Artificial intelligence for Improved Diagnosis and Treatment of Bacterial Infections

Md Habibur Rahman[1], Syeda Anjuman Ara Aunni[2*], Bulbul Ahmed[2], Md Moshiur Rahman[3], Md Mahedi Hasan Shabuj[2], Debashis Chandra Das[4], Mst. Shahana Akter[5], Abdullah Al Numan[6]

Abstract

Background: Artificial intelligence (AI) is assuming a progressively crucial role in healthcare, providing enhanced diagnostic precision, tailored treatment strategies, and superior patient outcomes. Through the analysis of extensive medical data, including genetic information, lifestyle choices, and medical histories, AI has become an influential instrument in personalized medicine, especially for cancer and infectious diseases. Methods: Oncology AI models evaluate genetic profiles and treatment histories to propose personalized chemotherapy protocols that minimize adverse effects while improving therapeutic efficacy. When treating infectious diseases, tools like CombiANT use automated image analysis to check how well antibiotics work together. Portable antimicrobial susceptibility testing methods quickly find bacterial infections and make treatment plans that work best for them. Advanced AI systems, like ChatGPT-3, deliver precise differential diagnoses, accelerating clinical decision-making. Results: AI-driven personal therapy strategies have demonstrated considerable potential in cancer by enhancing therapeutic efficacy through the assessment of individual genetic variants. In infectious illnesses, AI's capacity to evaluate bacterial susceptibility and anticipate therapeutic responses is transforming treatment accuracy. Furthermore, AI models have attained significant diagnostic precision, highlighting their capacity to enhance and expedite clinical methodologies. Conclusion: Although AI has significant potential to revolutionize personalized healthcare, several hurdles remain. This encompasses data privacy issues, the opaque nature of AI decision-making, and the sluggish progression of converting research into practical applications. Overcoming these challenges through cooperation, innovation, and comprehensive policy development is crucial for maximizing AI's potential to enhance personalized medicine and treatment outcomes.

Keywords: AI, personalized healthcare, diagnosis accuracy, treatment precision, bacterial infections

Significance | Artificial intelligence is transforming personalized healthcare by improving diagnostics, optimizing treatments, enhancing outcomes, increasing efficiency, and reducing healthcare costs.

*Correspondence. Syeda Anjuman Ara Aunni, Department of Microbiology, Jagannath University, Dhaka, Bangladesh
E-mail: anjumanara1508@gamil.com

Editor Md Fakruddin, Ph.D., And accepted by the Editorial Board Aug 15, 2024 (received for review Jun 04, 2024)

1.Introduction

Bacterial infections continue to provide a significant and intricate threat to worldwide public health and healthcare systems, resulting in millions of fatalities annually. On November 21, 2022, The Lancet published research identifying bacterial infections as a primary contributor to the global health burden, ranking second only to ischemic heart disease in terms of mortality globally (GBD, 2019). This underscores the pressing necessity for swift and precise

Author Affiliation.
[1] Department Computer Science and Engineering, North South University, Dhaka, Bangladesh.
[2] Department of Microbiology, Jagannath University, Dhaka, Bangladesh.
[3] Departmet of Biotechnology and Genetic Engineering, University of Development Alternative, Dhaka, Bangladesh.
[4] Department of TMSS Biomolecular Laboratory, TMSS Medical College and Rafatullah Community Hospital, Bangladesh.
[5] Department of Orthodontics, TMSS Medical College and Rafatullah Community Hospital, Bogura, Bangladesh.
[6] Department of Biochemistry and Molecular Biology, Tejgaon Collage, Dhaka, Bangladesh.

Please cite this article.
Md Habibur Rahman, Syeda Anjuman Ara Aunni et al. (2024). Artificial intelligence for Improved Diagnosis and Treatment of Bacterial Infections, 7(1), 1-18, 10036

pathogen identification and antibiotic resistance assessment, essential measures for commencing effective treatment, and decreasing fatality rates as antibiotic resistance is becoming more common against traditional antibiotics, especially in ICU patients (Salam et al. 2024). Nevertheless, conventional diagnostic techniques, sometimes reliant on protracted cultures, may need several days to yield findings. Delays in treatment augment dependence on broad-spectrum antibiotics; hence, they heighten the danger of antibiotic resistance. This emphasizes the urgent need for faster, more effective diagnostic technology. Moreover, effective surveillance and control measures are crucial to avert bacterial infection epidemics and protect public health.

The medical community is currently investigating novel methods and techniques to enhance the diagnosis, treatment, and prevention of bacterial infections in response to these obstacles. One of the most promising advances is artificial intelligence (AI), which possesses considerable potential to revolutionize the detection, management, and treatment of bacterial infections (Mintz & Brodie, 2019; Larentzakis & Lygeros, 2021; Ting Sim et al., 2023). AI uses sophisticated computing methods, including machine learning (particularly deep learning), natural language processing, computer vision, and robotics, to emulate human cognitive functions and decision-making processes.

In healthcare, AI has shown significant potential by improving epidemiological monitoring, expediting pathogen identification, forecasting antibiotic resistance, and assisting in the creation of novel pharmaceuticals and personalized treatments. Integrating AI into healthcare systems has a significant opportunity to transform the management of bacterial infections, resulting in more precise diagnosis, focused therapies, and perhaps lower fatality rates. This integration coincides with the overarching objectives of personalized medicine, providing customized and efficacious care (Wong et al., 2023). This study investigates the influence of AI on medical diagnosis and treatment efficacy, emphasizing how AI-generated insights might enhance the rapidity and accuracy of controlling bacterial infections while tackling obstacles in their practical application. This research seeks to provide healthcare practitioners with an in-depth understanding of AI applications in the diagnosis and treatment of bacterial infections through the analysis of recent breakthroughs and literature. Furthermore, it promotes the use of AI to address bacterial infections, enhancing patient care efficiency and efficacy while advancing global public health goals.

Moreover, geographic information systems (GIS), because of their sophisticated data integration and overlay functionalities, have become indispensable instruments in public health, improving the monitoring and visualization of infectious disease trends (Wells et al., 2021). The ToxPi GIS Toolkit enables the dynamic visualization and analysis of geographic data in the ArcGIS environment, integrating Python scripts and bespoke tools to create understandable representations of public health data (Fleming et al., 2022). Additional digital advancements, including cloud-based data storage and real-time monitoring systems such as Google Flu Trends, have demonstrated the capabilities of big data in illness tracking and surveillance (Pfeiffer and Stevens, 2015). While predominantly used in viral epidemiology, these sophisticated methods have considerable potential in bacterial epidemiology, especially as AI-driven models develop.

The significance of AI in diagnosing and controlling bacterial infections has demonstrated significant efficacy. Through the processing and analysis of extensive, intricate information, AI may detect early indicators of bacterial infection epidemics, direct preventative actions, and improve public health policies. Hospitalized patients employ machine learning algorithms to forecast the probability of Clostridioides difficile infections, enabling preventative measures before the onset of illness (Oh et al., 2018; Tilton and Johnson, 2019). Real-time locator systems in emergency departments enhance contact tracing efficiency, enabling quicker identification of possible exposures compared to conventional approaches and optimizing resource allocation (Hellmich et al., 2017), as quick diagnosis and treatment can improve morbidity and mortality not only bacterial but also other infectious disease such as hepatitis B and C induced hepatocellular carcinoma or non-infectious disease such as acute necrotizing pancreatitis (Tufael et al. 2024) (Rahman et al. 2024). AI and big data methodologies for monitoring pathogen transmission across hospitals demonstrate their efficacy in mitigating hospital-acquired illnesses (Ciccolini et al., 2014). These AI-driven technologies provide a novel paradigm in bacterial infection management, aiding in prevention, guiding public health choices, and bolstering worldwide initiatives against infectious illnesses.

2. Application of AI in epidemiological surveillance of bacterial infectious diseases

Artificial intelligence (AI) and big data technologies are transforming infectious disease epidemiology by improving the speed, precision, and scope of public health emergency (PHE) research and management. These advanced technologies facilitate the collecting, integration, and analysis of extensive information, greatly enhancing the capacity of scientists and healthcare practitioners to monitor, forecast, and address infectious disease epidemics. A major advancement is the use of infectious disease dynamics (IDD) models with dynamic Bayesian networks (DBNs). Infectious Disease Dynamics (IDD) models replicate the transmission patterns of infectious illnesses, enabling public health organizations to predict their dissemination and formulate proactive response plans. DBNs utilize probabilistic inference to examine intricate outbreak situations in real time, offering

significant insights into both short-term and long-term epidemic patterns (Gao & Wang, 2022). Collectively, these instruments augment early warning systems and boost outbreak preparedness and response. Cloud computing is essential for AI applications in epidemiology, facilitating the real-time processing and analysis of extensive data streams for effective monitoring of infectious illnesses. Although training AI models is computationally intensive, their capacity to analyze and understand extensive data in real time makes them essential for epidemic predictions and swift responses (Li et al., 2023).

Geographic Information Systems (GIS) enhance these initiatives by assimilating and analyzing spatial data to comprehend the geographical distribution of illnesses. The ToxPiGIS toolkit facilitates the visualization of numerous data layers in a spatial context, enabling public health organizations to identify risk factors and monitor disease hotspots. ToxPiGIS utilizes the ArcGIS platform, integrating Python scripts and custom tools to produce intuitive geospatial analytics that facilitate data-driven decision-making (Fleming et al., 2022). Geographic Information Systems (GIS) have emerged as a fundamental tool in epidemiology, allowing healthcare organizations to make educated decisions grounded in geographical data patterns (Wells et al., 2021). The incorporation of cloud-based data storage and real-time internet search data, shown by systems such as Google Flu Trends, highlights the capabilities of big data in disease surveillance beyond GIS. These systems utilize extensive data sources to deliver early warnings and augment conventional surveillance techniques, thereby improving real-time monitoring and epidemic response (Pfeiffer & Stevens, 2015).

Although primarily concentrated on viral epidemiology, these technologies are increasingly being used for bacterial illness monitoring. Hospitals are creating machine learning models to forecast the risk of Clostridioides difficile infections through the analysis of patient and environmental data. These models empower healthcare teams to execute preventative strategies, hence decreasing infection rates (Oh et al., 2018; Tilton and Johnson, 2019). Hospital emergency rooms have implemented real-time locator systems to more effectively trace patient contacts, enhancing the precision of exposure tracking and optimizing the utilization of healthcare resources (Hellmich et al., 2017). Artificial intelligence has furthered the investigation of disease transmission between hospitals. Researchers have employed Monte Carlo simulations to predict the transmission of methicillin-resistant Staphylococcus aureus (MRSA) throughout hospitals, thereby providing insights into infection routes and informing countermeasures (Lesosky et al., 2011). Similarly, researchers have used susceptible-infectious models to explore cross-hospital transmission, demonstrating the effectiveness of AI in the management of hospital acquired illnesses (Ciccolini et al., 2014).

The incorporation of AI in forecasting and preventing bacterial infections is revolutionizing worldwide initiatives to address infectious illnesses. AI driven models discover trends, anticipate epidemics, and deliver accurate, data informed insights to enhance preventative and control strategies. These talents are essential for public health decision making, facilitating more effective responses to the increasing problems posed by infectious diseases. Through the use of sophisticated data analysis and prediction technologies, artificial intelligence and big data are establishing new benchmarks in epidemiology, advancing efforts against viral and bacterial infections.

