoming more severe and is one of the primary causes of mortality [1, 2]. Nearly 5 million fatalities throughout the globe were attributed to antimicrobial resistance (AMR) caused by bacteria in 2019, with 1.27 million deaths specifically being driven by it [1]. The region of Western sub-Saharan Africa had the most significant mortality rate from resistance, with 27.3 fatalities per 100,000 inhabitants [1]. This region was the most dangerous area to live in. Every year,

antimicrobial resistance (AMR) to conventional antibiotics is responsible for more than two million illnesses and at least 23,000 fatalities in the United States [3]. Antibiotic-resistant bacteria were responsible for more than 2.8 million illnesses in the United States in 2019 [4]. Antimicrobial resistance may be responsible for 10 million fatalities annually by the year 2050 [5]. The Infectious Disease Society of America discussed six deadly viruses that are referred to as "ESKAPE" because they are rapidly growing resistant to antibiotics. The World Health Organization (WHO) compiled a list of "priority pathogens" that are in desperate need of new medicines. AMR is another concern in China, where an increasing number of bacteria are developing resistance to some medications. A decrease in the number of newly authorized antibiotics has occurred, with just four medications being approved between the years 2010 and 2014. Developing new drugs is difficult because the same antibiotics are discovered repeatedly, which makes it challenging to find new antibiotics. This is particularly true for the pathogens that are on the World Health Organization's list of priorities. Artificial

intelligence (A.I.) is a subfield of computer science that focuses on the development of intelligent computers that are capable of performing many of the same tasks as humans. The application of artificial intelligence is helping to expedite the discovery of new scientific findings, especially in the field of medicine, where it is assisting in the discovery of new medications and research. A.I. is also used in the fight against AMR. In this study, we will discuss the advancements that have been made in the production of novel antibacterial treatments as well as the problems that have been encountered. Additionally, we will discuss how artificial intelligence is being used to create new antibiotics, enhance their structures, and discover new ways that they may function [6].

## Literature Review

### A.I. Techniques for Identifying Drug Resistance:

Within the realm of supervised learning, prediction and classification issues are rather popular. These challenges require training models with input information in order to make predictions about a specified target or label. Collecting and pre-processing data, which often consists of whole-genome sequences (WGS) and single-nucleotide polymorphisms (SNPs) connected to certain features, is the first step in this process when it comes to the prediction of antimicrobial resistance (AMR) [7,8]. To investigate the resistance of *E. coli* strains to antibiotics like ciprofloxacin and ceftazidime, for instance, researchers in [7] employed whole genome sequencing in their study. In order to generate a final SNP matrix, data pre-processing entails the extraction of pertinent genetic information by means of reference and variant alleles, as well as their placements [7]. Using techniques such as chaotic game representation (CGR) or label encoding, single nucleotide polymorphisms (SNPs) may be represented [7]. To find genetic patterns that are associated with resistance, another method involves breaking sequences into shorter pieces that are referred to as k-mers [8].

After the data has been prepared, several machine learning models, such as logistic regression (LR), support vector machine (SVM), random forest (R.F.), and convolutional neural networks (CNN), may be used for prediction [7,9]. For making predictions, these models will learn patterns from the data. For example, CNNs attempt to imitate the organization of the human brain in order to recognize intricate patterns in genetic data [10]. The implementation of these models often involves the use of Python modules such as sci-kit-learn and TensorFlow. Before being used in applications that are based on the real world, the models are put through their paces by being tested using data that they have not encountered before. Utilizing evaluation criteria such as accuracy, precision,

recall, and confusion matrix, one may evaluate the performance of a model [10,11]. The availability of data and the quality of that data are some of the issues that are involved in AMR prediction. For training the models, researchers need a substantial quantity of genetic data that includes phenotypes (traits) that have been defined.

On the other hand, variations in testing procedures and laboratory practices might add noise to the data, which can have an impact on the accuracy of the Model. If you want your Model to work well, it is necessary to get a dataset that is well-balanced and has an adequate number of sensitive and resistant categories. Furthermore, in order to generalize, it is essential to have a solid grasp of the genetic variety of isolates as well as the geographical differences in resistance mechanisms. To increase the accuracy and reliability of AMR prediction models, it is necessary to address these problems [13-17].

