Artificial Intelligence in Microbiology: Transforming Diagnostics, Antimicrobial Resistance and Public Health: A Review

[1]Magimai Rufus A.J, *Deepa S*[4], *[2]Bharathi B, [3]Deepa C.Philip
[1]*II BSc Medical lab technology, MMM College of health sciences*
[2*]*Associate Professor, Microbiology, MMM College of health sciences*
[3]*Principal, MMM College of health sciences*
[4]*Assistant Professor, MMM College of Health Sciences*

Abstract - The new technologies based on AI are changing microbiology for the better by improving diagnostics, fighting against antimicrobial resistance (AMR), and even improving public health surveillance. The use of machine learning algorithms along with predictive modeling tools and neural networks has made it easier to identify different microorganisms and patterns in genomic data as well as predict future outbreaks. This review aims to analyze the application of AI in modern microbiological diagnostics, AI-powered research in smart antibiotics, and epidemiological interventions while also considering subsequent trends and outcome.

Key words: Artificial intelligence, machine learning, antimicrobial resistance, predictive modeling, neural networks, genomic data analysis, smart antibiotics, public health surveillance, AI-powered research, healthcare

1. INTRODUCTION

The field of AI and its branches, such as ML and DL, are streamlining efforts in microbiological diagnostics, AMR supervision, and even in the public health response systems by augmenting them with analytics far beyond human capabilities [Topol EJ., 2019]. The rapidly emergent ecosystem of forensic microbial genomics, electronic healthcare records, as well as imaging systems is enabling technologically advanced shifts that were previously unimaginable due to a lack of adequate infrastructure [Esteva *et al*., 2019].

2. AI IN MICROBIOLOGICAL DIAGNOSTICS

2.1 AI-Powered Pathogen Identification

AI-enabled algorithms are capable of analyzing genomic sequences as well as mass spectrometry data to detect pathogens. Bacteria classification is accomplished by convolutional neural networks (CNNs) on Gram-stained images, while NLP aids in identifying intricate patterns for diagnosis within unstructured clinical documents [Smith *et al*., 2020], [Rajkomar *et al*., 2020].
The identification of bacteria in clinical samples has been significantly improved with the application of MALDI-TOF MS in combination with machine learning, providing results in mere minutes [Weis *et al*., 2019].

2.2 Automated Culture Interpretation and Antimicrobial Susceptibility Testing

Robotic systems driven by artificial intelligence enable automated culture interpretation and antibiotic susceptibility testing while alleviating human error and enhancing efficiency in operational workflows [Doern CD., 2019]. Automated reading of plates is possible because computer vision systems are capable of identifying the morphology of bacterial colonies and the patterns of hemolysis [Jung *et al*., 2021].

3. COMBATING ANTIMICROBIAL RESISTANCE (AMR)

3.1 Predictive Modeling for Resistance Gene Detection

Now, with AI models, it is possible to obtain phenotype information based on genomic sequences which accelerates AST turn around time. Predictive deep learning has been effective in determining some genes associated with resistance and β-lactamase production in E. coli and K. pneumoniae species [Su *et al*., 2020].

One such example is DeepARG, a model known for successfully retrieving antibiotic resistance genes from metagenomic datasets [Arango-Argoty *et al*., 2018]. Equally effective is the tool PathoFact, which utilizes ensemble ML techniques for detection of ARGs as well as other virulence factors [de Nies *et al*., 2021].

3.2 AI-Enhanced Antimicrobial Stewardship and Resistance Surveillance

AI actively aids antimicrobial stewardship programs by assessing the issuing of prescriptions while hypothesizing probable suggested regimens that can dispensed based on pre-determined susceptibility profiles [Chokshi *et al*., 2021]. Linkage with electronic health record systems facilitates active monitoring of resistance patterns over time across multiple hospitals, enhancing control of infections [Kelly *et al*.,2019].