3. AI has revolutionized the study of bacterial infection mechanism

A complete awareness of bacterial infectious diseases necessitates an in-depth investigation into their etiology. This discipline investigates the intricate mechanisms via which bacteria establish residence, penetrate, and multiply within a host, alongside the host's immune response and its dynamic interactions with pathogens. This research focuses on pathogen-host interactions, which are essential to disease development. Historically, animal models have been essential for exploring these relationships, yielding significant insights into infection mechanisms, immune responses, and disease progression (Younes et al., 2020; Burkovski, 2022). Nonetheless, these methods sometimes incur high costs, require significant time investment, and provoke ethical issues about animal care. Improvement in artificial intelligence (AI), especially machine learning, is transforming the examination of pathogen host interactions by providing alternatives to animal experimentation. AI driven technologies integrate extensive information, employ advanced analytical methods, and replicate biological processes with exceptional precision, offering economical and efficient solutions for researchers. The PHISTO tool combines machine learning, text mining, and graph theory to combine data from different databases and run BLAST searches. This makes it easier to look at infection pathways in more detail (Durmuş Tekir et al., 2013).

Simultaneously, advancements in sophisticated imaging methods are yielding an unparalleled understanding of bacterial pathogenesis. A group of modular structural plasmids called pTBH (toolbox of Haemophilus) lets scientists watch how bacteria live together and infect each other in real time. Employing 3D microscopy in conjunction with quantitative image analysis, researchers may see fluorescently labeled bacterial strains, elucidating their adaptations to host conditions (Rapún-Araiz et al., 2023). These technologies enhance our comprehension of bacterial survival and adaptability within host tissues. AI models are improving our capacity to mimic pathogen-host interactions across diverse metabolic conditions. To describe the metabolic

adaptability of pathogenic bacteria, researchers have used machine learning techniques (Dillard et al., 2023). These techniques have led to new insights into how these organisms interact with their hosts (Figure 5). Furthermore, researchers have uncovered unique infection patterns for Staphylococcus aureus isolates in conditions such as osteomyelitis, bacteremia, and endocarditis, highlighting differences in bacterial behavior among various host cell types (Rodrigues Lopes et al., 2022). These methodologies enhance our understanding of microbial behavior in host contexts and facilitate the creation of customized treatments and vaccines by revealing pathogen-specific characteristics. AI driven modelling serves as a revolutionary instrument for forecasting and recreating the complex dynamics of pathogen-host interactions. By diminishing dependency on animal studies, these models optimize research methodologies, save expenses, and provide novel investigations into bacterial pathogenesis. Although AI cannot fully supplant animal models in every instance, it offers an indispensable tool for exploring hitherto unattainable aspects of infectious disease research. This technology enhances our capacity to address bacterial illnesses with more accuracy, facilitating the advancement of effective therapies and preventive measures.

4. AI application in the diagnosis of bacterial infections

Traditional methods of detecting bacterial infectious illnesses depend on a mix of microbiological and biochemical assays to identify pathogens. This procedure often entails growing bacteria, examining their physical traits, performing biochemical reaction assays, and utilizing serological methods to identify particular antigens or antibodies (Ernst et al., 2006; Váradi et al., 2017) (Table 1). Researchers extensively employ molecular biology methods, particularly polymerase chain reaction (PCR), due to their exceptional specificity in detecting bacterial DNA sequences (Wilson, 2015; Deusenbery et al., 2021). Nonetheless, despite its sophisticated capabilities, PCR can be time-consuming, constraining its effectiveness for swift diagnosis.

The use of artificial intelligence (AI) in diagnostic processes might transform the identification and treatment of bacterial illnesses. AI-driven methods not only make traditional diagnostic methods more accurate, but they also open up completely new ways to quickly and accurately find and treat bacterial infections (Ho et al., 2019) (Figure 2).

4.1. AI improves the efficiency and accuracy of pathogen identification

Advancements in artificial intelligence (AI) are transforming the swift and precise identification of bacterial infections, providing novel treatments to enhance patient outcomes. The amalgamation of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOFMS) with ClinProTools software has demonstrated significant effectiveness. This method facilitates the accurate identification of bacterial species with 100% precision in distinguishing two subspecies of Staphylococcus aureus. Thanks to better genetic analysis and a good classifier model, MALDI TOF MS has become a powerful tool for clinical uses that need to quickly identify bacteria (Pérez-Sancho et al., 2018) (Figure 3).

Findaureus, an open-source Python application, is a notable innovation that automates the localization of bacteria inside tissue slices through immunological fluorescence tagging. This program mitigates the inefficiencies associated with manual threshold setting, which can be arduous and variable. Findaureus improves the accuracy and reliability of diagnostics in cellular structures by automating the determination of thresholds for finding and analysing bacteria in complex tissue settings (Mandal et al., 2024). Pheno Matrix's Colorimetric Detection Module (CDM) signifies a significant advancement in high-throughput screening. The Walk Away Specimen Processor includes this module, which automates the detection of Group B streptococcus, offering sensitivity similar to molecular testing. This invention markedly improves laboratory efficiency and minimizes human error, making it especially beneficial in high-demand clinical environments (Baker et al., 2020).

Some DNA microarray technologies, like the DendrisChips platform, use machine learning algorithms and PCR to quickly find bacterial 16S rDNA that can be used to diagnose respiratory infections. This device can identify 11 bacterial species within four hours by hybridizing certain oligonucleotide sequences on a microarray chip with over 95% accuracy. This technology offers a rapid and accurate alternative to conventional microbiological procedures, markedly decreasing the diagnosis duration for respiratory tract infections (Senescau et al., 2018). Another revolutionary method uses a biosensor that can identify 16 bacterial species and employs neural networks to analyze bacterial response patterns. The sensor maintains stability for up to six months after preparation and necessitates less dye and sample volume relative to traditional approaches. This cost-effective approach has over 90% accuracy and shows significant potential for pathogen identification in resource-constrained environments, where conventional diagnostic equipment may be unavailable (Laliwala et al., 2022).

Sluggish processing rates and sensitivity limitations have hindered traditional microscopy approaches for tuberculosis (TB) and associated disorders. Neon Metafer, an automated smear microscopy scanner from Metasystems that integrates deep learning image analysis (Figure 1), overcomes these challenges by using a deep neural network (DNN) classifier to identify acid-fast bacilli (AFB)-negative slides. This technology diminishes analysis duration to around 10 seconds per slide, representing a substantial enhancement compared to traditional procedures that necessitate several minutes (Horvath et al., 2020). Using T-SPOT tests along

with deep learning-based computed tomography image analysis has also made it easier to tell the difference between pulmonary tuberculosis and nontuberculous mycobacterial lung disease, which is an important but often hard thing to do in clinical practice (Ying et al., 2022).

Artificial Neural Networks (ANNs) and other AI driven diagnostic instruments are becoming vital for the rapid and accurate identification of diseases. These technologies optimize diagnostic processes, reduce human errors, and improve overall dependability. AI powered solutions expedite the diagnostic process, facilitating the prompt and precise identification of infectious pathogens, essential for efficient disease treatment. Advanced AI technologies possess the capacity to revolutionize healthcare by enhancing access to effective diagnostic solutions, especially in resource-limited environments with significant clinical demands (Dande and Samant, 2018). These improvements represent a substantial advancement in enhancing the speed, accuracy, and accessibility of bacterial infection diagnostics, establishing a new benchmark for pathogen detection in contemporary medicine.

4.2. AI optimizes antimicrobial susceptibility testing

Modern clinical laboratories mostly use traditional culturing methods to find pathogens and do antimicrobial susceptibility testing (AST) to separate organisms and check how resistant they are to treatment (. The Clinical and Laboratory Standards Institute (CLSI, 2023) lists disc diffusion, microbroth dilution, and agar dilution as common techniques (Table 2). It usually takes two to three days or more after the first sample is collected to get clear results (Abu Aqil et al., 2022). Clinicians frequently employ empirical therapies with broad-spectrum antimicrobials to address infections, as initial symptoms alone are not sufficient for accurate diagnosis. Although empirical therapies may provide temporary infection control, their excessive usage fosters the development of drug-resistant bacteria. This escalating hazard underscores the pressing need for expedited and precise AST methodologies to guarantee prompt and efficient identification and therapy.

Progress in artificial intelligence (AI) and expedited testing methods is revolutionizing antimicrobial susceptibility testing (AST) by facilitating the swift and automated detection of resistant microorganisms. A significant advancement is the integration of Raman spectroscopy with image-stitching methodologies, allowing the identification of resistant bacteria at the single cell level with minimum human involvement (Nakar et al., 2022; Dou et al., 2023). A unique method integrates machine learning with infrared spectroscopy, facilitating the rapid detection of urinary tract infection bacteria and their resistance characteristics. This technique decreases the diagnostic duration for infections such as Escherichia coli, Proteus mirabilis, and Pseudomonas aeruginosa from 48 hours to around 40 minutes (Ciccolini et al., 2014; Tilton and Johnson, 2019; Younes et al., 2020; Burkovski, 2022). These developments enable doctors to make prompt, evidence-informed decisions for precise therapy. Microfluidic technologies, such as the SlipChip device, have emerged as efficient tools for accelerating antimicrobial susceptibility testing (AST). While SlipChip disperses pathogens in nanoscale broth droplets to facilitate concurrent multi-drug testing, electrophoresis directly separates bacteria from blood cultures. The concurrent inoculation method gives results for AST in 3–8 hours, which makes antibiotic treatments quick and accurate (Yi et al., 2019). Automation has significantly transformed the identification of drug-resistant organisms in clinical environments. MALDI-TOF mass spectrometry (MS) has demonstrated significant efficacy in swiftly detecting resistant strains, including methicillin-resistant Staphylococcus aureus (MRSA) and carbapenem-resistant Klebsiella pneumoniae (CRKP) (Wieser et al., 2012; Zhang et al., 2023). Recently, the incorporation of machine learning into MALDI-TOF MS procedures has further decreased identification times, yielding findings from labeled blood cultures in less than an hour (Yu et al., 2023a, b). Furthermore, computational analysis of MALDI-TOF MS data facilitates the discovery of specific protein markers that distinguish resistant from susceptible bacterial strains; hence, improving resistance profiling (Wang et al., 2021).

Automated tools like WASPLab have greatly cut down on the time needed to find vancomycin-resistant enterococci (VRE), which has improved the efficiency of the lab and the accuracy of the diagnosis (Cherkaoui et al., 2019). The Automated Plate Assessment System (APAS Independence) uses high-resolution digital imagery to categorize MRSA and methicillin-sensitive Staphylococcus aureus (MSSA) autonomously. This approach enhances efficiency in high-throughput laboratories by delivering quick and accurate pathogen classification using automated picture processing (Gammel et al., 2021). AI driven innovations in AST furnish clinical laboratories with powerful and automated instruments for the rapid identification of drug-resistant bacteria. These technologies significantly decrease the time from sample collection to diagnostic confirmation, thereby improving laboratory productivity and allowing doctors to provide prompt, customized antimicrobial therapies. The automated AST enhances infection control and bolsters laboratories' capacity to track antimicrobial resistance trends. These improvements provide more accurate and sustainable antimicrobial stewardship measures, eventually enhancing the battle against drug resistant bacteria.