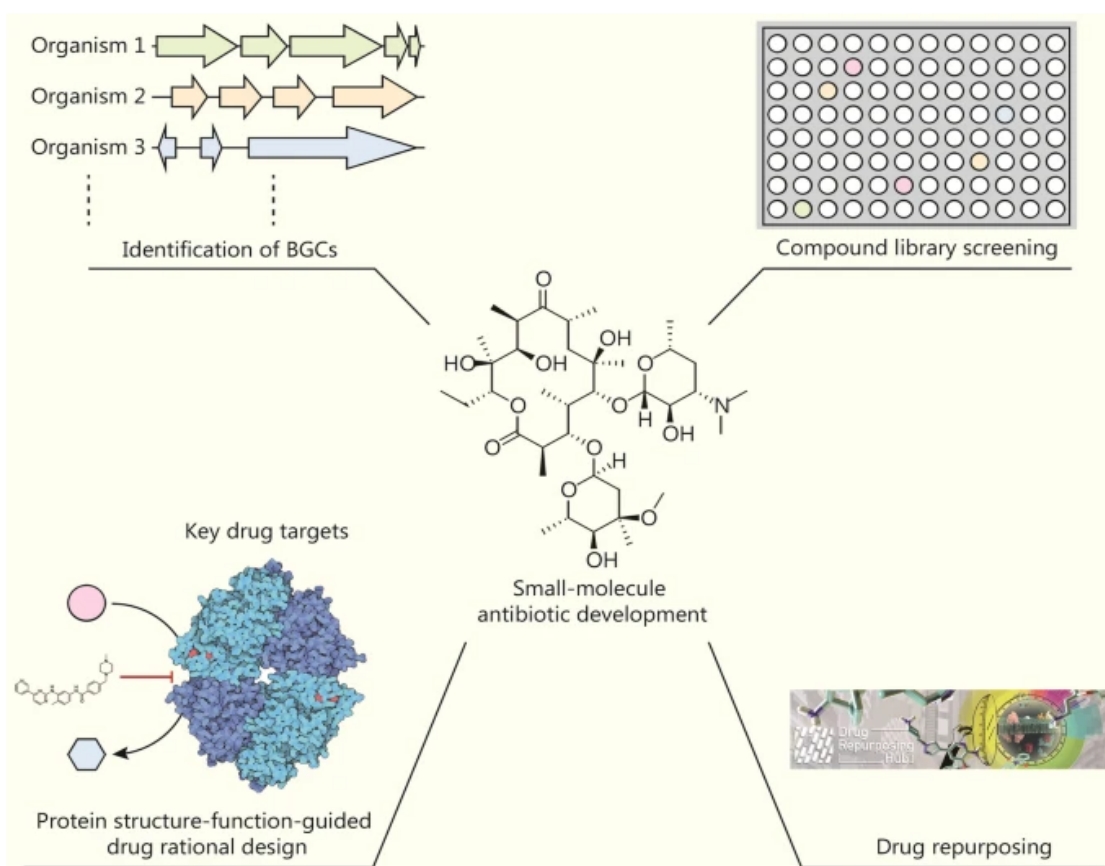
To put it another way, machine-learning models are trained on certain kinds of data in order to determine whether a germ will be resistant to some treatments or not. The genetic material contained inside the germ is broken down into smaller pieces known as k-mers in order to do this. The frequency of each k-mer is then determined by analysis of the data. Through the use of this information, vectors, which can be thought of as mathematical representations, are generated for each k-mer. Through the use of these vectors, the Model is able to better comprehend the genetic composition of the germ and forecast resistance. In addition, there are methods that entail identifying genes that are associated with resistance or doing an analysis of the germ's whole genetic composition. This serves to capture various genetic variants that have the potential to influence the way in which the germ reacts to medications. Scientists also take advantage of environmental data, such as information about the weather, in order to make predictions about the locations of drug-resistant microorganisms. In this way, it is possible to have a better understanding of when and where they are most likely to spread. In order to get an understanding of how many elements influence the result, the primary concept underlying machine-learning models is to make use of a large amount of data. The training of these models takes place on a dataset, and then they are tested using fresh content. It is necessary to separate the data into training, test, and validation sets in order to do this. For the purpose of determining the optimal parameters, the Model is trained using the training set. Several models are appropriate for various kinds of data. Simple neural networks, for instance, are helpful in solving some issues, but other types of decisions, such as decision trees, are more effective for determining how the Model concluded. Due to the fact that models that are more complicated may be more challenging to comprehend, it is essential to

choose the appropriate Model for the task. For instance, decision tree models are simple to understand because they allow one to see the process by which each choice is arriving at its conclusion.