AI powered interfaces like IBM Watson or MedAware have been used to overlooking inappropriate prescription and suggest better evidence-based alternatives along with their justifications which greatly improves clinical workflows reliance on documents provided by referring physicians to make decisions that may not be beneficial to the patient's health[Bates et 2018].

4. PUBLIC HEALTH APPLICATIONS OF AI IN MICROBIOLOGY

4.1 AI for Infectious Disease Outbreak Prediction and Monitoring

AI technologies are pivotal in monitoring infectious disease outbreaks using data from laboratories, social media, climate sensors, and electronic health records (EHRs). HealthMap and BlueDot are two programs that leverage AI to forecast influenza, COVID-19, and even some foodborne illnesses [Brownstein *et al*., 2019].

Throughout the COVID-19 pandemic, AI models played a significant role in predicting outbreak scenarios alongside analyzing the public health responses to control the spread [Chinazzi *et al*., 2020].

4.2 Genomic Epidemiology Enabled by Artificial Intelligence

The application of AI on whole genome sequencing (WGS) data for pathogens provides insights into transmission pathways, clonal expansion, zoonotic reservoirs, as well as phylogenetic tree reconstruction with emerging variant identification through clustering algorithms which supports targeted response actions [Armstrong *et al*., 2019].

The use of genomic surveillance has been effective in tracking other diseases such as MDR-TB and MRSA, which showcases its effectiveness when used with AI technology focusing on genomic data [Walker *et al*., 2015].

4.3 AI-Driven Wastewater Surveillance for Early Detection

Through the application of AI concepts in environmental health monitoring, it is possible to identify community infections long before they become apparent through testing by evaluating wastewater microbiological content. Combined with artificial intelligence (AI), this method can rapidly diagnose enteric diseases as well as SARS-CoV-2 and the dissemination of antimicrobial resistance (AMR) genes in the environment [Medema *et al*., 2020].

5. MACHINE LEARNING APPLICATIONS IN MICROBIOLOGICAL RESEARCH

5.1 Supervised Learning for Microbial Classification and Prediction

The classification of microbial species, resistance profiles, and virulence patterns has been commonly undertaken using supervised learning algorithms like SVMs, random forests, and logistic regression [Nguyen *et al*., 2021]. These methods depend on training datasets that are labeled and are created from EHRs or genomic databases.

5.2 Unsupervised and Reinforcement Learning in Microbial Data Analysis

K-means clustering and principal component analysis (PCA) are examples of unsupervised learning techniques that have been applied to the exploration of complex microbial community structures in metagenomics [Pasoli *et al*., 2016]. While not widely adopted, reinforcement learning can apply to the refinement of laboratory workflows as well as antibiotic treatment frameworks [Komorowski *et al*., 2018].

6. BARRIERS TO AI IMPLEMENTATION IN MICROBIOLOGY

6.1 Data Quality, Bias, and Generalizability

As with any technology, AI in healthcare is only as good as the data it has been trained on. Training datasets that are incomplete or contain harmful biases often lead to incorrect predictions or underrepresentation of infrequent pathogens [Char *et al*., 2018].

6.2 Technical Challenges: Interoperability and Infrastructure

The application of AI technology requires rigid standards for data formats, high-performance computing systems, inter-institutional collaborations, as well as experts in the given field – all resources which may be missing in poorly funded institutions [Shenoy A & Appel JM., 2020].

6.3 Ethical, Legal, and Governance Considerations

The implementation of AI technology in healthcare software brings up topics such as personal data usage policies, algorithm visibility and explainability, and responsibility attribution. The governance policies concerning AI technologies in microbiology are still preliminary [Gerke *et al*., 2020].

7. FUTURE DIRECTIONS AND INNOVATIONS

7.1 Custom-tailored Infection Risks and Microbiology

Using artificial intelligence alongside patient-specific data, such as microbiome compositions and immune statuses, could enable personalized profiling of infection risks and tailored treatment strategies [Lloyd-Price *et al*., 2017].

