THE EVIDENCE

E-ISSN:3048-7870
Vol. 2 No. 4 (2024)

Review Article | Public Health

Check for updates

Evolution of clinical and diagnostic microbiology in the era of artificial intelligence: a systematic review

Drishti Sagar[1*], Smriti Srivastava[1], Priyanka Banerjee[1]

[1] Department of Microbiology, Janakpuri Super Specialty Hospital, Delhi, India.

*Correspondence: drishsag14@gmail.com

Abstract

Background: Artificial intelligence (AI) is an upcoming field that focuses on the evolution of intelligent machines which can easily perform labor intensive tasks with great accuracy. It has the ability to promptly analyze large amounts of data in a short span of time due to which it has been used for pathogen identification, and to make predictions regarding culture plate interpretations in a clinical specimen. This study reviews AI's impact on clinical microbiology, focusing on microorganism identification, antimicrobial resistance detection, drug development, and record management, while highlighting key challenges.

Methods: A systematic review was conducted until June 1, 2024 by searching literature from various databases such asPubMed, Scopus, Web of Science, and manual search using keywords 'AI and clinical microbiology', 'AI and diagnostic microbiology', 'AI and microscopy', 'AI and antimicrobial resistance'. Only the articles focusing on the use of AI in clinical or diagnostic microbiology were included and others were excluded. As the involvement of AI in clinical microbiology is a relatively recent and upcoming modality, majority of the selected articles were published in the last 5 years only.

Results: AI algorithms can be used for pathogen identification, bacterial growth detection, microscopy, colony counting, antimicrobial susceptibility testing, and maintenance of electronic records in a clinical microbiology laboratory. This review focuses on the various AI algorithms that are relevant for clinical microbiology, some of which have already been used in pilot studies in many developed countries.

Conclusion: With the increasing number of publications on the use of AI in clinical microbiology, education and training regarding these technological advancements has become indispensable.

Keywords: *Algorithm, artificial intelligence, clinical microbiology, deep learning, machine learning, neural networks*

www.evidencejournals.com

Cite this Article

Sagar D, Srivastava S, Banerjee P. Evolution of Clinical and Diagnostic Microbiology in the era of Artificial Intelligence: A Systematic Review. THE EVIDENCE. 2024:2(4):1-10. DOI:10.61505/evidence.2024.2.4.106 Available From https://the.evidencejournals.com/index.php/j/article/view/106

Received:	2024-09-08
Revised:	2024-10-02
Accepted:	2024-10-09
Published:	2024-12-05

Evidence in Context

- AI is impacting clinical and diagnostic microbiology by analyzing large datasets quickly.
- It enhances objectivity, precision, and efficiency in reporting.
- Applications include microorganism identification, antimicrobial resistance detection, drug development, and hospital record management.
- AI uses machine learning, neural networks, and deep learning for improved outcomes.
- Limitations include difficulties in interpreting contamination, phenotypic polymorphisms, and overlapping resistance mechanisms.

To view Article

Introduction

Although diagnostic microbiology largely focuses on the laboratory analysis of infectious diseases, it is increasingly being replaced by clinical microbiology, which emphasizes the treatment and management of infections through pathogen characterization. Diagnostic microbiology has always played a critical role in the management of infectious diseases, outbreak containment, and combating antimicrobial resistance. In the last couple of years, clinical microbiology has been blessed with incredible breakthroughs that have immensely upgraded the quality of

Testing and enhanced patient safety. Artificial intelligence (AI), although in its nascent stage, has revolutionized our knowledge and potential by its integration into the healthcare world [1].

There is a margin of error associated with manual interpretation of culture plates with non-consensus between microbiologists, often reported in literature [2-4]. AI through its cutting-edge digital imaging applications, has systematized certain aspects of interpretive microbiology, such as increased objectivity, precision, and is time saving. AI can be used for a plethora of diagnostic microbiology activities, such as slide screening for pathogenic microorganisms, culture plate interpretations, and antimicrobial susceptibility results, as well as for the analysis of drug resistance mechanisms [5].

AI algorithms such as machine learning (ML), neural networks, and deep learning techniques are increasingly being used for analyzing large data sets in diagnostic microbiology.

Machine learning: ML is a branch of AI that is trained on historical data and uses it to read new data. With the advent of ML, the potential for improvement in quality, cost, and turn-around time of infectious diseases' diagnosis is increasingly being recognized [6]. Furthermore, there is an impending issue of antimicrobial resistance for which the development of newer antibiotics is a slow and expensive process with a scarcity of drugs in the pipeline. ML facilitated antibiotic discovery has been an upcoming modality, with AI facilitated innovations expected in the next decade [7]. ML often has an air of 'mystery' to it, giving the notion of an intelligent computer. It can be categorized as supervised, unsupervised, and reinforced learning [1]. It can be applied to clinical microbiology at various stages, such as pre analytical, analytical, and post analytical processes for sample tracking, image acquisition, and workstation operation. These are designed to minimize the human error that arises from repetitive, monotonous, and labor-intensive tasks, thus, overcoming the data integrity concerns in diagnostic microbiology [8]. ML has the advantage of rapid and detailed pattern analysis of data sets, which cannot be achieved using conventional spreadsheets.