This provides us with a better understanding of the reasons for the Model's predictions, particularly in the field of health and diagnostics [17].

**Table 1: Software used for detecting microbes [23].**

Software	Description
MetaPhlAn	A tool for profiling the composition of microbial communities from metagenomic shotgun sequencing data
Kraken	A taxonomic sequence classifier that assigns taxonomic labels to DNA sequences
MetaPhlAn2	An updated version of MetaPhlAn, offering improved accuracy and the ability to identify strains and species with high precision
IDseq	A cloud-based metagenomics platform for pathogen detection and outbreak tracking
PathSeq	A tool for identifying microbial sequences in metagenomic data
QIIME	A software package for analyzing microbial communities, including tools for clustering, diversity analysis, and taxonomic classification
Mothur	A software package for analyzing microbial communities that includes tools for clustering, classification, and diversity analysis
MG-RAST	A metagenomics analysis server that offers automated annotation and comparative analysis of metagenomic data
GOTTCHA	A tool for identifying pathogens in metagenomic samples
DIAMOND	A sequence aligner for comparing DNA, RNA, or protein sequences against a protein database, often used for metagenomic analysis.
MEGAN	A software tool for interactive exploration and analysis of large-scale microbiome sequencing data, including taxonomic and functional analysis



**Figure 1: Shows the use of the A.I. technique for screening and development of antibiotics [6].**

**Material and Methods**

**Study Design:** This systematic review was conducted following the Preferred Reporting Items

for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. Search Strategy: A comprehensive search was performed in electronic databases, including PubMed, Embase, and

Cochrane Library. The search strategy included relevant keywords and MeSH terms related to the topic of interest. Additionally, manual searches of

reference lists of relevant studies and reviews were conducted to identify additional articles.