7.2 Integrating AI with CRISPR Technologies

AI can be integrated with CRISPR gene-editing technologies to improve the editing of microbial genomes as well as synthetic biology and diagnostics with CRISPR-based biosensors [Wang *et al*., 2021].

7.3 AI's Role in Advancing the One Health Approach

One Health framework can be facilitated via AI models since they can concurrently track human, animal, and environmental reservoirs for zoonotic pathogens. This also strengthens surveillance of diseases transmitted from animals to humans [Destoumieux-Garzon *et al*., 2018].

8. CONCLUSION

The integration of artificial intelligence into microbiology is transforming the discipline by improving diagnostics, speeding up the detection of antimicrobial resistance, and enhancing surveillance systems. The relationship between microbiology and AI will improve infectious disease management and expand unprecedented opportunities when algorithms become more sophisticated and data grows increasingly abundant. Nevertheless, global ethical, infrastructural, and educational challenges need to be resolved to realize AI's full potential.

REFERENCE

[1] Topol, E. J. (2019). High-performance medicine: The convergence of human and artificial intelligence. *Nature Medicine, 25*(1), 44–56. https://doi.org/10.1038/s41591-018-0300-7

[2] Esteva, A., Robicquet, A., Ramsundar, B., Kuleshov, V., DePristo, M., Chou, K., Cui, C., Corrado, G., Thrun, S., & Dean, J. (2019). A guide to deep learning in healthcare. *Nature Medicine, 25*(1), 24–29. https://doi.org/10.1038/s41591-018-0316-z

[3] Smith, K. P., & Kirby, J. E. (2020). Image analysis and artificial intelligence in infectious disease diagnostics. *Clinical Microbiology and Infection, 26*(10), 1318–1323. https://doi.org/10.1016/j.cmi.2020.03.012

[4] Rajkomar, A., Dean, J., & Kohane, I. (2019). Machine learning in medicine. *New England Journal of Medicine, 380*(14), 1347–1358. https://doi.org/10.1056/NEJMra1814259

[5] Weis, C., Horn, M., Rieck, B., Cuénod, A., Egli, A., & Borgwardt, K. (2020). Topological and kernel-based microbial phenotype prediction from MALDI-TOF mass spectra. *Bioinformatics, 36*(Suppl_1), i30–i38. https://doi.org/10.1093/bioinformatics/btaa429

[6] Doern, C. D. (2018). The slow march toward rapid phenotypic antimicrobial susceptibility testing: Are we there yet? *Journal of Clinical Microbiology, 56*(4), e01999-17. https://doi.org/10.1128/JCM.01999-17

[7] Jung, H., Kim, S. J., Lee, J., Lee, J., & Kim, J. (2021). Deep learning-based automatic bacterial colony counting system using image processing. *Scientific Reports, 11*(1), 8594. https://doi.org/10.1038/s41598-021-87955-9

[8] Su, J. Q., An, X. L., Li, B., Chen, Q. L., Gillings, M. R., Chen, H., Zhang, T., & Zhu, Y. G. (2020). Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. *Trends in Microbiology, 28*(5), 398–407. https://doi.org/10.1016/j.tim.2020.01.009

[9] Arango-Argoty, G., Garner, E., Pruden, A., Heath, L. S., Vikesland, P., & Zhang, L. (2018). DeepARG: A deep learning approach for predicting antibiotic resistance genes from metagenomic data. *Microbiome, 6*(1), 23. https://doi.org/10.1186/s40168-018-0401-z

[10] de Nies, L., Lopes, S., Busi, S. B., Galata, V., Heintz-Buschart, A., Laczny, C. C., & Wilmes, P. (2021). PathoFact: A pipeline for the prediction of virulence factors and antimicrobial resistance genes in metagenomic data. *Bioinformatics, 37*(18), 2825–2832. https://doi.org/10.1093/bioinformatics/btab157

[11] Chokshi, A., Sifri, Z., Cennimo, D., & Horng, H. (2021). Artificial intelligence in antibiotic stewardship: A systematic review. *The Lancet Infectious Diseases, 21*(3), e60–e67. https://doi.org/10.1016/S1473-3099(20)30563-8