Neural networks: These are a subset of ML models and are based on neural networks in the human brain. It is an intricate network of interconnected neurons that collaborate to handle complicated tasks. It has many types- feed forward neural network (NN), convolutional neural network (CNN), and fully convolutional network (FCN). Feedforward NN allows unidirectional passage of information from input layer to hidden layer to the output layer. Large number of neurons are present in each layer which perform mathematical operations on the inputs of previous layer. Convolutional layers are the defining elements of CNN which carry out matrix multiplications in close proximity. This is adequate for capturing spatial information making them adequately suitable for image analysis. FCN have an edge in performing segmentation tasks such as microscopy images. Other NNs include vision transformer, generative adversarial network, and autoencoder [9].

Deep learning: A branch of AI that emulates how we learn and comprehend certain exercises, such as pattern recognition and classification of tasks. Through deep convolutional neural networks, urine sample analysis can be carried out by capturing images similar to the visual cortex region of the human brain. Deep neural networks can also predict antimicrobial properties from amino acid sequences [10]. In a study conducted in 2009, researchers have described the use of neural networks for predicting peptide activity against *Pseudomonas aeruginosa* [11, 12]. Antimicrobial resistance prediction has increased the interest and excitement among clinical microbiologists for inculcating AI in routine microbiology reporting.

These emerging technologies have the requisite potential to re-shape diagnostic microbiology as rapid microbiology. The development of an algorithm for accurate and precise interpretation of cultures and smears requires inputs from clinical microbiologists, software developers, AI specialists, and clinical leads. The United States Food and Drug Administration (FDA) has issued guidelines for 'Good Machine Learning Practice for Medical Device Development,' which provides a roadmap for AI enabled software for a variety of healthcare needs, including culture plate interpretations [13].

Intellect and reasoning of clinical microbiologists cannot be replaced by AI, however, combing the strengths of two can do wonders in augmenting the delivery of accurate results to the patient. In today's age and time, it has become imperative to study generative AI coupled with computer vision for welcoming the 'golden age' in clinical microbiology.

In view of the above, this systematic review includes a brief summary of the AI technologies coupled with their uses and limitations that can be used for clinical and diagnostic microbiology.

Methods

The Preferred Reporting Items for Systematic Review and Meta-analysis (PRISMA) guidelines were followed. A systematic review was conducted until June 1, 2024 by searching literature from various databases such as PubMed, Scopus, Web of Science, and manual search using keywords 'AI and clinical microbiology', 'AI and diagnostic microbiology', 'AI and microscopy', 'AI and antimicrobial resistance'. Only the articles focusing on the use of AI in clinical or diagnostic microbiology were included and others were excluded (Figure 1). As the involvement of AI in clinical microbiology is a relatively recent and upcoming modality, majority of the selected articles were published in the last 5 years only.