4.3 AI can improve bacterial genome sequencing

Genome sequencing technologies, like whole genome sequencing and next-generation sequencing (NGS), have changed how infectious diseases are found, how they are spread, and how the health effects of microbial communities on humans are studied

(d'Humières et al., 2021; Deusenbery et al., 2021). These methods provide rapid and thorough genetic study of pathogens, enabling accurate identification of infectious organisms and transmission routes, especially in hospital environments. In addition, genome sequencing is necessary for keeping an eye on and managing antimicrobial resistance (AMR) around the world. It gives researchers and medical professionals the tools they need to see patterns of resistance and deal with new threats (Waddington et al., 2022; Sherry et al., 2023). Conventional genetic testing techniques depend on sequence similarity to detect infections by contrasting sample sequences with those in reference databases. However, these methodologies encounter constraints when dealing with novel or significantly divergent species that lack closely comparable reference genomes. To address this constraint, sophisticated machine learning algorithms, such as PaPrBaG, have been created to precisely predict species occurrence despite poor genome coverage. These techniques improve pathogen detection capacities and facilitate the identification of previously uncharacterized species (Deneke et al., 2017).

The integration of machine learning with metagenomic sequencing has enhanced diagnostic precision for notoriously difficult illnesses, such as tuberculous meningitis. Algorithms using large genomic data can discern distinctive genetic patterns linked to challenging to diagnose disorders, hence enhancing the speed and accuracy of diagnoses (Ramachandran et al., 2022). With the reduction in high-throughput sequencing costs, the efficient interpretation of the extensive and intricate genomic data generated has emerged as a significant problem. This problem can be solved with machine learning, which predicts the health effects of pathogens like Escherichia coli, which makes Shiga toxin. This makes microbial risk assessment techniques better (Njage et al., 2019).

In AMR prediction, machine learning has facilitated substantial advancements by developing predictive models that surpass conventional techniques. Knowing more about AMR in Escherichia coli through knowledge maps made by machine learning has helped us find drug resistance genes we hadn't known about before, which has helped us understand how resistance works (Youn et al., 2022). Using advanced machine learning methods, like XGBoost and convolutional neural networks (CNNs), to predict the minimum inhibitory concentrations (MICs) of different antimicrobial drugs against clinical isolates of Klebsiella pneumoniae has been very successful. These models not only forecast MICs but also detect highly resistant or virulent strains, enhancing evaluations of bacterial pathogenicity (Nguyen et al., 2018; Liu et al., 2021; Lu et al., 2022). Treesist-TB is a new decision tree-based algorithm that has shown to be more accurate than other tools like TB-Profiler at finding mutant strains and predicting treatment resistance in tuberculosis (TB). This method underscores the capability of decision trees to examine resistance patterns and offers a framework for detecting drug-resistant strains in additional infections (Deelder et al., 2022).

The incorporation of artificial intelligence, especially machine learning, into genome sequencing has proved revolutionary. As sequencing technologies produce progressively larger and more intricate information, machine learning has become indispensable for addressing the shortcomings of conventional genetic detection methods, enabling the identification of new species, and enhancing the interpretation of high dimensional data. These models not only exceed conventional methods in predicting precision but also augment our comprehension of disease biology, antimicrobial resistance mechanisms, and microbial ecosystems. In combating AMR, machine learning serves as an essential instrument, facilitating the monitoring, forecasting, and alleviation of resistance patterns worldwide. This advancement is essential for protecting public health and promoting precision treatment.

5. Application of AI in the treatment of bacterial infections

The fast emergence of antimicrobial resistance (AMR), a pressing global health problem today, progressively impedes the management of bacterial infections. Antimicrobial resistance (AMR) arises when bacteria develop the capability to resist the effects of medications intended to eradicate them; hence, treatments are rendered ineffective. The United Nations General Assembly convened a high-level meeting on AMR in 2016, acknowledging the seriousness of the issue and urging nations to execute national action plans to address resistance. Current statistics clearly demonstrate the magnitude of the situation: drug-resistant illnesses linked to over 5 million fatalities in 2019 (Antimicrobial Resistance Collaborators, 2022). In the absence of appropriate treatments, estimations indicate that antimicrobial resistance (AMR) may result in 10 million fatalities per year by 2050 (Walsh et al., 2023).

The adaptive evolution of bacteria, which acquires resistance through genetic changes and natural selection, propels the emergence of antimicrobial resistance (AMR), thereby diminishing the effectiveness of conventional antibiotics. Contributing variables include the excessive and improper use of antibiotics in both medicine and agriculture, which intensifies the pressure for bacteria to develop resistance. The diversity of bacterial species and the intricacy of bacterial-host interactions hinder the advancement of broad-spectrum therapies, vaccines, and innovative medicines. To address antibiotic resistance (AMR), the advancement of novel antimicrobial techniques is essential, with artificial intelligence (AI) emerging as a pivotal instrument in this endeavor. AI offers advanced modeling tools to examine intricate interactions among infections, hosts, and medications, allowing researchers to elucidate microbial infection pathways with exceptional accuracy. Using extensive datasets, AI models may detect prospective therapeutic

targets, simulate drug pathogen interactions, and expedite the creation of optimized vaccines by identifying antigens likely to provoke successful immune responses. These developments are essential for formulating medicines that retain efficacy against swiftly changing bacterial populations. Artificial intelligence has furthered the advancement of phage treatment, which employs bacteriophages (viruses that target bacteria) to address resistant bacterial strains. By utilizing genetic sequencing and predictive modeling, AI can discern phages that precisely target resistant bacteria, establishing phage therapy as a significant adjunct to antibiotics, especially when conventional therapies prove ineffective.

5.1 AI revolutionizes drug discovery and development

In the field of pharmaceutical research and development, AI is revolutionizing conventional approaches and enabling novel techniques to address drug resistance. Researchers are making substantial progress in finding new therapeutic targets and improving drug discovery precision by merging AI driven methodologies with biophysical and computational tools.

Integrating high-throughput biophysical research with machine learning establishes a strong foundation for discovering bioactive targets in the development of antibiotics. This method facilitates the delineation of links among phenotypes, targets, and chemotypes crucial components for recognizing potential therapeutic candidates. Santa Maria et al. (2017) illustrated this technique by precisely forecasting bioactive targets, thereby facilitating the discovery of prospective antimicrobial drugs. Further advancement entails the amalgamation of fragment-based drug design with quantitative structure-activity relationship (QSAR) modeling. Artificial neural networks (ANNs) have demonstrated significant efficacy in forecasting therapeutic effectiveness by modeling correlations between chemical structure and biological function. Kleandrova and Speck-Planche (2020) employed this methodology to enhance drug candidate selection, illustrating the efficacy of artificial neural networks in the drug development process.

Machine learning has been important in the analysis of bacterial minimum inhibitory concentration (MIC) data, facilitating the identification of chemical characteristics that augment antibiotic efficacy. Gurvic et al. (2022) used matched molecular pair analysis to find molecular features related to antibacterial activity. This expanded the chemical landscape for broad-spectrum medicines and helped find effective compounds to fight resistant strains. AI driven approaches are transforming the development of antimicrobial drugs for diseases. We have used support vector machines (SVMs) to analyses genomic, metabolomic, and transcriptome data from Pseudomonas aeruginosa. This method showed clear genetic pathways that separate harm from harmless strains, revealing important areas for developing antibiotics (Larsen et al., 2014). In the fight against tuberculosis (TB), machine learning algorithms and neural networks have found two types of targets for dual inhibitors: leucyl-tRNA synthetase (LeuRS) and methionyl-tRNA synthetase (MetRS) in Mycobacterium tuberculosis. These targets, crucial for bacterial survival, signify prospective strategies for combating multidrug-resistant tuberculosis (Volynets et al., 2022). Ekins et al. (2017) found small-molecule inhibitors of topoisomerase I, offering possible remedies for the escalating problem of tuberculosis medication resistance. Machine learning applications for analyzing public datasets on M. tuberculosis have expedited drug discovery by facilitating the swift identification of potential compounds and establishing a knowledge repository for further study (Lane et al., 2022). This data-centric methodology optimizes the development process, facilitating quicker reactions to newly resistant strains.

Artificial intelligence profoundly transforms drug development by improving accuracy, speed, and efficiency while broadening the possibilities for identifying successful medicines. By utilizing modern computational methods, AI allows researchers to traverse the intricacies of biological systems with enhanced accuracy, promoting the creation of novel medicines. These technological developments are facilitating a new age in pharmaceutical research, marked by more intelligent, expedited, and precise drug discovery methods. In combating AMR, AI driven technologies provide essential capabilities to monitor, forecast, and address resistance patterns, offering optimism for successful therapies against some of the globe's most formidable illnesses.

5.2 AI brings breakthroughs in vaccine development

Recent developments in vaccine research and development have markedly enhanced the rapidity and efficacy of responses to viral illnesses, especially during developing epidemics. The use of computer-aided design technology has transformed the development process, as demonstrated by the swift production of COVID-19 vaccines. Computational modeling expedited the rapid discovery and assessment of potential vaccine candidates, allowing many to enter the market in unprecedented times (Abbasi et al., 2022). This milestone highlights a significant transformation in vaccine science, with computational methods increasingly integral to vaccine design and evaluation.

Bacterial vaccine development poses distinct and more intricate obstacles. Bacterial pathogens, in contrast to viruses, have significant genetic diversity, swiftly acquire resistance to therapies, and participate in complex host-pathogen interactions that hinder the development of effective and enduring vaccinations. To tackle these challenges, researchers are progressively using modern technologies such as artificial intelligence (AI), machine learning (ML), and immunological assessment methods. These novel techniques are improving the accuracy and efficacy of vaccine

creation while assisting scientists in combating the adaptive strategies employed by bacteria to circumvent immune responses. One important step in making a bacterial vaccine is finding antigens, which are molecular features on the pathogen's surface that might make the immune system remember the pathogen for a long time. To provide long-lasting protection, bacterial vaccines that work must trigger strong immune responses that include both humoral (antibody-mediated) and cellular immunity. Recent advancements in reverse vaccinology (RV) have demonstrated potential in fulfilling these needs. RV employs computational analysis of pathogen genomes to pinpoint vaccination targets; hence, it greatly enhances the development process. The Bexsero vaccine for Neisseria meningitidis serogroup B, produced by reverse vaccinology, represents a significant success and is currently extensively distributed worldwide (Heinson et al., 2015).

Computer methods like deep learning, immunoinformatic, and reverse vaccination have revolutionized the finding of antigens, fundamental to vaccine development. These techniques make it possible to study pathogen protein-coding genomes at a high level of detail. This speeds up the creation of multi-epitope subunit vaccines, which are made up of many antigenic components meant to trigger strong immune responses. Although further testing is necessary to validate the safety and immunogenicity of vaccines developed by computational approaches (Rawal et al., 2021), this strategy signifies significant progress. It diminishes dependence on laborious, conventional laboratory experiments, optimizes development, and offers a robust instrument for addressing drug-resistant bacterial species. Machine learning methods are significantly enhancing bacterial vaccination research by increasing the precision and sensitivity of predictions. An ML model has shown enhanced efficacy in recognizing critical antigenic characteristics of Mycobacterium tuberculosis, surpassing traditional techniques (Khanna and Rana, 2019). By eliminating the necessity of animal testing and labor-intensive experimentation, machine learning optimizes the vaccine development process, improving efficiency and decreasing costs.

