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ROLE OF ARTIFICIAL INTELLIGENCE IN BACTERIAL DIAGNOSIS

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Diagnosis is an important aspect in healthcare and is important in the identification of microorganisms responsible for infections and disorders. In the bacterial diagnostics field, artificial intelligence (AI) systems can be utilised to improve illness management, medication discovery, prediction of antibiotic resistance and epidemiological surveillance. Artificial intelligence systems may detect infections fast and accurately. Also, the development of AI programs for bacterial testing is important to reduce diagnostic errors and thus to provide adequate therapy. This paper intends to explore the function of AI in diagnosing harmful bacteria and to highlight the most reliable AI programs available. The report also discusses the major problems we have in applying AI to the diagnosis of harmful bacteria. AI has brought in the high motive in the bacterial prognosis by providing better instruments that surpass several barriers of the conventional tactics. AI-based totally approaches, especially in automated photo evaluation, colony counting, genome sequencing, phylogenetic evaluation, and immunological diagnostics, have substantially advanced the rate, accuracy, and reliability of pathogen identification. "These technologies minimise the need for guide interpretation and allow for more standardised, efficient lab workflows". In the future, the ongoing improvement and integration of AI technology are anticipated to convert bacterial diagnostics into a greater fast, precise, and on hand procedure, strengthening healthcare structures and advancing global public health.

Keywords: *Artificial Intelligence, Bacterial infections, Diagnosis, Deep learning, Machine learning.*

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1. INTRODUCTION

Infections caused by bacteria continue to be a major problem for medical and public health in the 21st century, resulting in the deaths of millions of patients annually. Bacterial infections are one of the leading causes of global health loss and the second leading cause of death worldwide, after ischemic heart disease, according to a study that was published in The Lancet on November 21, 2022 [1]. It is essential to quickly and accurately identify pathogens and their drug susceptibility profiles in order to select the appropriate treatment and reduce mortality. However, due to the long-term use of broad-spectrum antibiotics, most current bacterial identification and drug susceptibility testing require culture times of several days, which not only delays treatment initiation but also increases the risk of the development of resistant bacteria [2,3]. In order to safeguard public health and prevent their

spread, surveillance and management of bacterial infections are simultaneously essential. The medical community is urgently looking for new methods and tools to combat bacterial infections. A novel approach to treating bacterial infections is provided by the development of artificial intelligence technology [4]. The diagnosis and treatment of bacterial infections have recently shown great promise thanks to AI, a potent computational tool. AI is a field of study and technology that uses computers to imitate human intelligence, including cognitive abilities and decision-making processes [5]. Machine learning, particularly deep learning, natural language processing, computer vision, the knowledge graph, robotics, and other related terms ought to be the primary focus in medicine. [5,6]. The widespread application of AI is anticipated to fundamentally transform the management, diagnosis, and treatment of bacterial infection [7]. In addition, AI supports the research and development of new drugs, vaccines, and innovative therapies, thereby promoting the development advancement of personalized medicine. The fast development of artificial intelligence (AI) technology has made it possible to improve the epidemiological surveillance, to speed up the detection of pathogens

and to anticipate the sensitivity of bacteria to antimicrobial drugs [8]. This study aimed to examine how AI technology can improve the efficiency and accuracy of medical diagnosis of bacterial infections, as well as the level of personalized treatment, while focusing on the obstacles that may hinder its practical clinical application. It was based on a comprehensive analysis of the existing literature and the most recent research results. This will primarily give medical professionals a comprehensive understanding of how AI technology is used to diagnose bacterial infectious diseases, work together to promote AI's use in the fight against bacterial infections, provide patients with medical services that are more accurate and efficient, and help advance global public health.

2. DIFFICULTIES WITH CONVENTIONAL BACTERIAL DIAGNOSIS

One of the most important aspects of modern medicine and bacterial diagnosis faces difficulties throughout the entire procedure. A major initial obstacle is obtaining and transporting samples [9]. The initial step is to collect clinical specimens. However, it is extremely difficult to guarantee that clinical samples are collected correctly and transported to the laboratory in a timely manner. The risk of the viability and integrity of the microorganisms in the sample being compromised by improper handling, storage, and transport delays can result in inaccurate diagnostic results [10]. As a result, the primary traditional diagnostic method is microorganism culture and isolation. This process takes a long time to generate culture. False negative results may be obtained if the bacteria are not properly cultivated. Excessive use of antibiotics in clinical practice can further impair growth and isolation of certain organisms [11].