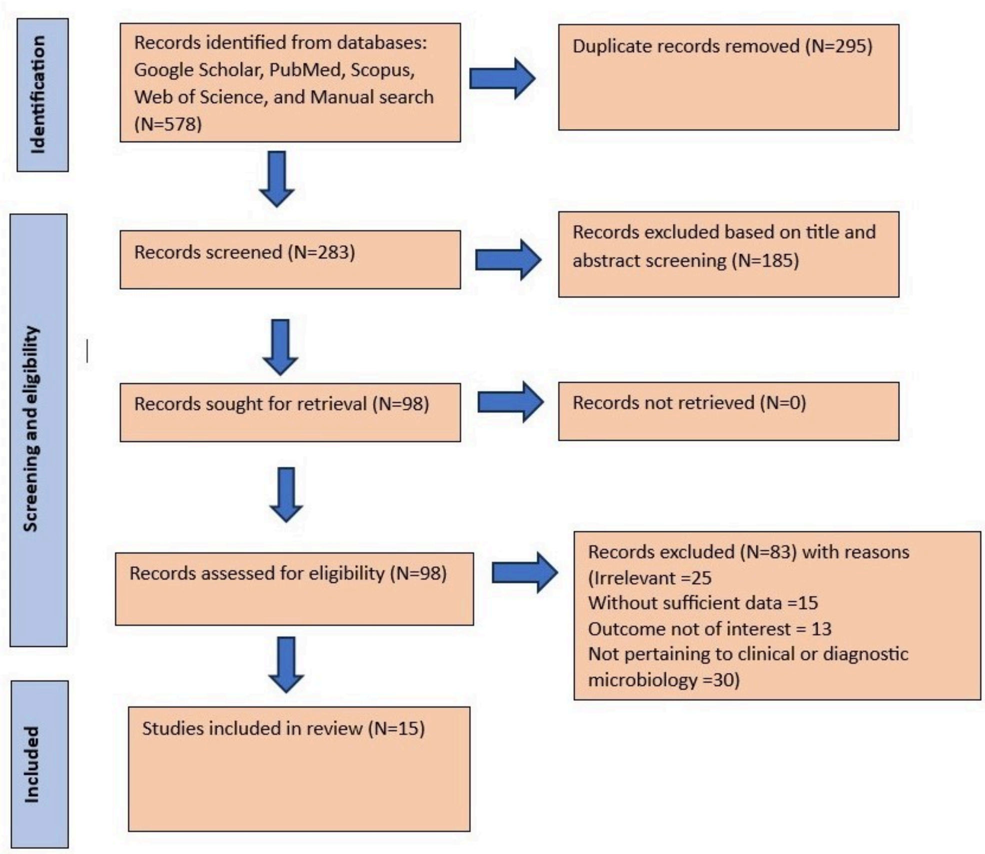

Figure 1: Flow diagram for study selection as per PRISMA guideline

Uses of AI in Clinical Microbiology

Identification of pathogenic microorganisms

Prominent manufacturers in life science technology have built a deep convolutional neural network for reproducing images in urine sample analysis, with authors reporting 98% accuracy for the overall model. The CNN is an AI model that is influenced by mammalian visual cortex. The convolutional layer detects the abstract features of an image. These can be rotated, shifted, or squashed. So, if a human can recognize the features, it is likely that CNN can too [10].

AI models can also predict the course of infections through analysis of patient symptoms, laboratory and other diagnostic tests. These can assist physicians to determine the most effective treatment modalities for their patients [14].

Genetic mutations associated with infectious diseases can also be identified by AI driven analysis of large amounts of data. ML works by identifying similarities in the DNA sequences of organisms

To trace their origins, and groups them according to their genetic sequences [15]. Consideration of contamination requires delineating whether the unknown organism is related to a previously characterized organism or is a novel identity. Identification of contamination requires a supervised approach, and is a focus of future studies [14].

Detection of bacterial growths

At present, the only class II medical device system with FDA clearance is Automated Plate Assessment System (APAS®) Independence (Clever Culture Systems). Gammel et al, used this technology to triage *Staphylococcus aureus* and methicillin-resistant *Staphylococcus aureus* (MRSA) cultures (with samples collected from the nares). The study confirmed the accuracy of digital image analysis with a negative predictive value (NPV) of 100%, implying that intervention by a microbiologist will only be required in cases of significant growths. No growths can be reliably reported using this system [2].

Glasson et al, used this technology to screen urine cultures, which displayed a sensitivity of 99% and specificity of 84.5%. Growth was detected on 99.5% of MacConkey agar plates and 99% of blood agar plates. Growth detection performance varied with the colony forming units (CFU). In blood agar plates, the sensitivity was 99.9% at 10^5 CFU, 99.6% at 10^4 CFU, and 97.3% at 10^3 CFU. In MacConkey agar plates, the sensitivity was 99.9% at 10^5 CFU, 99.6% at 10^4, and 98.65% at 10^3 CFU [3]. This technology is particularly useful in urine samples, as they are usually received in bulk since urinary tract infection is a common infection prevalent in both hospitals and the community [1].

PhenoMatrix™ (BioMerieux, Craponne, France) that a similar application system which has published literature on *Streptococcus pyogenes* and group B *Streptococcus* [16,17]. The user assesses the agar plate and decides whether to report the algorithm decision or perform subsequent testing.

Positive culture findings can be detected through a computational image analysis technique called Chromogenic media image detection system, which has high sensitivity and specificity. It has numerous advantages, such as overcoming the manual error that arises due to subjective variation, and assessing high volumes of samples even without an ample workforce [1].

Interpretation of culture plates using an expert image analysis system can be used as an effective screening tool for prompt and accurate reading of culture plates. It acts as a better differentiator of positive cultures from negative cultures. However, accurate assessment of contamination is a challenging task for AI, and the final decision for reporting rests with the microbiologist [4].

Given the applications described above, there are substantial reasons to expect more from AI. This will challenge the manufacturers of the media industry as AI requires strict adherence to physical and chemical conditions. The media was initially developed for a well-trained microbiologist’s eye, and not for an advanced imaging system. To the best of our knowledge there aren’t any existing industrial modifications that have been implemented to accommodate AI. This technology urges that individuals in regulatory positions are eventually bound to work with AI development specialists. This phenomenal shift will bring advancements in technology, decreasing laboratory turn-around times aiding in prompt and accurate patient management.