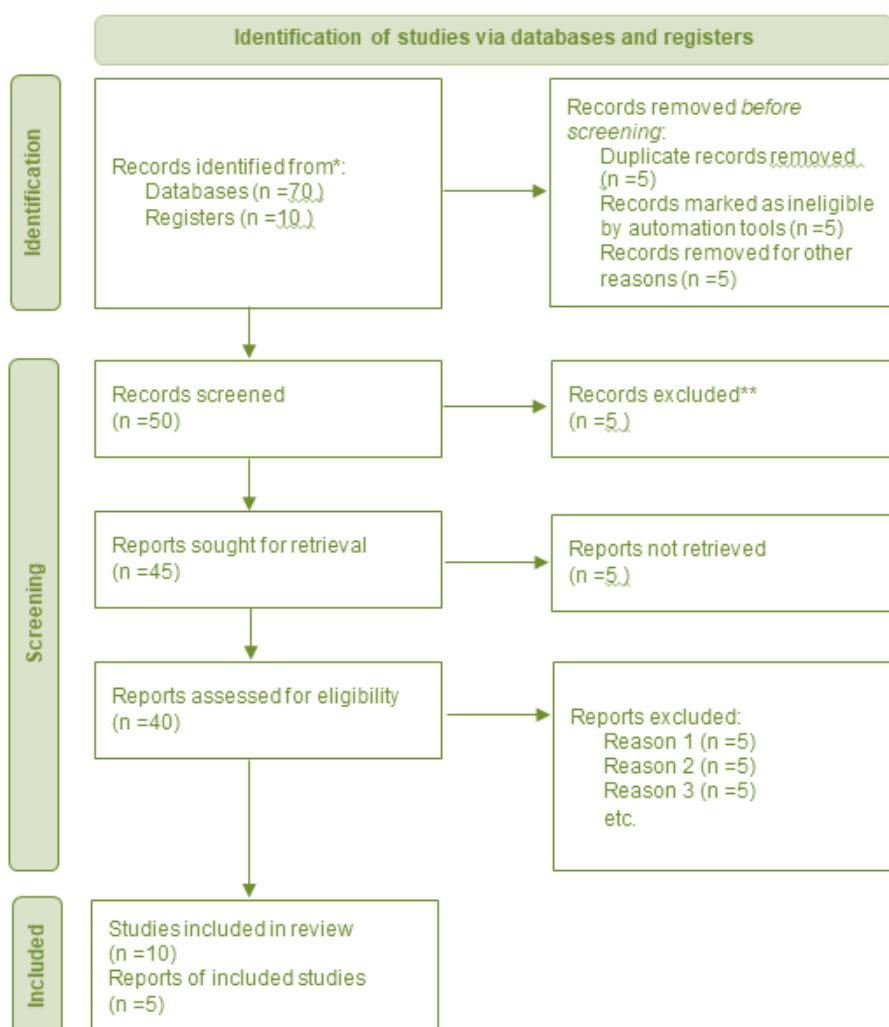


Figure 2: PRISMA flow chart

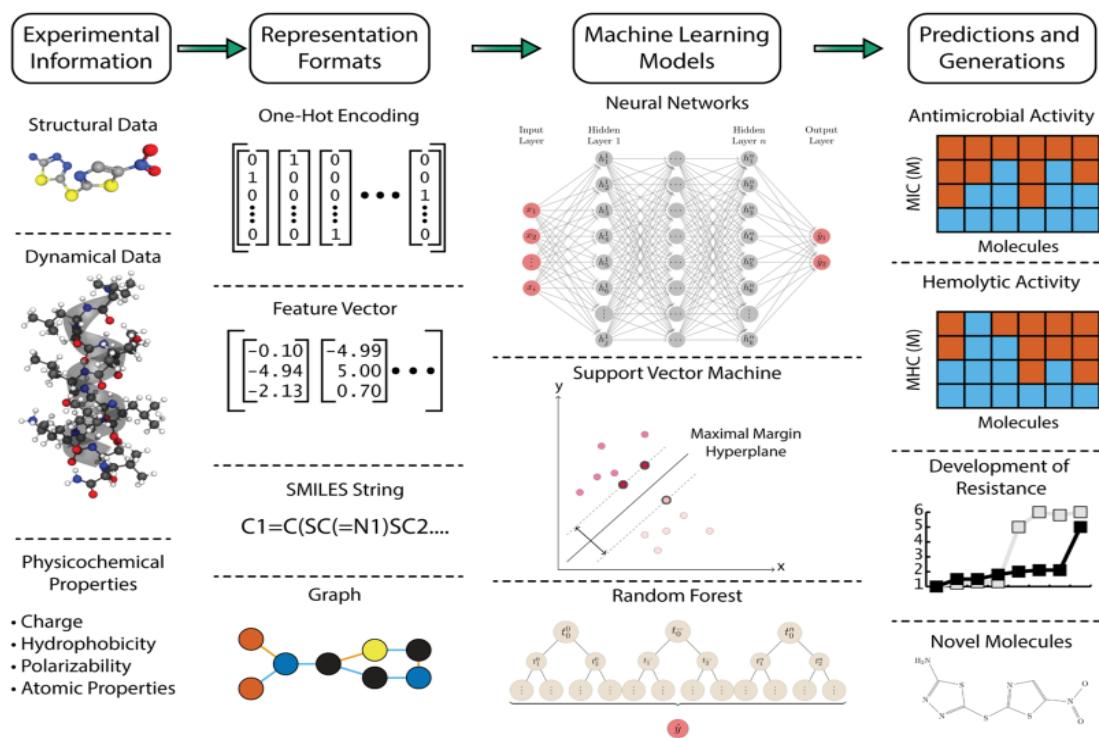
## Results and Discussion

Two of the most frequent methods that doctors employ to diagnose antimicrobial resistance (AMR) are now being used by clinical microbiologists. The first way is conventional culture-based testing, and the second method is the whole-genome sequencing method. Both of these methods are suitable for assessing antibiotic susceptibility. There is a shorter amount of time required to get results when using the culture-based method, but it is more uncomplicated. This may result in antibiotic treatments being delayed, which in turn raises the probability that the therapy will fail or that bacteria may acquire resistance to the antibiotics now being administered. In one technique, the amount of time needed to assess the susceptibility of bacteria has been decreased to less than three hours, while in another method; the required time has been cut to