Another major challenge is reliable identification and classification of bacterial species. Microorganisms possess deceptive physical traits or unusual behaviours that may not always be detected by conventional procedures such as biochemical testing and microscopy [12]. It is also hard to figure out how susceptible bacterial isolates are to antibiotics when choosing a treatment. Time-consuming and sometimes requiring precise predictions of the infecting strain's response to antibiotics, traditional susceptibility testing methods like disk diffusion [13] can lead to poor treatment choices and potential therapeutic complications. To diagnose medical conditions, traditional methods frequently necessitate a team of highly skilled personnel, specialized equipment, and significant resources. Due to the reliance on skilled professionals, environments with limited resources are more susceptible to human error. As a result, it is crucial to develop new and user-friendly diagnostic methods [14]. Traditional bacterial diagnosis frequently delays the first phase of treatment, allowing diseases to progress unchecked due to delayed results [15]. Empirical therapy increases antibiotic resistance, but traditional methods detect microorganisms, leading to

misdiagnosing emerging pathogens [16]. It is more difficult to perform conventional diagnosis because it is susceptible to cross-contamination and false positives. Due to the possibility of cross-contamination, traditional bacterial diagnosis may not provide sufficient real-time data for efficient epidemiological surveillance. Serological tests may return false-positive results as a result [17]. In diagnostic laboratories, inconsistent results that are less accurate and consistent may result from the absence of standardized procedures and quality measures [18].

Table 01: Comparison between conventional bacterial diagnostic methods and artificial intelligence-assisted approaches

Diagnostic criterion	Conventional methods	AI-assisted approaches	References
Turnaround time	Culture and susceptibility testing usually require several days	Results obtained within hours; sputum analysis reduced tuberculosis diagnosis from weeks to hours	[2,3,21]
Species identification	Biochemical tests and microscopy may fail with atypical or misleading morphology	Deep learning models classify morphology, arrangement, texture and colour beyond visual perception	[12,47,49]
Colony counting	Manual counting of a limited field; contaminants counted with target colonies	Automated counting of 100% of the plate with about 25% improvement in accuracy and exclusion of contaminants	[23,24]
Susceptibility testing	Disk diffusion and phenotypic assays are slow and	Machine learning predicts resistance from k-mer pattern	[13,56,57]

	may mispredict response	s, gene mutations or growth images	
Operator dependence	Requires highly skilled personnel; prone to human error in low-resource settings	Standardised automated interpretation reduces reliance on individual expertise	[14,52]
Reproducibility	Variable results due to absence of standardised procedures	Consistent, protocol-independent outputs once models are validated	[18,53]
Epidemiological use	Limited real-time data for surveillance	Genomic and epidemiological data integrated for outbreak tracking in near real time	[17,35,41]

3. ARTIFICIAL INTELLIGENCE AND ENHANCEMENT BACTERIAL DIAGNOSTICS

Artificial intelligence is becoming a major driver behind a paradigm shift in bacterial detection, especially in infectious diseases, amid the wave of digital revolution changing healthcare [19]. AI-powered diagnostic tools have proven to be very beneficial in identifying and tracking infectious diseases, particularly in terms of increasing diagnostic speed, accuracy, and accessibility. These devices apply machine learning methods such as convolutional neural networks and deep learning to provide great sensitivity and accuracy for detection of a wide spectrum of hazardous bacteria [20]. They are generally utilised at the site of wearable sensor platforms for fast screening. The success of AI-powered diagnostic tools in restricted resource settings has been excellent. For instance, in India, the combination of AI-powered sputum analysis with telemedicine reached 92% sensitivity in diagnosis of tuberculosis and reduced the diagnostic time from weeks to hours [21]. Mobile devices based on convolutional neural networks have achieved great sensitivity in Sub-Saharan Africa. AI-enhanced diagnostic technologies have improved the identification and management of infectious diseases by giving exceptionally accurate, rapid, and widely available testing capabilities, which have proved to be of

essential practical utility notably in settings with limited resources [19]. However, tackling concerns around device reliability, connectivity and constant user education is key for their sustainability. [22].