Microscopy

AI can also detect high resolution images from microscopic slides. A study at Beth Israel Deaconess Medical Centre revealed that AI enhanced microscopes have the potential to aid microbiologists in analyzing images of bacteria promptly and accurately [18]. Based on the bacterial morphology, such as cocci in clusters or chains, it can accurately detect *Staphylococcus* or *Streptococcus* respectively. ML algorithms extract knowledge from microscopy images by supervised and unsupervised learning. It sorts the images into 3 categories, namely, round clusters, round pairs or chains, and rod-shaped bacteria, with approximately 95% accuracy [8].

AI can also fuel microscopy-based virological research, aiding in the accurate diagnosis of viral infections. AI-driven algorithms have been applied for detection of virus-specific antibodies, viral immunosuppression, viral replication, and screening for antiviral targets [19-22]. Deep learning models such as neural networks have evolved the virus microscopy data interpretation through

Image acquisition and analysis. Feedforward neural networks, autoencoders, fully convolutional networks, and vision transformers are some of the artificial neural networks used for biological image analysis [9].

Routine clinical parasitology involves the labour-intensive task of examining smears for hours, which often turn negative for parasites such as protozoa [23, 24]. A study by Mathison et al, describes the detection of protozoa and helminthic ova in trichome stained faecal smears through deep convolutional neural networks. This study corroborated computer vision application through precision, accuracy, and limit of detection analysis [23]. A validation set is necessary for implementing any AI application for clinical and diagnostic use. This has made computer vision optimal for screening large amounts of data and images (identifying the negative smears), while human expertise can be utilized for critical thinking and complex pattern recognition (confirmation of the diagnosis of positive smears) [6, 23].

A study by Racsa et al described the use of CellaVision® (Lund, Sweden) for detecting *Plasmodium* and *Babesia* species in peripheral blood smears. The detection rate was 100% when parasitaemia was ≥2.5% and 63% when it was <0.1%. This software can also be used for storing images for training and educational purposes [25]. Having said that, more studies are required on the use of AI in microscopy before it can overtake the conventional procedures.

Colony counting

Culture plate interpretations require years of training and professional experience, and in spite of that, microbiologists are prone to making errors while colony counting. Through AI, advances have been made in visual assessment of images. ML can detect small and mixed colonies with a higher image resolution and sensitivity than a human eye. Various factors which affect this are- ability to segregate closely positioned colonies, zooming function for smaller colonies, counting colonies from all sectors of culture plate, visualization of fluorescent colonies, and differentiation between color and clear media. Although, considerable progress has been made, ML applications for colony counting are not completely reliable as of now. Main obstacles are colony forming units (CFUs) close to the boundary of petri dish, low image resolution, high CFU density, and artifacts on petri dish's boundary [8].

Diagnosis of antimicrobial resistance mechanisms and drug development

AI models have also been used for the development of new antimicrobial drugs and treatment modalities for infectious diseases. One can identify potential antimicrobial targets and the analyze their effectiveness. Along with this, AI is also being used for analysis of large amounts of data pertaining to the side effects of these drugs [14]. Wong F et al, have mentioned the development of a novel antibiotic class active against MRSA using deep learning in their study [26].

AI has the ability to quickly go through large data sets such as those generated from matrix-assisted laser desorption- ionization/ time of flight mass spectrometry (MALDI-TOF MS). These include data analysis from primary culture plates, metagenomic microorganism findings, and bacterial genetic data. Coupling of mass spectra data with ML algorithms can significantly improve organism and antimicrobial resistance detection through enhanced discrimination between closely related sub lineages. Use of supervised and unsupervised ML algorithms allows identification and differentiation of features whose expression is integral for species classification. Feucherolles et al, have revealed the use of MALDI-TOF MS in combination with ML in their study using the Python programming language. They have effectively detected antimicrobial resistance in *Campylobacter* species with a sensitivity of 92.3% and 81.2% precision [5]. Nguyen et al, have tested ML models for predicting minimum inhibitory concentrations (MIC) along with the genetic characteristics of non-typhoidal *Salmonella* (NTS) with accuracy as high as 95% [27].

CellaVision® (Lund, Sweden) is commonly used for classification of white blood cell morphology. Apart from this, it can be used for detecting vancomycin resistance in *Enterococci* and methicillin resistance in *Staphylococci* from culture specimens, acid-fast bacilli, malarial parasites, and even aid in antimicrobial susceptibility testing (AMST). It is a software that is based on computer vision but requires expert human opinion for the final diagnosis and reporting of the complex image patterns [28-36].