The use of machine learning and computational techniques in bacterial vaccine development possesses transformational potential. These technologies allow the modeling of intricate biological interactions, the virtual evaluation of vaccination candidates, and the prioritization of the most promising alternatives prior to conventional trial stages. As bacterial pathogens change and provide substantial public health risks, such scientific and technical breakthroughs are essential for expediting responses to bacterial outbreaks. Reducing worldwide reliance on medicines and implementing effective immunization techniques represents a crucial advancement in tackling the issues posed by bacterial diseases.

5.3 AI drives innovative applications of phage therapy

Phage treatment has garnered significant interest from the scientific community as a viable method to address antibiotic-resistant bacterial infections (Viertel et al., 2014; Kulshrestha et al., 2024). The global menace of antimicrobial resistance (AMR) is diminishing the efficacy of conventional antibiotics, necessitating the urgent development of new treatment techniques. Phage treatment utilizing bacteriophages viruses that specifically target and attack bacteria has emerged as a promising alternative. The intricate interactions among bacteriophages, their bacterial hosts, and the human organism impede the therapeutic efficacy of phage treatment. Aspects such as bacterial resistance mechanisms, phage specificity, and the physiological conditions at the infection site influence the interactions, making the precise prediction of treatment results a significant challenge (Cisek et al., 2017). Artificial intelligence (AI) and machine learning (ML) technologies provide robust instruments to tackle these issues, yielding innovative insights on phage-host-pathogen interactions. Through the analysis of large datasets and the discovery of patterns that guide therapeutic approaches, these advanced computational techniques make it easier to predict and improve phage treatments. Qiu et al. (2024) have devised a machine learning-based local K-mer approach to accurately anticipate phage-bacteria interactions. This approach examines certain DNA sequences termed K-mers to assess the probability of a phage infecting a given bacterial strain. This method facilitates silico predictions, enhancing the selection of suitable phage candidates for particular illnesses, hence markedly increasing treatment accuracy and efficacy.

Artificial intelligence has exhibited potential in enhancing the therapeutic uses of phage treatment. It is possible for machine learning algorithms to help find the best phages for targeted therapy in cases of urinary tract infections (UTIs) caused by multidrug-resistant Escherichia coli. This feature enables the creation of customized therapy strategies specific to the bacterial strain responsible for the infection, improving therapeutic efficacy and minimizing the likelihood of treatment failure. A significant innovation is the creation of tools like HostPhinder, which forecasts the genus and species of bacterial hosts that a certain phage is likely to infect. HostPhinder has exhibited remarkable precision, with 81% accuracy in forecasting the host genus and 74% in forecasting the host species (Villarroel et al., 2016). These prediction instruments enable researchers to identify the most appropriate therapeutic phages for bacterial illnesses, guaranteeing that phage treatment is both efficacious and accurately directed.

The combination of phage therapy with conventional antimicrobial therapies offers a viable solution for illnesses caused by drug-resistant organisms. AI-driven techniques expedite the identification and optimization of phage candidates, facilitate

Table 1. Advantages and limitations of the traditional bacterial identification methods.

Method	Advantages	Limitations
Bacterial culture (Baron, 2019)	✓ The cost is low ✓ Effective for various bacteria ✓ Easy to operate	• Long time consumption • Some bacteria cannot develop • Susceptible to contamination • It is not suitable for highly specific tests
Morphological observation (Periasamy, 2014)	✓ No special equipment ✓ Intuitive is strong ✓ Accumulation of experience	• Subjectivity is strong • Limited information • The lack of specificity • Need to develop
Biochemical reaction tests (Ohkusu, 2000)	✓ Cost-effective ✓ Easy to operate	• Limited specificity • Does not apply to all bacteria
Serological technique (Eldin et al., 2019)	✓ High specificity ✓ Quick results ✓ Quantifiable analysis	• Greatly influenced by sampling time • There were false positive and false negative results • A variety of pathogens have cross-reacted

Table 2. Artificial intelligence in the bacteria identification and drug sensitivity analysis.

Technology	Application	References
MALDI-TOF+ MS + ClinProTools software	Rapidly identified *Staphylococcus aureus* subspecies	Pérez-Sancho et al. (2018)
Findaureus	Automatic localization of bacteria in immunofluorescently labeled tissue sections	Mandal et al. (2024)
PM + CDM + WASP	High sensitivity to identify group B streptococcus	Baker et al. (2020)
Machine learning-based DNA micro-matrix technology	More than 95% accuracy in identifying respiratory bacteria	Senescau et al. (2018)
Neural network-based sensors	90% accuracy in bacterial identification	Laliwala et al. (2022)
AFB + Neon Metafer	Significantly improved the speed and accuracy of identification of acid- fighting bacilli (AFB) on smear-negative slides	Desruisseaux et al. (2024)
DNN + an automated slide scanning system	Significantly reduced slide analysis time	Horvath et al. (2020)
T-SPOT + DL-based technology	Significantly improved the classification accuracy of NTM—PD and PTB	Ying et al. (2022)
Raman spectroscopy based on image stitching technology	Automatically, efficiently and rapidly identified drug-resistant bacteria	Dou et al. (2023) and Nakar et al. (2022)
SlipChip microfluidic device	Significant reduction in bacterial drug sensitivity test time	Yi et al. (2019)
A novel MALDI-TOF MS method based on ML	Rapidly identified MRSA and CRKP	Yu et al. (2023a,b)
WASPLab automation system	Significantly shorten the vancomycin-resistant enterococcus (VRE) recognition time	Cherkaoui et al. (2019)
APAS Independence	Accurately distinguish MRSA and MSSA	Gammel et al. (2021)

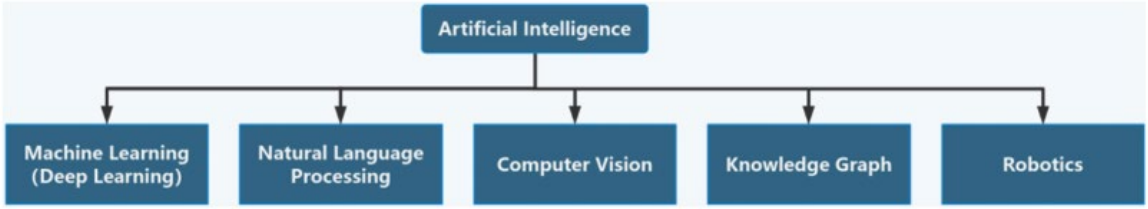

Figure 1. The relationship between machine learning (particularly deep learning), natural language processing, computer vision, knowledge graph, robotics, and artificial intelligence.

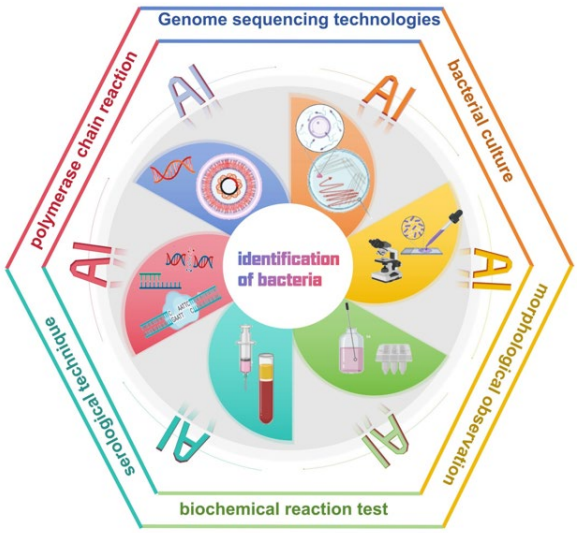

Figure 2. Artificial intelligence facilitates the diagnosis of bacterial infectious diseases.

Figure 3. AI technology can model complex interactions between pathogens, hosts, and drugs.

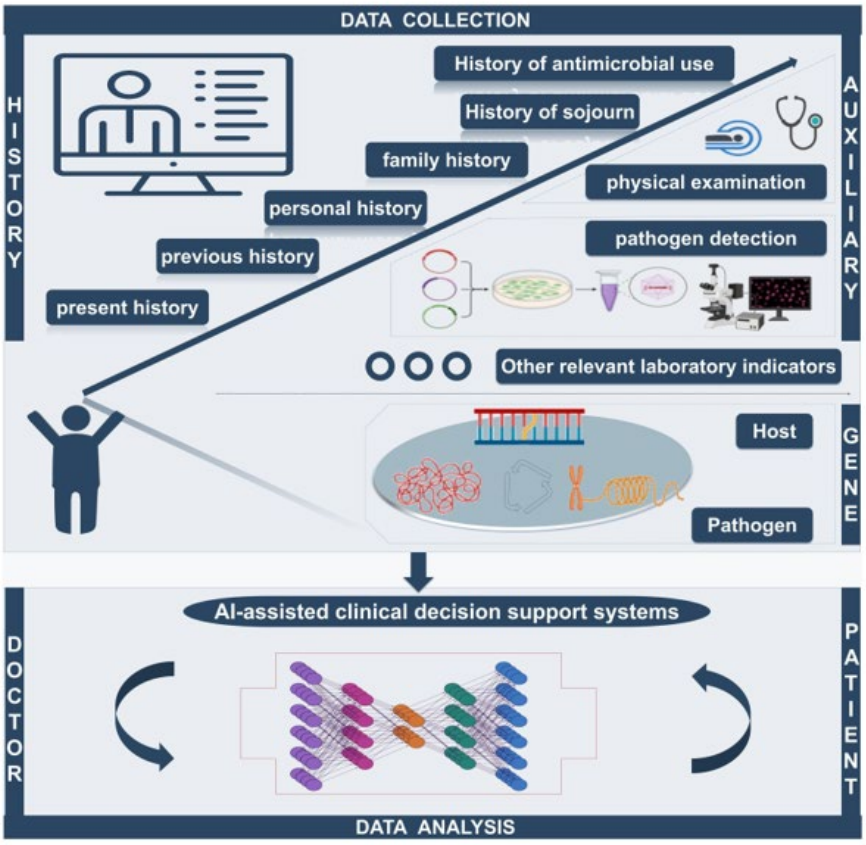

Figure 4. The AI-assisted clinical decision support system can quickly collect the patient's history of present disease, past history, personal history, family history, travel history, and antibiotic use history. Simultaneously, the system can integrate relevant auxiliary examination (including imaging examination and laboratory examination) and analysis of the genetic information of hosts and pathogens to provide the best treatment, becoming a bridge of effective communication between doctors and patients.