4. KEY ROLES OF AI IN BACTERIAL DIAGNOSIS

Artificial intelligence is still evolving its role in the diagnosis of bacteria and research in this field is moving at a fast pace. AI tackles the diagnosis from different points of view and we will focus in this study on the following major points:

4.1. Role Artificial Intelligence in Bacterial Colony Counting

A number of AI programs, most notably Scan AI, which offers unmatched performance and ongoing development potential, have been employed to count germs in order to assess the severity of diseases [23]. For the automated counting of bacterial colonies in labs, it is at the forefront of technical developments. Counting accuracy is consistent and about 25% better with AI capabilities compared with conventional counting techniques. 100% of the culture plate is counted by the automatic count, which ignores contaminants. AI recognizes and precisely counts colonies, differentiating between several microorganisms that contaminate the bacterial culture, including molds and yeasts [24]. In its most recent iterations, Scan AI incorporates new AI models (figure 1), such as MobIA, a cutting-edge new Scan AI technology created especially for mold classification. This technique improves the clarity of data and supports laboratory and quality control decision-making by enabling the automatic detection and classification of spore types based on image analysis [24,25]. Learn about the TSC AI model on Scan Ai, which is intended to count anaerobes that reduce sulfite.

This instrument is specifically made to count sulfite-reducing anaerobes and provides quality control through automated analysis and consistent results reading [26]. Scan Ai provides a model specifically designed to identify *Listeria monocytogenes* with Compass *Listeria*® AI. In compliance with regulatory regulations, this approach helps monitor the health of products and industrial settings. Another instance of artificial intelligence in action is the Perfecto Duo® AI model, which lists sulfite-reducing anaerobes and recognises *Clostridium perfringens* colonies on the same medium. It is a combination of two analytical functions [27,28] which allow to read and comprehend it.

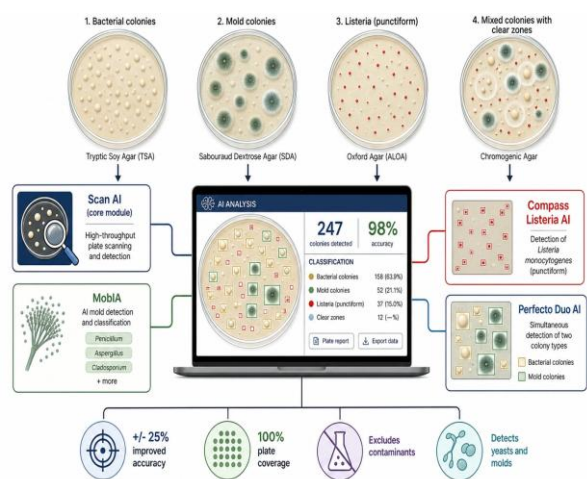


Figure 01: The role of artificial intelligence in bacterial colony counting and analysis

The main AI models currently embedded in automated colony-counting platforms are summarised in Table 2.

Table 02: Artificial intelligence models applied to automated bacterial colony counting and classification

AI model / platform	Target application	Principal function	References
Scan AI (core module)	Routine colony enumeration	Counts the entire culture plate, distinguishes colonies from contaminants and improves counting accuracy by about 25%	[23,24]
MobIA	Mould classification	Automatic detection and classification of spore types from plate images to support quality-control decisions	[24,25]
TSC AI model	Sulfite-reducing anaerobes	Automated enumeration with consistent reading and integrated quality control	[26]

Compass Listeria® AI	Listeria monocytogenes	Detection and monitoring of products and industrial environments in line with regulatory requirements	[27]
Perfecto Duo® AI	Clostridium perfringens	Simultaneous counting of sulfite-reducing anaerobes and detection of C. perfringens on the same medium	[27,28]
CNN-based counters	Research and reference laboratories	Convolutional networks and U ² -Net/ResNet 50 pipelines for high-throughput automated counting	[23,25,27]
Few-shot learning models	Limited-data laboratories	Edge-computing counting with small training sets, suitable for resource-limited settings	[26,28]

4.2. Role Artificial Intelligence in Gene Sequence and Phylogenetic Tree Identification

The advancement of bacterial diagnostics depends on the integration of gene sequencing and artificial intelligence (figure 2). According to recent research, machine learning algorithms can evaluate Next-Generation Sequencing data more quickly and precisely than conventional techniques [29]. According to a recent review research, AI not only aligns gene sequences but also classifies them, predicts gene functions, and uses a technique called resistome profiling to identify the genes that cause antibiotic resistance [30]. Deep learning methods can assess metagenomic data and identify bacterial species even in complicated samples, improving molecular diagnostics accuracy and speeding up turnaround times, according to another research [31]. On the other hand,