WASPLab Chromogenic Detection Module (CDM) (Copan, Brescia, Italy) software works by

Detecting pigmented colonies by a digital camera, followed by segregation into positive and negative cultures on chromogenic MRSA agar plates. Positive colonies are determined on the basis of hue, saturation, and value (HSV) score. A study by Faron ML et al, used digital camera for capturing images at 0 and 16-24 hours. If the HSV score falls into a set threshold, then it is deemed positive for MRSA. This automated digital analysis system was compared to manual reading, and exhibited a sensitivity and specificity of 100% and 90.7% respectively [28]. In another study, CDM was successful in determining vancomycin resistant *Enterococci* negative cultures from chromogenic agar plates with a sensitivity of 100% and a specificity of 89.5% [29].

Recently, AI algorithms have been shown to detect aminoglycoside resistance in *Escherichia coli* and *Staphylococcus aureus* [37]. Multiple large-scale laboratories are installing AI for pathogen identification and AMST. Kiestra TLA system (Becton Dickinson, Franklin Lakes, NJ, USA) and WASPLab (Copan Diagnostics Inc., Murrieta, CA, USA) are examples of such laboratories [38].

In a diagnostic microbiology laboratory that deals with molecular tests such as proteomics and genetic sequencing, AI systems can be beneficial not only for storage, but also for interpretation and analysis of large amounts of complex data that is being generated from these laboratories [6].

Table 1 summarizes AI technologies in clinical microbiology and their diagnostic benefits.

Table 1: Summary of AI technologies that can be used in clinical microbiology

Study	Type of AI algorithm	Commercial software/tool/organization	Clinical microbiology task
Mishra A et al [1]	Machine learning	Unknown	Hospital records (laboratory information system)
DeYoung B et al [4]	Machine learning	Automated Plate Assessment System (APAS®)	Detection of bacterial growths (MRSA)
Feucherolles et al [5]	Machine learning	Python programming language (v3.7.6) & Scikit-learn package (v0.22.1) in Jupyter NoteBook (v6.0.3)	Antimicrobial drug resistance detection in Campylobacter species
Sandle T et al [8]	Machine learning	Beth Israel Deaconess Medical Center (Boston, Massachusetts)	Morphology of Staphylococcus, Streptococcus; colony counting
Petkidis A et al [9]	Deep convolutional neural network	Atomwise (San Francisco, California)	Detection of virus-specific antibodies, viral immunosuppression, viral replication, and screening for antiviral targets
Alouani DJ et al [10]	Convolutional neural network	Xception and InceptionResNetV2 (BacterioSight platform)	Urine sample analysis
Khaledi A et al [12]	Machine learning	Support Vector Machine (SVM) classifier	Antimicrobial drug resistance detection in Pseudomonas aeruginosa
Baker J et al [16] and	Machine learning	PhenoMatrix™	Detection of bacterial growths (Group B Streptococcus and Streptococcus pyogenes
Van TT et al [17]			
Mathison BA et al [23]	Deep convolutional neural network	Pannoramic 250 Flash III (3DHISTECH, Budapest, Hungary) viewer software	Protozoa and helminthic ova detection in trichome stained smears
Racsa LD et al [25]	Deep convolutional neural network	CellaVision® DM96 (Lund, Sweden)	Plasmodium and Babesia detection in peripheral blood smears
Wong F et al [26]	Deep convolutional neural network	Chemprop	Novel class of antibiotic discovery against MRSA
Nguyen et al [27]	Machine learning	Extreme Gradient Boosting (XGBoost)	Detection of minimum inhibitory concentrations, and associated genotypic features of non-typhoidal Salmonella
Faron ML et al [30, 31]	Machine learning	WASPLab® image analysis software (Copan, Brescia, Italy)	Detection of methicillin-resistant Staphylococcus aureus and vancomycin resistant Enterococci on chromogenic agar plates

Hospital records

ML is the predominant form of AI that is being used in healthcare. Natural language processing

(NLP) is a technique of AI that helps in the maintenance of electronic records generated from laboratory information systems (LIS). This can be used for providing valuable information regarding clinical signs and symptoms aiding in the diagnosis of infectious diseases. Speech analysis is an application of NLP that can develop a conversational form of AI translating patient interaction with the clinician, thereby, helping the laboratory personnel in the analysis of health records and clinical notes [1]. Some of the AI algorithms that are used for maintenance of health records are Augmedix (San Francisco, California), CloudMedX (Palo Alto, California), and Regard (Los Angeles, California) [39-41].