only thirty minutes [18,19]. It has been possible to speed up the testing procedure with the use of machine learning (ML). It is important to note, however, that these machine-learning approaches need highly trained personnel as well as expensive equipment. It is feasible to identify microbes in a short period and at a cheap cost by combining matrix-assisted laser desorption/ionization with time-of-flight mass spectrometry, which is better known by its acronym, MALDI-TOF MS. Recent studies [20-21] are investigating the possibility of using it in combination with machine learning to determine the presence of antibiotic resistance in clinical illnesses. The Food and Drug Administration (FDA) has given its clearance to a number of MALDI algorithms that are based on machine learning with the aim of identifying microorganisms [21]. It is possible to evaluate

antimicrobial resistance (AMR) using reference methods such as the Kirby-Bauer disk-diffusion and microdilution antibiograms [22]. In spite of the fact that they are effective, they require a significant amount of time, and they do not assist medical practitioners in picking the proper antibiotic in a

timely setting. For the purpose of maximizing the use of antibiotics and minimizing the risk of antibiotic resistance, it is vital to have diagnostic tests that are not only rapid and accurate but also economical [20, 22].



**Figure 3: Shows the antibiotic screening methods using machine-learning principles [24]**

For more than half a century, researchers have been making efforts to discover the most effective methods for predicting the efficacy of new medications. It is possible for them to do this by using computers to create predictions about the activity of these new molecules. This may save both time and money since it eliminates the need to produce and test a large number of distinct compounds. For the purpose of doing this, scientists make use of computer models to depict these molecules. However, accurately defining molecules in a manner that computers can comprehend is a complex task. This may soon become overwhelming due to the fact that there are many different methods to characterize molecules. When it comes to simple amino acid residues, which are the fundamental components of proteins, there are over 400 distinct methods to define them. When describing the structure and characteristics of small-molecule medications, scientists use a variety of different methodologies. Having said that, it is only feasible to use some of these distinct names. In order to simplify these descriptions and ensure that they include the most essential information, scientists have devised methods to integrate them. With this information, they are able to make more accurate

predictions about how well these molecules will function [25-30].

In the pursuit of clear and insightful representations, machine learning (ML) tools and principles have completely replaced more conventional approaches such as principal component analysis (PCA) and singular value decomposition. In the following examples, we will see how improvements in machine learning theory and methodology may be adapted to enable the development of antibiotics powered by machine learning. One significant illustration of this is the use of graph convolutional networks, which allow neural networks to learn directly from the chemical structure itself [31]. These networks make use of the geometry and linkages of molecules, transforming them into graphs. This methodology has also been used for the purpose of analyzing and forecasting the structures of proteins [32]. Not only may neural networks enhance the process of defining a medicine based on molecular descriptors, but they can also improve the determination of these descriptors, according to a thorough benchmark, analysis performed using existing methodologies and datasets [33]. This study was expanded to include the prediction of a number of antimicrobial compounds that were accurately

recognized as active regardless of the fact that they were structurally distinct from antibiotics that are already in use [24].