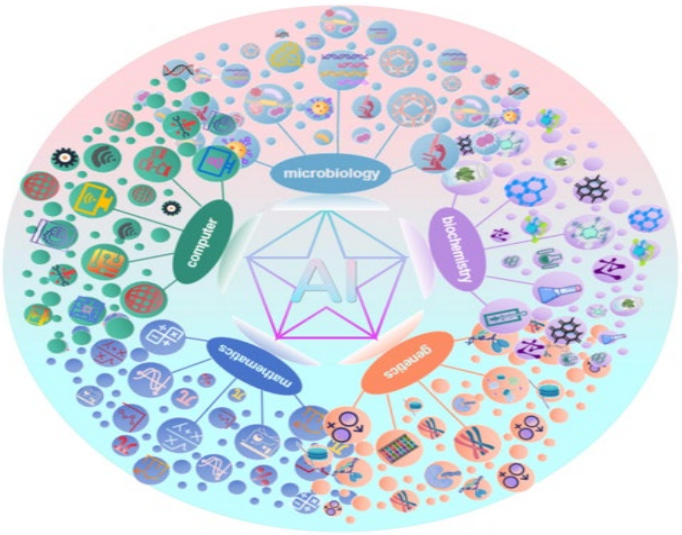

Figure 5. The successful application of AI models in medicine relies on multidisciplinary collaboration.

personalized therapies, and enhance clinical results. Additionally, combining phages with common antimicrobial drugs can lead to more effective treatments that kill bacteria faster and get around their resistance mechanisms. Combination strategies are especially beneficial in instances when traditional antibiotics have demonstrated ineffectiveness (Tagliaferri et al., 2019). The escalating AMR epidemic highlights the transformational potential of AI in phage treatment. By providing swift and precise predictions of phage-bacteria interactions and permitting customized therapy tactics, AI-driven methodologies will significantly contribute to the fight against drug-resistant diseases. The incorporation of these technologies into clinical practice provides a means to achieve more efficient and sustainable solutions for tackling the worldwide issue of antimicrobial resistance (AMR).

5.4 AI-assisted clinical decision support systems

The timing of effective antimicrobial administration is a critical factor in determining morbidity and mortality in the management of infectious diseases, particularly in the case of septic shock (Evans et al., 2021). Early and accurate identification of the infection is essential, as it can drastically reduce the negative outcomes associated with delayed treatment. Prompt treatment not only improves prognosis but also helps prevent unnecessary medical interventions, ultimately reducing healthcare costs and enhancing patient survival rates and quality of life. Therefore, timely antimicrobial therapy is a cornerstone in managing infections, with early intervention being a key driver in improving patient outcomes.

In the context of the increasing emphasis on personalized and precision medicine, advancements in artificial intelligence (AI) and machine learning (ML) offer new opportunities to revolutionize the diagnosis and treatment of infectious diseases. These technologies are streamlining clinical workflows, enhancing decision-making, and supporting the development of individualized treatment plans tailored to each patient's unique needs (Langford et al., 2024). AI and ML models can process vast amounts of data quickly and accurately, allowing clinicians to make informed decisions more efficiently. For example, ML models have been successfully employed to diagnose respiratory syncytial virus (RSV) and pertussis in children by integrating clinical symptoms with laboratory test results (McCord-De Iaco et al., 2023). Additionally, ML algorithms such as LightGBM have been used to predict the etiology of classical fever of unknown origin (FUO) in patients, by leveraging clinically relevant indicators such as age and sex (Yan et al., 2021). This predictive capability significantly enhances diagnostic accuracy, leading to faster and more effective treatment. Furthermore, ML models are increasingly being utilized to predict the risk of infections caused by drug-resistant pathogens. For instance, ML models can predict the likelihood of methicillin-resistant Staphylococcus aureus (MRSA) infection in patients with community-acquired pneumonia, allowing for more targeted antimicrobial treatment (Rhodes et al., 2023). Clinical decision trees, which are often generated through recursive methods, have also proven valuable in assessing the likelihood of extended-spectrum beta-lactamase (ESBL)-producing strains in patients with bacteremia, further refining antimicrobial therapy (Goodman et al., 2016).

Additionally, AI driven systems, such as the K-CDSTM system, have been developed to provide early warnings of antimicrobial drug allergies. These systems help prevent adverse drug reactions by alerting clinicians to potential allergies before antimicrobial drugs are prescribed (Han et al., 2024). Similarly, ontology-driven clinical decision support systems, which utilize big data and machine learning algorithms, help bridge the gap between patients and healthcare providers by assisting in the decision-making process for treating infectious diseases (Shen et al., 2018).

The application of AI in predictive disease modeling has also led to more accurate and reliable predictions than traditional methods. Machine learning models, especially those trained on large datasets, outperforming conventional techniques in forecasting disease risks and outcomes. A noteworthy example includes a study utilizing a computerized clinical decision support system (CDSS), which showed that the system reduced the time needed for diagnosis by approximately one hour and resulted in savings of about $84,000 in antimicrobial costs over a three-month period (McGregor et al., 2006).

AI and ML technologies are transforming the landscape of infectious disease diagnosis and treatment. By improving diagnostic accuracy, enhancing risk predictions, and reducing the time and costs associated with antimicrobial treatment, these technologies are not only making healthcare more efficient but also improving patient outcomes. As these tools continue to evolve, they hold the potential to reshape traditional diagnostic and treatment paradigms, leading to more personalized, effective, and cost-efficient healthcare. Machine learning models, with their superior predictive capabilities and accuracy, are emerging as indispensable tools in modern clinical decision making (Figure 4).

6. AI helps personalized medical development

Advanced analysis of complicated algorithms has enabled artificial intelligence (AI) to effectively process and understand extensive medical data, encompassing genetic information, lifestyle variables, and past health records. This ability to analyze various datasets allows AI to greatly enhance medical diagnosis accuracy and precision. In addition to diagnostics, AI is crucial in formulating personalized treatment regimens customized to the specific requirements of each patient. In oncology, AI can aid physicians in determining the most effective combinations of chemotherapy

agents by analyzing a patient's genetic profile, cancer classification, and treatment response history. This tailored methodology not only augments treatment effectiveness but also reduces adverse effects, thereby enhancing the overall success rate of cancer therapy. Moreover, AI can forecast possible consequences, assess treatment efficacy, and provide personalized health management plans tailored to a patient's unique circumstances and therapeutic responses (Bilgin et al., 2024; Elemento, 2024).

In the domain of infectious illnesses, AI has demonstrated significant potential in enhancing treatment options. An exemplary instance is CombiANT, a technique that uses automated image analysis to swiftly evaluate antimicrobial synergy from a single assay. This method delivers tailored clinical insights, enhancing combination therapy for bacterial infections and resulting in better patient outcomes (Fatsis Kavalopoulos et al., 2020). Kuo-Wei Hsu and colleagues created a portable, automated method for antibiotic susceptibility testing that can identify infections from four prevalent urinary tract bacterial strains. This technology allows the swift customization of treatment strategies according to unique bacterial susceptibilities, achieving results within 4.5–9 hours. This breakthrough has considerable potential for tackling prevalent and essential illnesses; hence, it enhances the implementation of personalized medicine in the management of infectious diseases (Hsu et al., 2021).

Artificial intelligence is advancing in diagnostics. Connor Rees and his colleagues revealed that ChatGPT-3, a sophisticated AI model, attained an accuracy rate of 90% in producing differential diagnoses for clinical cases. This diagnostic performance underscores AI's capacity to improve clinical decision-making and accelerate diagnoses, facilitating swifter treatment actions. Nonetheless, the complete realization of AI's promise in healthcare necessitates continuous research and assessment. Subsequent studies need to concentrate on addressing more intricate problems and enhancing AI models to accommodate a wider array of healthcare situations. An important focus is the enhancement of AI powered diagnostic chatbots, which may increase diagnosis accuracy, deliver thorough evaluations of patient situations, and facilitate more personalized treatment strategies. The applications of AI in medicine are many, including enhancements in diagnostic precision, tailored treatment plans, and optimizing healthcare services. By utilizing data from various sources and perpetually enhancing its algorithms, AI has the capacity to transform personalized healthcare, rendering therapies more effective, efficient, and tailored to the individual. We anticipate future innovations to enhance diagnostic accuracy and treatment specificity, leading to significant improvements in healthcare and improved patient outcomes.

7. Challenges of AI in the medical field

While the use of artificial intelligence (AI) in the treatment of bacterial infections holds significant promise, achieving its full effectiveness requires overcoming significant obstacles. A fundamental impediment is the matter of data encompassing both its volume and integrity. Privacy issues and legislative limitations frequently obstruct the aggregation, standardization, and dissemination of data pertaining to bacterial infections. These restrictions make it harder to get access to large, varied datasets that are needed to build strong AI models. This makes AI applications in healthcare settings less useful and applicable in other settings (Cath, 2018; Baowaly et al., 2019; Hummel and Braun, 2020).

A significant concern is the "black box" issue intrinsic to several deep learning techniques. These models frequently exhibit a lack of transparency, complicating the elucidation of their predictions. The absence of interpretability erodes the confidence of healthcare professionals and patients, which is essential for the integration of AI in clinical practice. Furthermore, the lack of comprehensive understanding of AI systems' decision-making processes might adversely affect predicted accuracy and therapeutic outcomes (Schwartz et al., 2024).

Despite considerable progress in AI research in controlled, non-clinical settings, the conversion of these discoveries into viable clinical applications continues to be a protracted and intricate endeavor. Numerous AI technologies in healthcare remain in experimental phases, and their adaptation to various clinical environments poses significant challenges. The diversity in patient demographics, healthcare systems, and infection patterns between geographies hampers the application of AI in practical settings (Alami et al., 2020). The intrinsic intricacy of bacterial illnesses poses further challenges. The rapid mutation rates and varied infection mechanisms of bacterial pathogens complicate the prediction of bacterial behavior and the precise evaluation of antibiotic sensitivity. AI models in this field must amalgamate information from other fields, including microbiology, genetics, biochemistry, and computer science. Creating integrative models necessitates substantial resources and experience, presenting a formidable task for researchers operating under limitations.

The absence of a comprehensive legal framework and standardized norms for AI applications in healthcare is a significant obstacle. As AI technology advances, it is crucial to formulate and consistently revise laws to guarantee its ethical, safe, and successful application in the treatment of bacterial diseases. Establishing clear criteria and monitoring will be crucial in mitigating issues pertaining to accountability, bias, and the fair implementation of AI systems in clinical practice (Rees and Müller, 2022). Confronting these difficulties necessitates interdisciplinary collaboration, the establishment of stringent data sharing rules, the implementation of transparent AI models, and the formulation of extensive

regulatory frameworks. By surmounting these challenges, AI can substantially improve the detection and treatment of bacterial infections, enabling novel and personalized healthcare solutions.

8. Conclusion

Artificial intelligence technology has the capacity to transform the treatment and management of bacterial infections by enhancing the speed and precision of medical decision-making. Its uses include improving pathogen identification, forecasting antibiotic susceptibility, and formulating customized treatment strategies for specific patients. AI significantly enhances epidemiological surveillance, facilitating the prompt monitoring and management of infectious illnesses. Notwithstanding its potential, the incorporation of AI in healthcare encounters obstacles, such as the necessity for greater transparency in AI driven decision-making and the resolution of ethical issues pertaining to data utilization and patient confidentiality. Overcoming these difficulties necessitates multidisciplinary collaboration, continuous technical advancement, and the creation of strong policy frameworks. As AI advances, it has the potential to revolutionize healthcare practice by offering more accurate and efficient diagnostic and treatment options. AI enhances patient outcomes and optimizes healthcare delivery, marking a substantial advancement in combating bacterial infections and ushering in a new age of personalized, effective medical treatment.

Author contributions

M.H.R. and S.A.A.A. conceptualized and developed the methodology. B.A., M.M.R. and M.M.H.S. prepared the original draft and reviewed and edited the writing. D.C.D., M.S.A. and A.A.N. analyzed the data and reviewed and edited the writing.

Acknowledgment

None declared.

Competing financial interests

The authors have no conflict of interest.