Limitations of AI

Although AI seems beneficial in the foresight, there are certain challenges that should be addressed at the earliest. Firstly, AI interprets single nucleotide polymorphisms (SNPs) that are phenotypically distinct as separate organisms. SNPs are variations at a single nucleotide position in the DNA sequence among individuals of the same species. These variations can lead to phenotypic differences. Secondly, interpretation of AMST data might become a hurdle when distinct classes show overlapping mechanisms of action with multidrug resistant mechanisms often co-existing in the same organism [1]. Thirdly, interpretation of contamination might be an issue as it requires broad and varied experience with insight into the type of specimen and overall clinical picture of the case [4]. Fourthly, the algorithm is developed for a designated set of variables, which should remain fixed and under strict control. For any given AI system, based on the visual detection of patterns or arrays, changing the lighting and camera angles will develop new images, affecting the overall performance of the algorithm [1]. This will require algorithm remediation followed by re-validation activities. These issues can be addressed as they are not insurmountable but require repeated patterns of learning.

Conclusion

A generation ago, polymerase chain reaction was the latest modality, and today nucleic acid amplification-based molecular tests are an integral component of a clinical diagnostic laboratory, especially after the COVID-19 pandemic. Similarly, AI is set to become an indispensable technological advancement in the field of diagnostic microbiology in the next decade. In the era of creative diagnostic laboratories being more accessible, clinical microbiologists should be encouraged to partner with information technology specialists to explore artificial intelligence and develop an in-depth knowledge of computer vision specific to clinical microbiology.

Future Perspectives and the Road Ahead

In conjunction with automation, AI can pave the way for rapid microbiology, which will be instrumental in overcoming the error-prone, time-consuming, and slow processes. Having said that, one should consider some key aspects before adopting the routine use of AI. Firstly, it may not be possible to bypass the human intelligence of clinical microbiologists; however, reporting can be enhanced by introducing more precision. Secondly, one should use AI as a strong screening tool and expert human opinion for verification of the computer algorithm. A bimodal approach of utilizing both AI (increasing sensitivity by analyzing large data promptly) and expert human opinion (increasing specificity with objective analysis and complex pattern recognition) should be used for effective patient outcomes. Attempts should be carried out to welcome these technologies in the rural and remote areas where there is a dire shortage of laboratory personnel. Addressing the hurdles with AI is essential before its amalgamation in the routine diagnostic microbiology. AI has the potential to dramatically reconstruct diagnostic microbiology, and with the present knowledge, we have only scratched the tip of the iceberg.

Abbreviations

AI: Artificial intelligence

CFUs: Colony forming units

CNN: Convolutional neural network

FCN: Fully convolutional network

Supporting information: None

Ethical Considerations: Not applicable

Acknowledgments: None

Funding: This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Author contribution statement: All authors (Initials of authors) contributed equally and attest they meet the ICMJE criteria for authorship and gave final approval for submission.

Data availability statement: Data included in article/supp. material/referenced in article.

Additional information: No additional information is available for this paper.

Declaration of competing interest: The authors declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

Clinical Trial: Not applicable

Consent for publication: Note applicable

References

[1] Mishra A, Khan S, Das A, Das BC. Evolution of diagnostic and forensic microbiology in the era of artificial intelligence. Cureus. 2023;15 (9): 45738. *[Crossref][PubMed][Google Scholar]*

[2] Gammel N, Ross TL, Lewis S, Olson M, Henciak S, Harris R, et al. 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. J Clin Microbiol. 2021;59(11):10-128. *[Crossref][PubMed][Google Scholar]*

[3] Glasson J, Hill R, Summerford M, Giglio S. Observations on variations in manual reading of cultures. J Clin Microbiol. 2016;54(11):2841. *[Crossref][PubMed][Google Scholar]*

[4] DeYoung B, Morales M, Giglio S. Microbiology 2. 0–A “behind the scenes” consideration for artificial intelligence applications for interpretive culture plate reading in routine diagnostic laboratories. Front Microbiol. 2022;13:2898. *[Crossref][PubMed][Google Scholar]*

[5] Feucherolles M, Nennig M, Becker SL, Martiny D, Losch S, Penny C, et al. Combination of MALDI-TOF mass spectrometry and machine learning for rapid antimicrobial resistance screening: The case of Campylobacter spp. Front microbiol. 2022; 12:804484. *[Crossref][PubMed][Google Scholar]*

[6] Rhoads DD. Computer vision and artificial intelligence are emerging diagnostic tools for the clinical microbiologist. J Clin Microbiol. 2020; 58(6):10-128. *[Crossref][PubMed][Google Scholar]*

[7] Melo MC, Maasch JR, de la Fuente-Nunez C. Accelerating antibiotic discovery through artificial intelligence. Commun Biol. 2021; 4(1):1050. *[Crossref][PubMed][Google Scholar]*

[8] Sandle T. Enhancing rapid microbiology methods: how AI is shaping microbiology. Eur Pharm Rev. 2021; 26(6): 38-40. *[Crossref][PubMed][Google Scholar]*

[9] Petkidis A, Andriasyan V, Greber UF. Machine learning for cross-scale microscopy of viruses. Cell Rep Methods. 2023; 3:100557. *[Crossref][PubMed][Google Scholar]*