phylogenetic trees are now a crucial diagnostic tool for identifying germs and the cause of infection and are no longer just useful for understanding evolution. For instance, a study employing 16S rRNA sequencing showed that phylogenetic tree analysis can precisely diagnose bacterial species like *E. coli* and *Klebsiella pneumoniae* by accurately determining the relationship between bacterial isolates and reference strains with up to 99% accuracy. Additionally, phylogenetic analysis can trace the horizontal gene transfer of antibiotic resistance genes between strains, offering a deeper knowledge of resistance transmission, according to current whole-genome sequencing research [32,33]. Artificial intelligence has advanced even further in the creation and study of phylogenetic trees. Algorithms are able to automatically classify bacterial strains according to genetic similarity and examine complex genetic variants [34]. By connecting genetic data to epidemiological transmission, these methods also make it possible to track resistant bacterial strains and accurately identify the source of illness. Artificial intelligence and evolutionary analysis, particularly when paired with whole-genome sequencing data, have been demonstrated in recent applications to improve early diagnosis and epidemiological monitoring systems [35]. The combination of accurate pathogen identification, understanding of its evolutionary relationship, and prediction of its resistance behaviour by artificial intelligence, linking gene sequence analysis and evolutionary trees, is a qualitative leap in bacterial diagnostics. It increases the diagnostic accuracy and accelerates the decision for therapy when faced with antibiotic resistance [36]. Figure 02 [37] illustrates that biodatabases such as NCBI GenBank and SRA are basic building blocks in the construction of modern computer models for artificial intelligence research in genomics and infectious disease detection. SRA has a lot of high throughput raw data generated from clinical and environmental sequencing. GenBank has a lot of library of annotated genomic sequences from different diseases including bacteria. These sources are the training and testing basis for AI models with algorithms for critical tasks such as the accurate classification of metagenomic data, rapid detection of harmful bacteria and the detection of antibiotic resistance genes [38]. Machine learning techniques have been integrated into genetic databases, disrupting genomic analysis, as they allow computers to evaluate huge amounts of complex data and uncover trends that are not visible using traditional methodologies [39]. SRA data are used to assess epidemics and monitor genetic changes almost in real time, modern genomic classification approaches are based on comparison with GenBank databases for rapid identification of bacterial species. Besides, even with limited genome coverage, AI models have surpassed the limitations of conventional methods that rely exclusively on sequence similarity, resulting in the identification of novel bacterial species and the prediction of their hazardous properties [40]. Hence, the merging of AI and genetic databases is essential for

accurate diagnosis, improved surveillance of antibiotic resistance and rapid public health responses. [41]. Through evaluating and forecasting the health effects of Shiga toxin-producing *Escherichia coli* infections, machine learning algorithms have demonstrated their promise in processing vast genomic data, offering fresh approaches and viewpoints for microbial risk assessment [42]. Furthermore, the analysis of genetic association studies was accelerated and variant strains of infection were accurately and rapidly identified by Bayesian neural networks employing a nonparametric Bayesian approach. Excellent performance in predicting pathogen resistance has been demonstrated by combining machine-learning models with genomics technology, which is far better than current approaches [43]. A knowledge map of antimicrobial resistance in *Escherichia coli* has been created by certain researchers using machine learning. This map identifies unknown drug resistance genes and accomplishes the automatic finding of knowledge of antimicrobial resistance in *Escherichia coli*. In addition to correctly predicting the minimum inhibitory concentrations of *Klebsiella pneumoniae* clinical isolates against 20 antimicrobial drugs, the researchers were able to identify strains with high virulence or drug resistance using the XGBoost and convolutional neural network approaches [43,44]. In a similar vein, some researchers have developed a decision tree method called Treesist-TB for identifying mutant strains and predicting drug resistance, which has a recognition ability beyond the current TB-Profiler tools. This technique not only shows the usefulness of decision trees in the field of tuberculosis but also offers a reference template for identifying other drug-resistant pathogens. AI has demonstrated significant promise in the field of genome sequencing [45].