When it comes to signal processing and natural language processing (NLP), recurrent neural networks (RNNs) are a popular tool. However, they have been modified to handle simplified molecular-input line-entry system (SMILES) representations of chemical structures. These representations encode structures by utilizing simple text strings. Researchers made use of long short-term memory (LSTM) generative neural networks in one of their studies [34], which allowed them to learn from SMILES representations of existing medications and build novel molecules. Alternately, reinforcement learning has been integrated with recurrent neural networks (RNNs) in order to generate an embedded representation for pharmaceuticals that is based on their SMILES representations [35]. As a result of its capacity to analyze sequence-based inputs, RNNs have been shown to be effective for antimicrobial peptide (AMP) sequences. A multiplicative LSTM neural network and an LSTM-based auto-encoder have both been trained to construct embedded representations for peptide sequences [36]. This training was accomplished by using a one-hot encoding of amino acid residues. An embedded representation was produced as a consequence of the latter, which was capable of determining the secondary structure of a protein, its thermal stability, the categorization of deep mutational scanning, and even the functional effect of mutations [37]. Predicting antimicrobial activity is essential to incorporating machine learning into the process of developing antibiotics. This has been the driving force behind more than a decade of effort to solve the quantitative structure-activity relationship (QSAR) issue. [38] This region has been the subject of a number of investigations. Take multinomial logistic regression as an example. It was used to identify molecular fragments in a training set, which improved upon earlier attempts to develop novel medications by studying chemical fragments and their attributes [39]. Through the use of this method, a "vocabulary" of fragments was established, which could be assembled in order to suggest novel medicines that are efficacious towards the Gram-negative bacteria *Pseudomonas aeruginosa* [24], [40].

The use of artificial intelligence (A.I.) in the process of detecting and analyzing bacteria has entirely revolutionized the sector, making the process both more efficient and reliable than the conventional approaches. In order to assist scientists and medical professionals in identifying germs, predicting how they could resist drugs, and even discovering new forms of germs, artificial intelligence systems can evaluate genetic data. Through the rapid discovery of intricate patterns in data, machine learning may

also increase the speed and accuracy of the process of recognizing germs. The use of this technology has become an indispensable instrument for the study of germs, as it enables the identification of patterns, the formulation of predictions, and the enhancement of the efficiency of germ analysis. Through the analysis of vast quantities of germ data, artificial intelligence has revolutionized the game by identifying patterns and distinctions that would be difficult for humans to recognize in a timely and precise manner. It is incredibly vital to have the capacity to notice patterns in order to swiftly identify infectious illnesses and to get knowledge of how viruses travel, which enables us to create more effective methods to prevent their spread.

Additionally, artificial intelligence is essential for creating predictions, using historical data to speculate on how bacteria could behave in the future and assisting us in making better decisions. This capacity for prediction is essential for determining when infections can spread, comprehending the process by which bacteria develop resistance to medications, and creating more effective treatment strategies [42]. For instance, machine learning can examine the genetic codes of bacteria and viruses to make educated guesses about the likelihood that these organisms may evolve and become resistant to specific therapies, assisting medical professionals in selecting the most appropriate treatments [42]. In addition, A.I. may speed up processes such as the preparation of samples, the analysis of pictures, and the comprehension of data. Not only does this let the process of detecting diseases go more quickly, but it also enables medical professionals to concentrate on the most crucial aspects of patient care [41,43].

The use of artificial intelligence in the detection of germs is not only altering the way that physicians operate, but it is also transforming the way that we discover new treatments. Using artificial intelligence, researchers are able to identify potential targets for medications, enhance the process of drug development, and uncover novel strategies to combat diseases. A.I. has a significant influence on the process of identifying targets by analyzing the genes and proteins of microorganisms and the way in which they function. By making educated guesses about how effectively certain medications could bind to microbial targets, machine learning helps speed up the process of developing new treatments. This, in turn, speeds up the process of selecting which compounds to test in studies. By analyzing the effects that pharmaceuticals have on the body, artificial intelligence may also assist in the discovery of novel applications for current medications. By doing data analysis, artificial intelligence may locate pharmaceuticals that have previously been authorized for use in the treatment of infections. This saves time in comparison to the process of generating new therapies. The ability to forecast

how medications flow through the body and how they function is another benefit of artificial intelligence [44].