[10] Alouani DJ, Ransom EM, Jani M, Burnham CA, Rhoads DD, Sadri N. Deep convolutional neural networks implementation for the analysis of urine culture. Clin Chem. 2022; 68(4): 574-83. *[Crossref][PubMed][Google Scholar]*

[11] Fjell CD, Jenssen H, Hilpert K, Cheung WA, Panté N, Hancock RE, et al. Identification of novel antibacterial peptides by chemoinformatics and machine learning. J Med Chem. 2009; 52(7): 2006-15. *[Crossref][PubMed][Google Scholar]*

[12] Khaledi A, Weimann A, Schniederjans M, Asgari E, Kuo TH, Oliver A, et al. Predicting antimicrobial resistance to Pseudomonas aeruginosa with machine learning-enabled molecular diagnostics. EMBO Mol Med. 2020;12(3):e10264. [Crossref][PubMed][Google Scholar]

[13] The United States Food and Drug Administration. Good Machine Learning Practice for Medical Device Development: Guiding Principles, 2021. [Internet]. [cited 2024 May 28]. *Available from: [Article][Crossref][PubMed][Google Scholar]*

[14] Leo S, Cherkaoui A, Renzi G, Schrenzel J. Mini review: clinical routine microbiology in the era of automation and digital health. Front Cell Infect Microbiol. 2020; 10:582028. *[Crossref][PubMed][Google Scholar]*

[15] Barman RK, Mukhopadhyay A, Maulik U, Das S. Identification of infectious disease-associated host genes using machine learning techniques. BMC Bioinf. 2019;20:736. *[Crossref][PubMed][Google Scholar]*

[16] Baker J, Timm K, Faron M, Ledeboer N, Culbreath K. Digital image analysis for the detection of Group B Streptococcus from ChromID Strepto B medium using PhenoMatrix algorithms. J Clin Microbiol. 2020;59(1):10-128. *[Crossref][PubMed][Google Scholar]*

[17] Van TT, Mata K, Dien Bard J. Automated detection of Streptococcus pyogenes pharyngitis by use of Colorex Strep A CHROMagar and WASPLab artificial intelligence chromogenic detection module software. J Clin Microbiol. 2019; 57(11):10-128. *[Crossref][PubMed][Google Scholar]*

[18] Smith KP, Kang AD, Kirby JE. Automated interpretation of blood culture gram stains by use of a deep convolutional neural network. J Clin Microbiol. 2018; 56(3):10-128. *[Crossref][PubMed][Google Scholar]*

[19] Pape C, Remme R, Wolny A, Olberg S, Wolf S, Cerrone L, et al. Microscopy-based assay for semi-quantitative detection of SARS-CoV-2 specific antibodies in human sera: A semi-quantitative, high throughput, microscopy-based assay expands existing approaches to measure SARS-CoV-2 specific antibody levels in human sera. Bioessays. 2021;43(3):2000257. *[Crossref][PubMed][Google Scholar]*

[20] Jiang S, Chan CN, Rovira-Clavé X, Chen H, Bai Y, Zhu B, et al. Combined protein and nucleic acid imaging reveals virus-dependent B cell and macrophage immunosuppression of tissue microenvironments. Immunity. 2022;55(6):1118-34. *[Crossref][PubMed][Google Scholar]*

[21] Lee JY, Wing PAC, Gala DS, Noerenberg M, Järvelin AI, Titlow J, et al. Absolute quantitation of individual SARS-CoV-2 RNA molecules provides a new paradigm for infection dynamics and variant differences. Elife. 2022;11:e74153. *[Crossref][PubMed][Google Scholar]*

[22] Kratzel A, Kelly JN, V'kovski P, Portmann J, Brüggemann Y, Todt D, et al. A genome-wide CRISPR screen identifies interactors of the autophagy pathway as conserved coronavirus targets. PLoS Biol. 2021;19(12):e3001490. *[Crossref][PubMed][Google Scholar]*

[23] Mathison BA, Kohan JL, Walker JF, Smith RB, Ardon O, Couturier MR. Detection of intestinal protozoa in trichrome-stained stool specimens by use of a deep convolutional neural network. J Clin Microbiol. 2020;58(6):10-128. *[Crossref][PubMed][Google Scholar]*

[24] Khan M, Gentile N, Zhou YS, B A, Yen E. An audit of stool ova and parasite (O&P) testing in a multi-hospital health system. Am J Gastroenterol. 2016;111:S429-30. *[Crossref][PubMed][Google Scholar]*

[25] Racsa LD, Gander RM, Southern PM, McElvania TeKippe E, Doern C, Luu HS. Detection of intracellular parasites by use of the CellaVision DM96 analyzer during routine screening of peripheral blood smears. J Clin Microbiol. 2015;53(1):167-71. *[Crossref][PubMed][Google Scholar]*