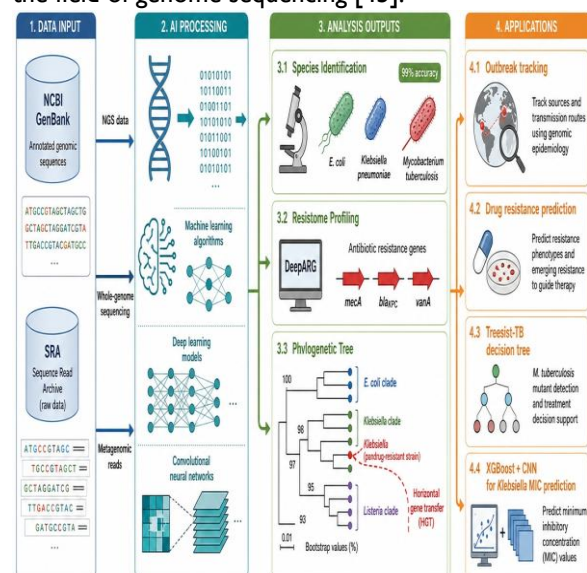


Figure 02: Role AI in analysis genes sequences and identification of phylogenetic tree of infectious bacteria Representative artificial intelligence tools used in genomic analysis, phylogenetic identification and resistance-gene detection are listed in Table 03.

Table 03: Artificial intelligence applications in bacterial gene sequence analysis, phylogenetics and resistome profiling

Approach / tool	Data source	Diagnostic task and reported outcome	References
Machine learning on NGS data	Whole-genome and metagenomic reads	Faster and more precise evaluation than conventional pipelines; species identification in complex samples	[29,31]
DeepARG and related deep models	Metagenomic sequences	Prediction of antibiotic resistance genes (resistome profiling) without prior isolation	[30]
16S rRNA phylogenetic analysis	Ribosomal gene sequences	Discrimination of <i>E. coli</i> and <i>Klebsiella pneumoniae</i> from reference strains with accuracy reported up to 99%	[32,33]
Whole-genome phylogenomics	Complete bacterial genomes	Tracing horizontal transfer of resistance genes and linking genotype to transmission chains	[33,35,41]
GenBank / SRA-trained models	Public genomic repositories	Training and benchmarking of classifiers for pathogen identification and	[37,38,39]

		resistance-gene detection	
XGBoost and CNN models	<i>Klebsiella pneumoniae</i> isolates	Prediction of minimum inhibitory concentrations against 20 antimicrobial agents and detection of hypervirulent strains	[43,44]
Treesist-TB decision tree	<i>Mycobacterium tuberculosis</i> genomes	Identification of mutant strains and drug-resistance prediction exceeding current TB-Profiler performance	[45]
Bayesian neural networks	Genetic association datasets	Accelerated identification of variant infectious strains and microbial risk assessment	[42,43]

4.3. Role Artificial Intelligence in Automated Image Analysis

One of the most significant current uses of AI in the identification of infectious microorganisms is automated bacterial image analysis. Intelligent devices that can quickly and accurately analyze microscopic pictures and culture plates have replaced traditional, error-prone visual inspection in laboratory operations [46]. In order to extract morphological patterns like shape (cocci or bacilli), arrangement, size, and density, as well as subtle color and textural features that are difficult to see with the unaided eye, these systems mainly rely on deep learning techniques, specifically convolutional neural networks that are trained on a large number of bacterial images [47]. Digital picture capture is the first step in the analysis process, which is then processed to enhance quality and eliminate noise. Then, using sophisticated methods like AI-based segmentation, bacterial cells or colonies are separated from the backdrop [48]. Lastly, pre-trained deep learning models are used to extract and classify unique

features. Research has shown that these technologies, whether using Gram staining or measuring colony growth on culture media, can diagnose bacteria with a high degree of accuracy. They are able to recognize various species, count colonies, and reduce human involvement in the assessment process [48,49]. Based on morphological and histological alterations, in figure 3, several methods may even forecast the type of bacteria and perhaps drug resistance. Additionally, real-time monitoring of bacterial growth and tracking its dynamics over time are made possible by the integration of these technologies with automated laboratory equipment and high-resolution digital imaging sensors [50]. This is essential for researching bacterial resistance and assessing the effectiveness of antibiotics. By offering quick and accurate results that make it easier to choose the best course of action for each patient, the application of artificial intelligence in this field further supports the idea of precision medicine [51]. Additionally, it contributes to reducing long-term operational expenses and enhancing laboratory efficiency, particularly considering the global shortage of microbiologists [52]. However, there are challenges include the need for large, diverse and highly precise datasets, the need to standardise imaging and culture techniques to minimise laboratory variation, and issues of model explainability and reliability. Knowing how models make decisions is important in healthcare settings [53]. To summarise, this sector, which combines digital technology with medical diagnostics, represents a huge step forward in pathogenic microbiology in general and bacteriology in particular.. With the advancement of AI technologies and their growing incorporation into contemporary healthcare systems, more growth is anticipated [54].