References

Abbasi, B. A., Saraf, D., Sharma, T., Sinha, R., Singh, S., Sood, S., et al. (2022). Identification of vaccine targets & design of vaccine against SARS-CoV-2 coronavirus using computational and deep learning-based approaches. PeerJ, 10, e13380. https://doi.org/10.7717/peerj.13380

Abu-Aqil, G., Lapidot, I., Salman, A., & Huleihel, M. (2023). Quick detection of Proteus and Pseudomonas in patients' urine and assessing their antibiotic susceptibility using infrared spectroscopy and machine learning. Sensors (Basel), 23, 8132. https://doi.org/10.3390/s23198132

Alami, H., Lehoux, P., Denis, J.-L., Motulsky, A., Petitgand, C., Savoldelli, M., et al. (2020). Organizational readiness for artificial intelligence in health care: Insights for decision-making and practice. Journal of Health Organization and Management, 35, 106–114. https://doi.org/10.1108/JHOM-03-2020-0074

Antimicrobial Resistance Collaborators. (2022). Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. The Lancet, 399, 629–655. https://doi.org/10.1016/S0140-6736(21)02724-0

Baker, J., Timm, K., Faron, M., Ledeboer, N., & Culbreath, K. (2020). Digital image analysis for the detection of group B Streptococcus from ChromID Strepto B medium using PhenoMatrix algorithms. Journal of Clinical Microbiology, 59, e01902–e01919. https://doi.org/10.1128/JCM.01902-19

Baowaly, M. K., Lin, C.-C., Liu, C.-L., & Chen, K.-T. (2019). Synthesizing electronic health records using improved generative adversarial networks. Journal of the American Medical Informatics Association, 26, 228–241. https://doi.org/10.1093/jamia/ocy142

Baron, E. J. (2019). Clinical microbiology in underresourced settings. Clinical Laboratory Medicine, 39, 359–369. https://doi.org/10.1016/j.cll.2019.05.001

Beam, A. L., Motsinger-Reif, A., & Doyle, J. (2014). Bayesian neural networks for detecting epistasis in genetic association studies. BMC Bioinformatics, 15, 368. https://doi.org/10.1186/s12859-014-0368-0

Bilgin, G. B., Bilgin, C., Burkett, B. J., Orme, J. J., Childs, D. S., Thorpe, M. P., et al. (2024). Theranostics and artificial intelligence: New frontiers in personalized medicine. Theranostics, 14, 2367–2378. https://doi.org/10.7150/thno.94788

Burkovski, A. (2022). Host–pathogen interaction 3.0. International Journal of Molecular Sciences, 23, 12811. https://doi.org/10.3390/ijms232112811

Cath, C. (2018). Governing artificial intelligence: Ethical, legal and technical opportunities and challenges. Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences, 376, 20180080. https://doi.org/10.1098/rsta.2018.0080

Cherkaoui, A., Renzi, G., Charretier, Y., Blanc, D. S., Vuilleumier, N., & Schrenzel, J. (2019). Automated incubation and digital image analysis of chromogenic media using Copan WASPLab enables rapid detection of vancomycin-resistant Enterococcus. Frontiers in Cellular and Infection Microbiology, 9, 379. https://doi.org/10.3389/fcimb.2019.00379

Ciccolini, M., Donker, T., Grundmann, H., Bonten, M. J. M., & Woolhouse, M. E. J. (2014). Efficient surveillance for healthcare-associated infections spreading between hospitals. Proceedings of the National Academy of Sciences of the United States of America, 111, 2271–2276. https://doi.org/10.1073/pnas.1308062111

Cisek, A. A., Dąbrowska, I., Gregorczyk, K. P., & Wyżewski, Z. (2017). Phage therapy in bacterial infections treatment: One hundred years after the discovery of bacteriophages. Current Microbiology, 74, 277–283. https://doi.org/10.1007/s00284-016-1166-x

CLSI. (2023). Performance standards for antimicrobial susceptibility testing (33rd ed., CLSI supplement M100). Clinical and Laboratory Standards Institute. https://iacld.com/UpFiles/Documents/672a1c7c-d4ad-404e-b10e-97c19e21cdce.pdf [Accessed April 7, 2024].

d'Humières, C., Salmona, M., Dellière, S., Leo, S., Rodriguez, C., Angebault, C., et al. (2021). The potential role of clinical metagenomics in infectious diseases: Therapeutic perspectives. Drugs, 81(12), 1453–1466. https://doi.org/10.1007/s40265-021-01572-4

Dande, P., & Samant, P. (2018). Acquaintance to artificial neural networks and use of artificial intelligence as a diagnostic tool for tuberculosis: A review. Tuberculosis (Edinburgh), 108, 1–9. https://doi.org/10.1016/j.tube.2017.09.006

Deelder, W., Napier, G., Campino, S., Palla, L., Phelan, J., & Clark, T. G. (2022). A modified decision tree approach to improve the prediction and mutation discovery for drug resistance in Mycobacterium tuberculosis. BMC Genomics, 23(1), 46. https://doi.org/10.1186/s12864-022-08291-4

Deneke, C., Rentzsch, R., & Renard, B. Y. (2017). PaPrBaG: A machine learning approach for the detection of novel pathogens from NGS data. Scientific Reports, 7, 39194. https://doi.org/10.1038/srep39194

Desruisseaux, C., Broderick, C., Lavergne, V., Sy, K., Garcia, D.-J., Barot, G., et al. (2024). Retrospective validation of MetaSystems' deep-learning-based digital microscopy platform with assistance compared to manual fluorescence microscopy for detection of mycobacteria. Journal of Clinical Microbiology, 62(1), e0106923. https://doi.org/10.1128/jcm.01069-23

Deusenbery, C., Wang, Y., & Shukla, A. (2021). Recent innovations in bacterial infection detection and treatment. ACS Infectious Diseases, 7(3), 695–720. https://doi.org/10.1021/acsinfecdis.0c00890

Dillard, L. R., Glass, E. M., Lewis, A. L., Thomas-White, K., & Papin, J. A. (2023). Metabolic network models of the Gardnerella pangenome identify key interactions with the vaginal environment. mSystems, 8(1), e0068922. https://doi.org/10.1128/msystems.00689-22

Dou, X., Yang, F., Wang, N., Xue, Y., Hu, H., & Li, B. (2023). Rapid detection and analysis of Raman spectra of bacteria in multiple fields of view based on image stitching technique. Frontiers in Bioscience-Landmark, 28(1), 249. https://doi.org/10.31083/j.bl2810249

Durmuş Tekir, S., Çakır, T., Ardıç, E., Sayılırbaş, A. S., Konuk, G., Konuk, M., et al. (2013). PHISTO: Pathogen–host interaction search tool. Bioinformatics, 29(11), 1357–1358. https://doi.org/10.1093/bioinformatics/btt137

Ekins, S., Godbole, A. A., Kéri, G., Orfi, L., Pato, J., Bhat, R. S., et al. (2017). Machine learning and docking models for Mycobacterium tuberculosis topoisomerase I. Tuberculosis (Edinburgh), 103, 52–60. https://doi.org/10.1016/j.tube.2017.01.005

Eldin, C., Parola, P., & Raoult, D. (2019). Limitations of diagnostic tests for bacterial infections. Médecine et Maladies Infectieuses, 49(2), 98–101. https://doi.org/10.1016/j.medmal.2018.12.004

Elemento, O. (2024). How artificial intelligence unravels the complex web of cancer drug response. Cancer Research, 84(15), 1745–1746. https://doi.org/10.1158/0008-5472.CAN-24-1123

Ernst, D., Bolton, G., Recktenwald, D., Cameron, M. J., Danesh, A., Persad, D., et al. (2006). Bead-based flow cytometric assays: A multiplex assay platform with applications in diagnostic microbiology. In Advanced Techniques in Diagnostic Microbiology (pp. 427–443). Springer US.

Evans, L., Rhodes, A., Alhazzani, W., Antonelli, M., Coopersmith, C. M., French, C., et al. (2021). Surviving sepsis campaign: International guidelines for management of sepsis and septic shock 2021. Intensive Care Medicine, 47(11), 1181–1247. https://doi.org/10.1007/s00134-021-06506-y

Fatsis-Kavalopoulos, N., Roemhild, R., Tang, P.-C., Kreuger, J., & Andersson, D. I. (2020). CombiANT: Antibiotic interaction testing made easy. PLOS Biology, 18(e3000856). https://doi.org/10.1371/journal.pbio.3000856

Fleming, J., Marvel, S. W., Supak, S., Motsinger-Reif, A. A., & Reif, D. M. (2022). ToxPi*GIS toolkit: Creating, viewing, and sharing integrative visualizations for geospatial data using ArcGIS. Journal of Exposure Science & Environmental Epidemiology, 32(6), 900–907. https://doi.org/10.1038/s41370-022-00433-w

Gammel, N., Ross, T. L., Lewis, S., Olson, M., Henciak, S., Harris, R., et al. (2021). Comparison of an automated plate assessment system (APAS Independence) and artificial intelligence (AI) to manual plate reading of methicillin-resistant and methicillin-susceptible Staphylococcus aureus CHROMagar surveillance cultures. Journal of Clinical Microbiology, 59(e00971-21). https://doi.org/10.1128/JCM.00971-21

Gao, S., & Wang, H. (2022). Scenario prediction of public health emergencies using infectious disease dynamics model and dynamic Bayes. Future Generation Computer Systems, 127, 334–346. https://doi.org/10.1016/j.future.2021.09.028

GBD Antimicrobial Resistance Collaborators. (2019). Global mortality associated with 33 bacterial pathogens in 2019: A systematic analysis for the Global Burden of Disease Study 2019. The Lancet, 400(10369), 2221–2248. https://doi.org/10.1016/S0140-6736(22)02185-7

Goodman, K. E., Lessler, J., Cosgrove, S. E., Harris, A. D., Lautenbach, E., Han, J. H., et al. (2016). A clinical decision tree to predict whether a bacteremic patient is infected with an extended-spectrum β-lactamase-producing organism. Clinical Infectious Diseases, 63(7), 896–903. https://doi.org/10.1093/cid/ciw425

Goodswen, S. J., Barratt, J. L. N., Kennedy, P. J., Kaufer, A., Calarco, L., & Ellis, J. T. (2021). Machine learning and applications in microbiology. FEMS Microbiology Reviews, 45(1), fuab015. https://doi.org/10.1093/femsre/fuab015

Gurvic, D., Leach, A. G., & Zachariae, U. (2022). Data-driven derivation of molecular substructures that enhance drug activity in gram-negative bacteria. Journal of Medicinal Chemistry, 65(9), 6088–6099. https://doi.org/10.1021/acs.jmedchem.1c01984

Han, N., Oh, O. H., Oh, J., Kim, Y., Lee, Y., Cha, W. C., et al. (2024). The application of knowledge-based clinical decision support systems to detect antibiotic allergy. Antibiotics (Basel), 13(3), 244. https://doi.org/10.3390/antibiotics13030244

Heinson, A. I., Woelk, C. H., & Newell, M.-L. (2015). The promise of reverse vaccinology. International Health, 7(2), 85–89. https://doi.org/10.1093/inthealth/ihv002

Hellmich, T. R., Clements, C. M., El-Sherif, N., Pasupathy, K. S., Nestler, D. M., Boggust, A., et al. (2017). Contact tracing with a real-time location system: A case study of increasing relative effectiveness in an emergency department. American Journal of Infection Control, 45(12), 1308–1311. https://doi.org/10.1016/j.ajic.2017.08.014