[26] Wong F, Zheng EJ, Valeri JA, Donghia NM, Anahtar MN, Omori S, et al. Discovery of a structural class of antibiotics with explainable deep learning. Nature. 2024;626:177-85. *[Crossref][PubMed][Google Scholar]*

[27] Nguyen M, Long SW, McDermott PF, Olsen RJ, Olson R, Stevens RL, et al. Using machine learning to predict antimicrobial mics and associated genomic features for nontyphoidal Salmonella. J Clin Microbiol. 2019;57(2):10-128. *[Crossref][PubMed][Google Scholar]*

[28] Fader RC, Weaver E, Fossett R, Toyras M, Vanderlaan J, Gibbs D, et al. Multilaboratory study of the biomic automated well-reading instrument versus MicroScan WalkAway for reading MicroScan antimicrobial susceptibility and identification panels. J Clin Microbiol. 2013;51(5):1548-54. *[Crossref][PubMed][Google Scholar]*

[29] Cherkaoui A, Renzi G, Fischer A, Azam N, Schorderet D, Vuilleumier N, et al. Comparison of the Copan WASPLab incorporating the BioRad expert system against the SIRscan 2000 automatic for routine antimicrobial disc diffusion susceptibility testing. Clin Microbiol Infect. 2020;26(5):619-25. *[Crossref][PubMed][Google Scholar]*

[30] Faron ML, Buchan BW, Vismara C, Lacchini C, Bielli A, Gesu G, et al. Automated scoring of chromogenic media for detection of methicillin-resistant Staphylococcus aureus by use of WASPLab image analysis software. J Clin Microbiol. 2016;54(3):620-4. *[Crossref][PubMed][Google Scholar]*

[31] Faron ML, Buchan BW, Coon C, Liebregts T, van Bree A, Jansz AR, et al. Automatic digital analysis of chromogenic media for vancomycin-resistant-Enterococcus screens using Copan WASPLab. J Clin Microbiol. 2016;54(10):2464-9. *[Crossref][PubMed][Google Scholar]*

[32] Panicker RO, Soman B, Saini G, Rajan J. A review of automatic methods based on image processing techniques for tuberculosis detection from microscopic sputum smear images. J Med Syst. 2016;40:1-3. *[Crossref][PubMed][Google Scholar]*

[33] Zingue D, Weber P, Soltani F, Raoult D, Drancourt M. Automatic microscopic detection of mycobacteria in sputum: a proof-of-concept. Sci Rep. 2018;8(1):11308. *[Crossref][PubMed][Google Scholar]*

[34] Prasad K, Winter J, Bhat UM, Acharya RV, Prabhu GK. Image analysis approach for development of a decision support system for detection of malaria parasites in thin blood smear images. J Digit Imaging. 2012;25:542-9. *[Crossref][PubMed][Google Scholar]*

[35] Kuo PC, Cheng HY, Chen PF, Liu YL, Kang M, Kuo MC, et al. Assessment of expert-level automated detection of Plasmodium falciparum in digitized thin blood smear images. JAMA Netw Open. 2020;3(2):e200206. *[Crossref][PubMed][Google Scholar]*

[36] Poostchi M, Silamut K, Maude RJ, Jaeger S, Thoma G. Image analysis and machine learning for detecting malaria. Transl Res. 2018; 194: 36-55. *[Crossref][PubMed][Google Scholar]*

[37] Peiffer-Smadja N, Dellière S, Rodriguez C, Birgand G, Lescure FX, Fourati S, et al. Machine learning in the clinical microbiology laboratory: has the time come for routine practice? Clin Microbiol Infect. 2020;26(10):1300-9. *[Crossref][PubMed][Google Scholar] [Crossref][PubMed][Google Scholar]*

[38] Croxatto A, Prod'hom G, Faverjon F, Rochais Y, Greub G. Laboratory automation in clinical bacteriology: what system to choose? Clin Microbiol Infect. 2016; 22(3): 217-35. *[Crossref][PubMed][Google Scholar]*

[39] Fox A. HCA deploys AI from Augmedix for acute care documentation in Eds Healthcare IT News2025. [Internet]. [cited 2024 May 6]. *Available from: [Article][Crossref][PubMed][Google Scholar]*

[40] Medsphere Systems corporation. Medsphere adds CloudMedx Artificial Intelligence to CareVue HER Platform [Press Release], Carlsbad, California July 9, 2019. [Internet]. [cited 2024 May 10]. *Available from: [Article][Crossref][PubMed][Google Scholar]*

[41] Aquino S. How healthcare firm Regard uses Artificial Intelligence to usher medicine into modern age. [Internet]. [cited 2024 May 12]. *Available from: [Article][Crossref][PubMed][Google Scholar]*