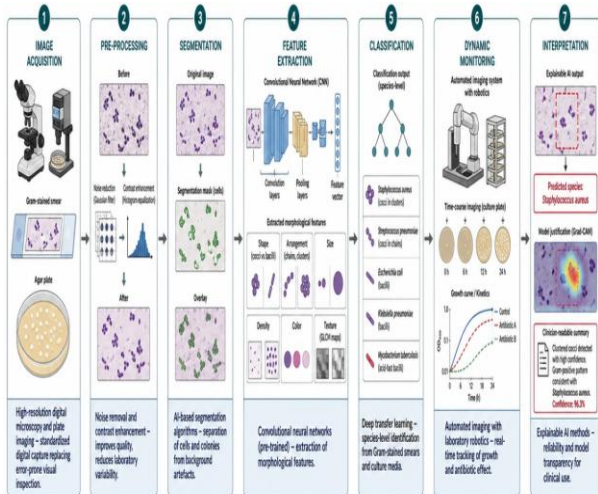


Figure 03: Schematic representation of the Automated Bacterial Image Analysis workflow using deep learning models for microbial classification

The deep learning architectures most frequently reported for automated bacterial image analysis, together with their inputs and outputs, are presented in Table 04.

Table 04: Deep learning approaches used in automated bacterial image analysis

Processing stage	Technique applied	Function and diagnostic value	References
Image acquisition	High-resolution digital microscopy and plate imaging	Standardised digital capture replacing error-prone visual inspection	[46,50]
Pre-processing	Noise removal and contrast enhancement	Improves image quality and reduces laboratory-to-laboratory variability	[48]
Segmentation	AI-based segmentation algorithms	Separation of bacterial cells and colonies from background artefacts	[48]
Feature extraction	Convolutional neural networks (pre-trained)	Extraction of shape (cocci or bacilli), arrangement, size, density, colour and texture features	[47,49]
Classification	Deep transfer learning models	Species-level identification from Gram-stained smears and growth on culture media	[46,49]
Dynamic monitoring	Automated imaging integrated with laboratory robotics	Real-time tracking of growth kinetics and antibiotic effect	[50,51]
Interpretation	Explainable AI methods	Addresses reliability and model	[53,54]

		transparen cy required for clinical use	
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4.4. Artificial Intelligence and Antibiotic Susceptibility Testing

Antibiotic susceptibility testing (AST) and bacterial resistance prediction both heavily rely on artificial intelligence. It uses phenotypic and genetic data analysis to provide highly accurate predictions about how bacteria will react to drugs [55]. This theory has been validated by a number of recent research. Whole genome sequencing research showed that resistance prediction using machine learning algorithms is based on the analysis of k-mer patterns and gene mutations [56]. Studies with algorithms such as Random Forest and Support Vector Machine have shown a high degree of accuracy in predicting resistance in bacteria such as *Staphylococcus aureus* and *Escherichia coli*. Other investigations have also shown that deep learning techniques, especially convolutional neural networks, can evaluate images of bacterial growth in culture media or even microscopic images to determine antibiotic susceptibility in hours rather than days, thus enhancing the speed and precision of clinical diagnosis [57,58]. Furthermore, artificial intelligence can predict resistance from complex samples directly without the need for bacterial separation, representing an important leap in rapid diagnosis as demonstrated in the metagenomics research [59]. Despite these results, most research agree on common concerns, such as the need for large, high-quality datasets, the problem of generalising models to other settings, and the limitations of interpreting some deep learning models. However, using artificial intelligence with conventional lab methods is a promising way to increase AST speed and accuracy while slowing the spread of antibiotic resistance [60].