Hirosawa, T., Harada, Y., Yokose, M., Sakamoto, T., Kawamura, R., & Shimizu, T. (2023). Diagnostic accuracy of differential-diagnosis lists generated by generative pretrained transformer 3 chatbot for clinical vignettes with common chief complaints: A pilot study. International Journal of Environmental Research and Public Health, 20(4), 3378. https://doi.org/10.3390/ijerph20043378

Ho, C.-S., Jean, N., Hogan, C. A., Blackmon, L., Jeffrey, S. S., Holodniy, M., et al. (2019). Rapid identification of pathogenic bacteria using Raman spectroscopy and deep

learning. Nature Communications, 10, 4927. https://doi.org/10.1038/s41467-019-12898-9

Horvath, L., Hänselmann, S., Mannsperger, H., Degenhardt, S., Last, K., Zimmermann, S., et al. (2020). Machine-assisted interpretation of auramine stains substantially increases throughput and sensitivity of microscopic tuberculosis diagnosis. Tuberculosis (Edinburgh), 125, 101993. https://doi.org/10.1016/j.tube.2020.101993

Howard, A., Aston, S., Gerada, A., Reza, N., Bincalar, J., Mwandumba, H., et al. (2024). Antimicrobial learning systems: An implementation blueprint for artificial intelligence to tackle antimicrobial resistance. The Lancet Digital Health, 6, e79–e86. https://doi.org/10.1016/S2589-7500(23)00221-2

Hsu, K.-W., Lee, W.-B., You, H.-L., Lee, M. S., & Lee, G.-B. (2021). An automated and portable antimicrobial susceptibility testing system for urinary tract infections. Lab on a Chip, 21, 755–763. https://doi.org/10.1039/d0lc01315c

Hummel, P., & Braun, M. (2020). Just data? Solidarity and justice in data-driven medicine. Life Sciences, Society and Policy, 16, 8. https://doi.org/10.1186/s40504-020-00101-7

Jiang, Y., Luo, J., Huang, D., Liu, Y., & Li, D. (2022). Machine learning advances in microbiology: A review of methods and applications. Frontiers in Microbiology, 13, 925454. https://doi.org/10.3389/fmicb.2022.925454

Keith, M., Park de la Torriente, A., Chalka, A., Vallejo-Trujillo, A., McAteer, S. P., Paterson, G. K., et al. (2024). Predictive phage therapy for Escherichia coli urinary tract infections: Cocktail selection for therapy based on machine learning models. Proceedings of the National Academy of Sciences of the United States of America, 121, e2313574121. https://doi.org/10.1073/pnas.2313574121

Khanna, D., & Rana, P. S. (2019). Ensemble technique for prediction of T-cell Mycobacterium tuberculosis epitopes. Interdisciplinary Sciences, 11, 611–627. https://doi.org/10.1007/s12539-018-0309-0

Kleandrova, V. V., & Speck-Planche, A. (2020). The QSAR paradigm in fragment-based drug discovery: From the virtual generation of target inhibitors to multi-scale modeling. Mini Reviews in Medicinal Chemistry, 20, 1357–1374. https://doi.org/10.2174/1389557520666200204123156

Kulshrestha, M., Tiwari, M., & Tiwari, V. (2024). Bacteriophage therapy against ESKAPE bacterial pathogens: Current status, strategies, challenges, and future scope. Microbial Pathogenesis, 186, 106467. https://doi.org/10.1016/j.micpath.2023.106467

Laliwala, A., Svechkarev, D., Sadykov, M. R., Endres, J., Bayles, K. W., & Mohs, A. M. (2022). Simpler procedure and improved performance for pathogenic bacteria analysis with a paper-based ratiometric fluorescent sensor array. Analytical Chemistry, 94, 2615–2624. https://doi.org/10.1021/acs.analchem.1c05021

Lane, T. R., Urbina, F., Rank, L., Gerlach, J., Riabova, O., Lepioshkin, A., et al. (2022). Machine learning models for Mycobacterium tuberculosis in vitro activity: Prediction and target visualization. Molecular Pharmaceutics, 19, 674–689. https://doi.org/10.1021/acs.molpharmaceut.1c00791

Langford, B. J., Branch-Elliman, W., Nori, P., Marra, A. R., & Bearman, G. (2024). Confronting the disruption of the infectious diseases workforce by artificial intelligence: What this means for us and what we can do about it. Open Forum Infectious Diseases, 11, ofae053. https://doi.org/10.1093/ofid/ofae053

Larentzakis, A., & Lygeros, N. (2021). Artificial intelligence (AI) in medicine as a strategic valuable tool. Pan African Medical Journal, 38, 184. https://doi.org/10.11604/pamj.2021.38.184.28197

Larsen, P. E., Collart, F. R., & Dai, Y. (2014). Using metabolomic and transportomic modeling and machine learning to identify putative novel therapeutic targets for antibiotic-resistant pseudomonad infections. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 314–317. https://doi.org/10.1109/EMBC.2014.6943592

Lesosky, M., McGeer, A., Simor, A., Green, K., Low, D. E., & Raboud, J. (2011). Effect of patterns of transferring patients among healthcare institutions on rates of nosocomial methicillin-resistant Staphylococcus aureus transmission: A Monte Carlo simulation. Infection Control & Hospital Epidemiology, 32, 136–147. https://doi.org/10.1086/657945

Li, R., Shen, M., Liu, H., Bai, L., & Zhang, L. (2023). Do infrared thermometers hold promise for an effective early warning system for emerging respiratory infectious diseases? JMIR Formative Research, 7, e42548. https://doi.org/10.2196/42548

Liu, W., Ying, N., Mo, Q., Li, S., Shao, M., Sun, L., et al. (2021). Machine learning for identifying resistance features of Klebsiella pneumoniae using whole-genome sequence single nucleotide polymorphisms. Journal of Medical Microbiology, 70. https://doi.org/10.1099/jmm.0.001474

Lu, J., Chen, J., Liu, C., Zeng, Y., Sun, Q., Li, J., et al. (2022). Identification of antibiotic resistance and virulence-encoding factors in Klebsiella pneumoniae by Raman spectroscopy and deep learning. Microbial Biotechnology, 15, 1270–1280. https://doi.org/10.1111/1751-7915.13960

Mandal, S., Tannert, A., Löffler, B., Neugebauer, U., & Silva, L. B. (2024). Findaureus: An open-source application for locating Staphylococcus aureus in fluorescence-labelled infected bone tissue slices. PLoS ONE, 19, e0296854. https://doi.org/10.1371/journal.pone.0296854

Mc Cord-De Iaco, K. A., Gesualdo, F., Pandolfi, E., Croci, I., & Tozzi, A. E. (2023). Machine learning clinical decision support systems for surveillance: A case study on pertussis and RSV in children. Frontiers in Pediatrics, 11, 1112074. https://doi.org/10.3389/fped.2023.1112074

McGregor, J. C., Weekes, E., Forrest, G. N., Standiford, H. C., Perencevich, E. N., Furuno, J. P., et al. (2006). Impact of a computerized clinical decision support system on reducing inappropriate antimicrobial use: A randomized controlled trial. Journal of the American Medical Informatics Association, 13, 378–384. https://doi.org/10.1197/jamia.M2049

Mintz, Y., & Brodie, R. (2019). Introduction to artificial intelligence in medicine. Minimally Invasive Therapy & Allied Technologies, 28, 73–81. https://doi.org/10.1080/13645706.2019.1575882

Nakar, A., Pistiki, A., Ryabchykov, O., Bocklitz, T., Rösch, P., & Popp, J. (2022). Detection of multi-resistant clinical strains of E. coli with Raman spectroscopy. Analytical and Bioanalytical Chemistry, 414, 1481–1492. https://doi.org/10.1007/s00216-021-03800-y

Nguyen, M., Brettin, T., Long, S. W., Musser, J. M., Olsen, R. J., Olson, R., et al. (2018). Developing an in silico minimum inhibitory concentration panel test for Klebsiella pneumoniae. Scientific Reports, 8(1), 421. https://doi.org/10.1038/s41598-017-18972-w

Njage, P. M. K., Leekitcharoenphon, P., & Hald, T. (2019). Improving hazard characterization in microbial risk assessment using next generation sequencing data and machine learning: Predicting clinical outcomes in shigatoxigenic Escherichia coli. International Journal of Food Microbiology, 292, 72–82. https://doi.org/10.1016/j.ijfoodmicro.2018.11.016

Oh, J., Makar, M., Fusco, C., McCaffrey, R., Rao, K., Ryan, E. E., et al. (2018). A generalizable, data-driven approach to predict daily risk of Clostridium difficile infection at two large academic health centers. Infection Control & Hospital Epidemiology, 39(4), 425–433. https://doi.org/10.1017/ice.2018.16

Ohkusu, K. (2000). Cost-effective and rapid presumptive identification of gram-negative bacilli in routine urine, pus, and stool cultures: Evaluation of the use of CHROMagar orientation medium in conjunction with simple biochemical tests. Journal of Clinical Microbiology, 38(12), 4586–4592. https://doi.org/10.1128/JCM.38.12.4586-4592.2000

Paquin, P., Durmort, C., Paulus, C., Vernet, T., Marcoux, P. R., & Morales, S. (2022). Spatio-temporal-based deep learning for rapid detection and identification of bacterial colonies through lens-free microscopy time-lapses. PLOS Digital Health, 1(1), e0000122. https://doi.org/10.1371/journal.pdig.0000122

Pérez-Sancho, M., Vela, A. I., Horcajo, P., Ugarte-Ruiz, M., Domínguez, L., Fernández-Garayzábal, J. F., et al. (2018). Rapid differentiation of Staphylococcus aureus subspecies based on MALDI-TOF MS profiles. Journal of Veterinary Diagnostic Investigation, 30(6), 813–820. https://doi.org/10.1177/1040638718805537

Periasamy, A. (2014). Advanced light microscopy. Methods, 66(1), 121–123. https://doi.org/10.1016/j.ymeth.2014.03.011

Pfeiffer, D. U., & Stevens, K. B. (2015). Spatial and temporal epidemiological analysis in the big data era. Preventive Veterinary Medicine, 122(1–2), 213–220. https://doi.org/10.1016/j.prevetmed.2015.05.012

Qiu, J., Nie, W., Ding, H., Dai, J., Wei, Y., Li, D., et al. (2024). PB-LKS: A python package for predicting phage-bacteria interaction through local K-mer strategy. Briefings in Bioinformatics, 25, bbae010. https://doi.org/10.1093/bib/bbae010

Rahman, M. M., Tasnim, M., Li, M., Devadas, H., & Mamoon, M. Y. (2024). Necrotizing Pancreatitis Due to Very High Triglyceride Level: A Case Report. Cureus, 16(9), e69761. https://doi.org/10.7759/cureus.69761

Ramachandran, P. S., Ramesh, A., Creswell, F. V., Wapniarski, A., Narendra, R., Quinn, C. M., et al. (2022). Integrating central nervous system metagenomics and host response for diagnosis of tuberculosis meningitis and its mimics. Nature Communications, 13(1), 1675. https://doi.org/10.1038/s41467-022-29353-x