Artificial intelligence modelling has the potential to lessen the severity of adverse effects, determine optimal dosages, and ensure that medications are safe, effective, and available for clinical testing. A further use of artificial intelligence is the prediction of how microorganisms can grow resistant to medications by analyzing their genomes. This helps to create medications that are less prone to produce resistance, which in turn makes them more potent and increases their duration of action. The identification of potential therapeutic targets Artificial intelligence looks at the genes and proteins of microorganisms and analyzes how they function in order to identify potential drug targets. This helps to speed up the process of developing new treatments by making educated guesses about how effectively certain pharmaceuticals could adhere to microbial targets. This gives researchers a better idea of which compounds to try in tests. A repurposing of drugs to uncover pharmaceuticals that may be used for new reasons, such as treating infections, artificial intelligence leverages what we already know about current medications and how they function. When compared to the process of creating new medications, this saves time. A modelling approach for pharmacokinetics and pharmacodynamics the application of artificial intelligence allows for the prediction of how medications flow through the body and how they function. Artificial intelligence modelling has the potential to lessen the severity of adverse effects, determine optimal dosages, and ensure that medications are safe, effective, and available for clinical testing. Artificial intelligence examines the DNA of bacteria in order to make predictions about the methods by which they can develop resistance to treatments. This contributes to the production of pharmaceuticals that are less prone to produce resistance, which in turn makes them more effective and last for a longer period of time [44].

Rapid advancements in the use of A.I. in the diagnosis of microorganisms provide exciting new possibilities for healthcare reform. Having said that, it does bring up some moral questions. There is a risk of hacking and exploitation of healthcare data originating from places like bioinformatics, genetic testing, and social media. Healthcare professionals' general accountability, data security, accessibility, algorithmic biases, and patient's right to privacy are all examples of such ethical concerns. Due to their reliance on massive datasets that may include personally identifiable information (PHI), A.I. systems raise serious concerns about patient privacy. Obtaining informed permission from patients before utilizing their data for A.I. diagnoses is crucial to protect their privacy. To ensure the ethical use of data, it is necessary to strike a balance between

protecting patient names via anonymization and retaining therapeutic relevance. It is possible that A.I. has biases related to culture, language, and other characteristics, which might affect the inclusion of specific patients in healthcare records. As a result, automated services may end up being inconsistent. One example is the possibility of gender and racial biases manifesting themselves in natural language processing. Strong protocols for identifying and managing biases are required of healthcare organizations and developers. New worries over data security have emerged with the proliferation of linked systems and cloud-based data storage. Ethically, it is vital to prevent cyberattacks and illegal access to patient data. In order to keep patient data secure, healthcare companies and developers of A.I. should put money into cybersecurity measures, encryption, and compliance with privacy regulations [44].

Understanding how A.I. arrives at diagnostic conclusions is crucial for both patients and physicians. Ethical guidelines advocate for A.I. models to be transparent and provide rapid explanations for their forecasts. As a result, medical practitioners will have more faith in A.I. recommendations and be able to employ them with more ease. Guaranteeing universal access to AI-powered diagnostic tools is a moral imperative. Healthcare providers should make an effort to bridge the digital divide so that low-income areas may have access to cutting-edge A.I. diagnoses. People with impairments should also be considered in AI-driven healthcare solutions to provide equal access to healthcare. Artificial intelligence (A.I.) has the potential to enhance the precision of diagnoses, but it should not replace human doctors. Ethical practice and patient safety need a balance between AI-driven automation and human intellect. The onus for patient care rests squarely on the shoulders of healthcare personnel; A.I. just supplements and improves upon expert medical judgment. Artificial intelligence (A.I.) diagnostic tools will become more important as computing power and machine learning capabilities increase. By rapidly detecting infections—including novel and drug-resistant strains—A.I. systems have already revolutionized disease treatment. People may one day be able to monitor their vitals and identify infectious illnesses caused by microbes as they happen. As A.I. becomes more integrated into vaccine research, antibiotic resistance, and epidemiological monitoring, it will enhance our capacity to address infectious disease outbreaks. Medical professionals anticipate that artificial intelligence (A.I.) in microbiological diagnosis will play an increasingly important role in the future of healthcare thanks to its ability to provide precise and individualized diagnoses, safeguard patient data, and promote universal access to cutting-edge medical technology [44].