Table 05: Machine learning models applied to antibiotic susceptibility testing and resistance prediction

Model / algorithm	Input data	Reported diagnostic performance	References
Random Forest and Support Vector Machine	Whole-genome sequences	High accuracy in predicting resistance in <i>Staphylococcus aureus</i> and <i>Escherichia coli</i>	[56,57]
k-mer based machine learning	Genomic k-mer patterns and	Rapid genotypic prediction of resistance in	[56]

	mutations	clinical isolates	
Convolutional neural networks	Images of bacterial growth and microscopy	Susceptibility determination within hours instead of days	[57,58]
Deep learning on metagenomes	Direct clinical samples	Resistance prediction without bacterial isolation, overcoming the culture bottleneck	[59]
MALDI-TOF MS with machine learning	Mass spectra of isolates	Rapid detection of carbapenem-resistant <i>Klebsiella pneumoniae</i>	[4,5,6,7,8]
Raman spectroscopy with deep learning	Spectral fingerprints	Identification of resistance and virulence-encoding factors	[2]
Hybrid AI-laboratory workflows	Phenotypic and genotypic data combined	Improved speed and accuracy of AST and support for antimicrobial stewardship	[55,60]

4.5. Role Artificial Intelligence in Immunological Diagnosis of Bacterial Infections

With the development of AI technology, bacterial immunodiagnosis is making impressive strides. By examining immunological interactions such as antigen-antibody binding in figure 4, AI has made it possible to significantly increase the speed and accuracy of infection identification [61]. Conventional immunological techniques, such as lateral flow tests and Enzyme-Linked Immunosorbent Assay (ELISA), rely on limited measurements or visual interpretation, which may result in human error or decreased sensitivity [62]. However, the development of deep learning and machine learning algorithms has made it possible to identify patterns that are undetectable to the human eye and analyze complicated biosignals with extreme accuracy [63]. AI is particularly relevant to the analysis of immunological biosensor data. It can interpret signals generated by immune interactions, such as fluorescent or electrochemical signals, allowing for the early detection of bacteria even at very low concentrations [64]. Furthermore, integrating AI with engineered biosensors allows for improved design of

immunosensors and increased sensitivity and selectivity by modeling the relationship between molecular structure and biological response. Convolutional neural networks are also utilised to analyse images from immunological assays such as quick test strips or microscopic images [65]. - Automatic classification of results, less dependence on human expertise, thereby enhancing accuracy of diagnosis and minimising turnaround time. AI may also integrate immunological data with other data such as genomic or clinical data to provide a holistic view that can help in identifying the type of bacterium and predicting its drug resistance [66]. One of the greatest benefits of employing AI in immunodiagnosis is the possibility of creating fast, mobile diagnostic systems with smartphones or cloud platforms. This makes them appropriate for usage in resource limited contexts, and decreases human error, therefore boosting the accuracy of the results in real time [67]. However, the issues still exist including data quality, protocol standardisation, privacy assurance and the requirement to train models on varied datasets to ensure appropriate generalisations. The integration of AI and immunology tools, however, is ongoing, and has the potential to revolutionise bacterial diagnostics, resulting in better healthcare and more successful antibiotic resistance [68].

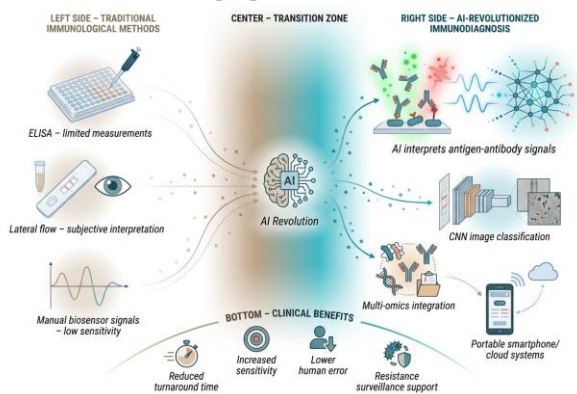


Figure (4): Schematic overview of the evolution from traditional immunological methods to AI-revolutionized bacterial immunodiagnosis and biosensor data analysis.

5. CHALLENGES FACING THE APPLICATION OF ARTIFICIAL INTELLIGENCE IN BACTERIAL DIAGNOSIS

One of the interesting breakthroughs in clinical microbiology is the application of AI for bacterial diagnosis. However there are various barriers which could limit its widespread use or reduce its efficiency in particular scenarios [70].

The first of these challenges is data quality and accessibility. Artificial intelligence (AI) systems, notably machine learning and deep learning, depend on large quantities of accurate, labelled data. In many laboratories, the bacterial identification is inaccurate because of incomplete or biased model training due to the missing or inconsistent data [71].

The second difficulty is the biological complexity and diversity of bacterial strains. Such AI models must be

flexible to the high genetic and phenotypic diversity of bacteria. Models could struggle to distinguish between closely related strains. Genome sequencing techniques generate complicated data that require skilled analysis [70]. Third is the difficulty of explainability. Many AI models, especially deep neural networks, are “black boxes” making it hard for clinicians to grasp how judgements are made. This reduces the trust of clinicians and impacts the acceptance of these systems in the practice of medicine [71].