Rapún-Araiz, B., Sorzabal-Bellido, I., Asensio-López, J., Lázaro-Díez, M., Ariz, M., Sobejano de la Merced, C., et al. (2023). In vitro modeling of polyclonal infection dynamics within the human airways by Haemophilus influenzae differential fluorescent labeling. Microbiology Spectrum, 11(3), e00993-23. https://doi.org/10.1128/spectrum.00993-23

Rawal, K., Sinha, R., Abbasi, B. A., Chaudhary, A., Nath, S. K., Kumari, P., et al. (2021). Identification of vaccine targets in pathogens and design of a vaccine using computational approaches. Scientific Reports, 11(1), 17626. https://doi.org/10.1038/s41598-021-96863-x

Rees, C., & Müller, B. (2022). All that glitters is not gold: Trustworthy and ethical AI principles. AI and Ethics, 3(3), 1241–1254. https://doi.org/10.1007/s43681-022-00232-x

Rhodes, N. J., Rohani, R., Yarnold, P. R., Pawlowski, A. E., Malczynski, M., Qi, C., et al. (2023). Machine learning to stratify methicillin-resistant Staphylococcus aureus risk among hospitalized patients with community-acquired pneumonia. Antimicrobial Agents and Chemotherapy, 67(1), e01023-22. https://doi.org/10.1128/aac.01023-22

Rodrigues Lopes, I., Alcantara, L. M., Silva, R. J., Josse, J., Vega, E. P., Cabrerizo, A. M., et al. (2022). Microscopy-based phenotypic profiling of infection by Staphylococcus aureus clinical isolates reveals intracellular lifestyle as a prevalent feature. Nature Communications, 13, 7174. https://doi.org/10.1038/s41467-022-34790-9

Salam, M. T., Bari, K. F., & others. (2024). Emergence of antibiotic-resistant infections in ICU patients. Journal of Angiotherapy, 8(5), 1–9. https://doi.org/10.25163/angiotherapy.859560

Santa Maria, J. P., Park, Y., Yang, L., Murgolo, N., Altman, M. D., Zuck, P., et al. (2017). Linking high-throughput screens to identify MoAs and novel inhibitors of Mycobacterium tuberculosis dihydrofolate reductase. ACS Chemical Biology, 12, 2448–2456. https://doi.org/10.1021/acschembio.7b00468

Schwartz, I. S., Link, K. E., Daneshjou, R., & Cortés-Penfield, N. (2024). Black box warning: Large language models and the future of infectious diseases consultation. Clinical Infectious Diseases, 78, 860–866. https://doi.org/10.1093/cid/ciad633

Senescau, A., Kempowsky, T., Bernard, E., Messier, S., Besse, P., Fabre, R., & François, J. M. (2018). Innovative DendrisChips® technology for a syndromic approach of in vitro diagnosis: Application to the respiratory infectious diseases. Diagnostics, 8(4), 77. https://doi.org/10.3390/diagnostics8040077

Shen, Y., Yuan, K., Chen, D., Colloc, J., Yang, M., Li, Y., et al. (2018). An ontology-driven clinical decision support system (IDDAP) for infectious disease diagnosis and antibiotic prescription. Artificial Intelligence in Medicine, 86, 20–32. https://doi.org/10.1016/j.artmed.2018.01.003

Sherry, N. L., Horan, K. A., Ballard, S. A., Gonçalves da Silva, A., Gorrie, C. L., Schultz, M. B., et al. (2023). An ISO-certified genomics workflow for identification and surveillance of antimicrobial resistance. Nature Communications, 14, 60. https://doi.org/10.1038/s41467-022-35713-4

Stracy, M., Snitser, O., Yelin, I., Amer, Y., Parizade, M., Katz, R., et al. (2022). Minimizing treatment-induced emergence of antibiotic resistance in bacterial infections. Science, 375, 889–894. https://doi.org/10.1126/science.abg9868

Tagliaferri, T. L., Jansen, M., & Horz, H.-P. (2019). Fighting pathogenic bacteria on two fronts: Phages and antibiotics as a combined strategy. Frontiers in Cellular and Infection Microbiology, 9, 22. https://doi.org/10.3389/fcimb.2019.00022

Tilton, C. S., & Johnson, S. W. (2019). Development of a risk prediction model for hospital-onset Clostridium difficile infection in patients receiving systemic antibiotics. American Journal of Infection Control, 47, 280–284. https://doi.org/10.1016/j.ajic.2018.08.021

Ting Sim, J. Z., Fong, Q. W., Huang, W., & Tan, C. H. (2023). Machine learning in medicine: What clinicians should know. Singapore Medical Journal, 64, 91–97. https://doi.org/10.11622/smedj.2021054

Tufael, M., Rahman, M. M., & others. (2024). Combined biomarkers for early diagnosis of hepatocellular carcinoma. Journal of Angiotherapy, 8(5), 1–12. https://doi.org/10.25163/angiotherapy.859665

Váradi, L., Luo, J. L., Hibbs, D. E., Perry, J. D., Anderson, R. J., Orenga, S., et al. (2017). Methods for the detection and identification of pathogenic bacteria: Past, present, and future. Chemical Society Reviews, 46, 4818–4832. https://doi.org/10.1039/c6cs00693k

Viertel, T. M., Ritter, K., & Horz, H.-P. (2014). Viruses versus bacteria: Novel approaches to phage therapy as a tool against multidrug-resistant pathogens. Journal of Antimicrobial Chemotherapy, 69, 2326–2336. https://doi.org/10.1093/jac/dku173

Villarroel, J., Kleinheinz, K. A., Jurtz, V. I., Zschach, H., Lund, O., Nielsen, M., et al. (2016). HostPhinder: A phage host prediction tool. Viruses, 8(116). https://doi.org/10.3390/v8050116

Volynets, G. P., Usenko, M. O., Gudzera, O. I., Starosyla, S. A., Balanda, A. O., Syniugin, A. R., et al. (2022). Identification of dual-targeted Mycobacterium tuberculosis aminoacyl-tRNA synthetase inhibitors using machine learning. Future Medicinal Chemistry, 14(1223–1237). https://doi.org/10.4155/fmc-2022-0085

Waddington, C., Carey, M. E., Boinett, C. J., Higginson, E., Veeraraghavan, B., & Baker, S. (2022). Exploiting genomics to mitigate the public health impact of antimicrobial resistance. Genome Medicine, 14(15). https://doi.org/10.1186/s13073-022-01020-2

Waddington, C., Carey, M. E., Boinett, C. J., Higginson, E., Veeraraghavan, B., & Baker, S. (2022). Exploiting genomics to mitigate the public health impact of antimicrobial resistance. Genome Medicine, 14, 15. https://doi.org/10.1186/s13073-022-01020-2

Walsh, T. R., Gales, A. C., Laxminarayan, R., & Dodd, P. C. (2023). Antimicrobial resistance: Addressing a global threat to humanity. PLOS Medicine, 20, e1004264. https://doi.org/10.1371/journal.pmed.1004264

Walsh, T. R., Gales, A. C., Laxminarayan, R., & Dodd, P. C. (2023). Antimicrobial resistance: Addressing a global threat to humanity. PLoS Medicine, 20, e1004264. https://doi.org/10.1371/journal.pmed.1004264

Wang, H., Ceylan Koydemir, H., Qiu, Y., Bai, B., Zhang, Y., Jin, Y., et al. (2020). Early detection and classification of live bacteria using time-lapse coherent imaging and deep learning. Light: Science & Applications, 9(118). https://doi.org/10.1038/s41377-020-00358-9

Wang, H., Ceylan Koydemir, H., Qiu, Y., Bai, B., Zhang, Y., Jin, Y., et al. (2020). Early detection and classification of live bacteria using time-lapse coherent imaging and deep learning. Light: Science & Applications, 9, 118. https://doi.org/10.1038/s41377-020-00358-9

Wang, H.-Y., Chung, C.-R., Wang, Z., Li, S., Chu, B.-Y., Horng, J.-T., et al. (2021). A large-scale investigation and identification of methicillin-resistant Staphylococcus aureus based on peaks binning of matrix-assisted laser desorption ionization-time of flight MS spectra. Briefings in Bioinformatics, 22, bbaa138. https://doi.org/10.1093/bib/bbaa138

Wang, H.-Y., Chung, C.-R., Wang, Z., Li, S., Chu, B.-Y., Horng, J.-T., et al. (2021). A large-scale investigation and identification of methicillin-resistant Staphylococcus aureus based on peaks binning of matrix-assisted laser desorption ionization-time of flight MS spectra. Briefings in Bioinformatics, 22, bbaa138. https://doi.org/10.1093/bib/bbaa138

Wang, M., Wei, Z., Jia, M., Chen, L., & Ji, H. (2022). Deep learning model for multi-classification of infectious diseases from unstructured electronic medical records. BMC Medical Informatics and Decision Making, 22(41). https://doi.org/10.1186/s12911-022-01776-y

Wang, M., Wei, Z., Jia, M., Chen, L., & Ji, H. (2022). Deep learning model for multi-classification of infectious diseases from unstructured electronic medical records. BMC Medical Informatics and Decision Making, 22, 41. https://doi.org/10.1186/s12911-022-01776-y

Wells, J., Grant, R., Chang, J., & Kayyali, R. (2021). Evaluating the usability and acceptability of a geographical information system (GIS) prototype to visualize socio-economic and public health data. BMC Public Health, 21(2151). https://doi.org/10.1186/s12889-021-12072-1

Wells, J., Grant, R., Chang, J., & Kayyali, R. (2021). Evaluating the usability and acceptability of a geographical information system (GIS) prototype to visualize socio-economic and public health data. BMC Public Health, 21, 2151. https://doi.org/10.1186/s12889-021-12072-1

Wieser, A., Schneider, L., Jung, J., & Schubert, S. (2012). MALDI-TOF MS in microbiological diagnostics—Identification of microorganisms and beyond (mini-review). Applied Microbiology and Biotechnology, 93, 965–974. https://doi.org/10.1007/s00253-011-3783-4

Wieser, A., Schneider, L., Jung, J., & Schubert, S. (2012). MALDI-TOF MS in microbiological diagnostics: Identification of microorganisms and beyond (mini review). Applied Microbiology and Biotechnology, 93, 965–974. https://doi.org/10.1007/s00253-011-3783-4

Wilson, M. L. (2015). Diagnostic microbiology: The accelerating transition from culture-based to molecular-based methods. American Journal of Clinical Pathology, 143, 766–767. https://doi.org/10.1309/AJCPIC9GPLHCV1NT

Wilson, M. L. (2015). Diagnostic microbiology: The accelerating transition from culture-based to molecular-based methods. American Journal of Clinical Pathology, 143, 766–767. https://doi.org/10.1309/AJCPIC9GPLHCV1NT

Wong, F., De La Fuente-Nunez, C., & Collins, J. J. (2023). Leveraging artificial intelligence in the fight against infectious diseases. Science, 381, 164–170. https://doi.org/10.1126/science.adh1114

Wong, F., De La Fuente-Nunez, C., & Collins, J. J. (2023). Leveraging artificial intelligence in the fight against infectious diseases. Science, 381, 164–170. https://doi.org/10.1126/science.adh1114

Yan, Y., Chen, C., Liu, Y., Zhang, Z., Xu, L., & Pu, K. (2021). Application of machine learning for the prediction of etiological types of classic fever of unknown origin. Frontiers in Public Health, 9, 800549. https://doi.org/10.3389/fpubh.2021.800549