Plants and animals have naturally occurring compounds called antimicrobial peptides (AMPs) that aid in the defence against bacterial infections. They help the body fight off harmful germs by destroying their cell walls or disrupting their metabolic activities [46]. Because bacteria have not evolved a broad resistance to AMPs, they may be particularly useful in the battle against illnesses, even though they have been around for millions of years [46]. Horseshoe crabs contain polyphemusin I, one of the strongest naturally occurring AMPs. Nevertheless, AMPs synthesized in a lab tend to be more powerful than their natural counterparts, and some chemicals in the body may even reduce the potency of natural AMPs [47]. Scientists are always exploring novel methods to increase AMPs, whether by changing their structure or using A.I. to create peptides with better antibacterial capabilities [47]. Through analysis of the peptide's amino acid interactions, A.I. may aid in the identification of peptides with improved antibacterial activity. This method takes into account the impact of amino acids on the peptide's overall structure, which is crucial to its function [47]. To further understand the efficacy of AMPs, A.I. may model their molecular

interactions with bacteria [47]. One further A.I. method that might assist in finding potential AMP candidates in huge datasets is virtual screening. Using computer algorithms, this technique selects compounds with the highest probability of being effective against bacteria, improving the likelihood of discovering novel antimicrobial drugs [48]. The database RiPPquest, which uses mass spectrometry to unearth novel AMPs, is an instance of an effective use of A.I. in AMP research. Informatipeptin is a new antibacterial peptide that RiPPquest discovered by analyzing genetic data [49]. There is hope for combating infections by combining AMPs with antibiotics. Recent research has shown that some bacteria, such as *Pseudomonas aeruginosa* and methicillin-resistant *Staphylococcus aureus* (MRSA), maybe more effectively treated by combining antibiotics with aminopeptidases (AMPs) [50]. Although AMPs show great promise, they do come with certain drawbacks, including toxicity, administration issues, high manufacturing costs, and worries about bacterial resistance. To overcome these obstacles and make AMPs a practical choice for addressing bacterial infections, researchers are hard at work [45-46].

**Table 2: Summary of Analysis**

Topic	Summary
<b>Diagnostic Methods</b>	ML has sped up bacterial susceptibility testing, reducing time to results. MALDI-TOF MS with ML is evaluated to detect AMR. ML-based MALDI algorithms, like the MALDI Biotyper CA System, are FDA-approved. Kirby-Bauer disk-diffusion and microdilution antibiograms are reference methods. Rapid, accurate, low-cost tests are needed for optimal antibiotic use and reducing AMR risk [18-22].
<b>Drug Prediction and Development</b>	A.I. predicts drug activity by analyzing molecules, saving time and money. Methods like PCA and neural networks are used. Graph convolutional networks and LSTM generative neural networks are applied for drug design. A.I. improves QSAR studies and antibiotic development [24-25, 30-40].
<b>A.I. in microbe study</b>	A.I. analyzes genetic data to identify and predict germs, aiding in understanding diseases. A.I. speeds up drug development, finds new drug uses, and predicts resistance mechanisms. A.I. is crucial for prospective therapeutic target identification, drug repurposing and pharmacokinetic/pharmacodynamics modelling [41-44].
<b>Ethical considerations</b>	A.I. raises concerns about patient data privacy, algorithm biases, data security, and healthcare access. Ethical guidelines are crucial for A.I. diagnostics. Balancing privacy and clinical relevance is important. A.I. biases need recognition and management. Data security is necessary [44].
<b>Antimicrobial peptides (AMP)</b>	AMPs are natural substances that protect against bacterial infections. A.I. is used to improve AMPs by designing peptides with enhanced antimicrobial properties. Virtual screening and database analysis help identify promising AMP candidates. Combining AMPs with antibiotics enhances effectiveness [45-49].

## Conclusion

The use of A.I. is changing how we diagnose infections, making it faster and more accurate. It helps us detect pathogens quickly, find antibiotic resistance early, and improve our diagnostic methods. A.I. is also crucial for spotting diseases

early, developing new drugs, personalizing treatments, and detecting outbreaks sooner. Because of this, public health and healthcare have gotten much better. However, as A.I. becomes more involved in medical decisions, we need to think about things like keeping patient information private, making sure A.I. is fair, keeping data safe,



being clear about how A.I. works, making sure everyone can access A.I. tools, and having humans oversee A.I. decisions. With more advancement in A.I. for diagnosing infections, we can expect even better ways to treat and prevent diseases in the future while also making sure healthcare practices are ethical and fair.

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