The fourth challenge is infrastructure and expense. Implementing standard artificial intelligence (AI) systems involves complex technology, specialised software and qualified people. These conditions are difficult for many countries or laboratories with limited resources to fulfill [69]. A major challenge lies in the integration with existing lab systems. Common technologies are Polymerase Chain Reaction (PCR) and ELISA. The integration of AI in these technologies requires technological and organisational adaptations [72]. Finally, regulatory and ethical challenges such as protection of patient data, the acquisition of regulatory approvals, and the verification of accuracy of systems before to clinical usage. Also, the absence of standardised criteria globally can hinder the use of these technologies [73]. To summarise, despite the great potential of AI in improving the accuracy and speed of bacterial diagnosis, overcoming these challenges will require collaboration between researchers, clinicians and software engineers, as well as supportive policies and adequate infrastructure.

Table 06: Challenges and solutions of the clinical application of artificial intelligence in bacterial diagnosis

Challenge	Description	Proposed solution	References
Data quality and availability	Missing, inconsistent or biased datasets lead to inadequate model training	Multicentre curated and standardised image and genome repositories	[71]
Biological diversity	Wide genetic and phenotypic variation hinders discrimination of closely related strains	Training on genetically and phenotypically diverse isolates	[70]
Explainability	Deep neural networks act as black boxes,	Explainable AI methods producing clinician-readable	[71,53]

	limiting clinical confidence	justifications	
Infrastructure and cost	Sophisticated hardware, software and trained personnel are required	Cloud-based and smartphone platforms suited to low-resource laboratories	[69,67]
Workflow integration	PCR and ELISA platforms require technical and organisational adjustment	Middleware connecting AI engines to existing laboratory information systems	[72]
Regulation and ethics	Patient data protection, approval pathways and absent global standards	Harmonised validation criteria, governance frameworks and human oversight	[73,75]
Clinical adoption	Limited collaboration between laboratories, clinicians and developers	Joint clinician-engineer frameworks and supportive institutional policy	[74,75]

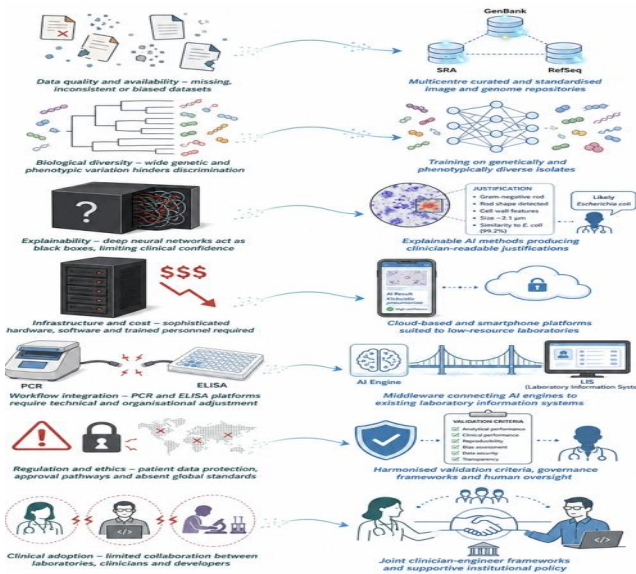


Figure 05: Principal barriers to the clinical implementation of artificial intelligence in bacterial diagnosis and the corresponding mitigation strategies proposed in the literature

6. CONCLUSIONS

Artificial intelligence is changing the diagnosis of bacteria, offering faster, more accurate and automated solutions that address the limits of traditional, time-consuming methodologies. Its applications cover the complete diagnostic workflow from initial pathogen detection to treatment planning and public health surveillance. The method of microbiological diagnosis is evolving as a consequence of the incorporation of AI. It provides rapid and precise detection of pathogens, early identification of antibiotic resistance and enhanced diagnostic technologies. AI is also critical in early illness detection, medication discovery, personalised healthcare, and outbreak prediction. This has led to tremendous improvements in public health benefits and health care outcomes. However, with the increasing role of AI in medical decision-making, ethical issues such as patient confidentiality, algorithmic biases, data security, openness, accessibility and human supervision need to be addressed. In the future, with the development of AI in microbiological detection, more advancements in illness treatment and prevention are acceptable, also ensuring ethical and just healthcare practices.

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