[12] Kelly, C. J., Karthikesalingam, A., Suleyman, M., Corrado, G., & King, D. (2019). Key challenges for delivering clinical impact with artificial intelligence. *BMC Medicine, 17*(1), 195. https://doi.org/10.1186/s12916-019-1426-2

[13] Bates, D. W., & Hong, J. C. (2018). Artificial intelligence in health care: Applications and legal implications. *Journal of the American Medical Informatics Association, 25*(8), 1036–1042. https://doi.org/10.1093/jamia/ocy072

[14] Brownstein, J. S., Freifeld, C. C., & Madoff, L. C. (2009). Digital disease detection—Harnessing the Web for public health surveillance. *New England Journal of Medicine, 360*(21), 2153–2157. https://doi.org/10.1056/NEJMp0900702

[15] Chinazzi, M., Davis, J. T., Ajelli, M., Gioannini, C., Litvinova, M., Merler, S., Pastore Y Piontti, A., Mu, K., Rossi, L., Sun, K., Viboud, C., Xiong, X., Yu, H., Halloran, M. E., Longini, I. M. Jr., & Vespignani, A. (2020). The effect of travel restrictions on the spread of the 2019 novel coronavirus (COVID-19) outbreak. *Science, 368*(6489), 395–400. https://doi.org/10.1126/science.aba9757

[16] Armstrong, G. L., MacCannell, D. R., Taylor, J., Carleton, H. A., Neuhaus, E. B., Bradbury, R. S., Posey, J. E., & Gwinn, M. (2019). Pathogen genomics in public health. *New England Journal of Medicine, 381*(26), 2569–2580. https://doi.org/10.1056/NEJMsr1813907

[17] Walker, T. M., Kohl, T. A., Omar, S. V., Hedge, J., Del Ojo Elias, C., Bradley, P., Iqbal, Z., Feuerriegel, S., Niehaus, K. E., Wilson, D. J., Clifton, D. A., Kapatai, G., Ip, C. L. C., Bowden, R., Drobniewski, F. A., Allix-Béguec, C., Gaudin, C., Parkhill, J., Diel, R., Supply, P., Crook, D. W., Smith, E. G., Walker, A. S., Ismail, N., Niemann, S., & Peto, T. E. A. (2015). Whole-genome sequencing for prediction of *Mycobacterium tuberculosis* drug susceptibility and resistance: A retrospective cohort study. *The Lancet Infectious Diseases, 15*(10), 1193–1202. https://doi.org/10.1016/S1473-3099(15)00062-6

[18] Medema, G., Heijnen, L., Elsinga, G., Italiaander, R., & Brouwer, A. (2020). Presence of SARS-Coronavirus-2 RNA in sewage and correlation with reported COVID-19 prevalence in the early stage of the epidemic in the Netherlands. *Environmental Science & Technology, 54*(23), 14263–14271. https://doi.org/10.1021/acs.est.0c03895

[19] Nguyen, M., Long, S. W., McDermott, P. F., Olsen, R. J., Olson, R., Stevens, R. L., Tyson, G. H., Zhao, S., & Davis, J. J. (2021). Using machine learning to predict antimicrobial MICs and associated genomic features for nontyphoidal *Salmonella*. *Briefings in Bioinformatics, 22*(3), bbaa225. https://doi.org/10.1093/bib/bbaa225

[20] Pasolli, E., Truong, D. T., Malik, F., Waldron, L., & Segata, N. (2016). Machine learning meta-analysis of large metagenomic datasets: Tools and biological insights. *Cell Host & Microbe, 20*(5), 690–702. https://doi.org/10.1016/j.chom.2016.10.012

[21] Komorowski, M., Celi, L. A., Badawi, O., Gordon, A. C., & Faisal, A. A. (2018). The Artificial Intelligence Clinician learns optimal treatment strategies for sepsis in intensive care. *Nature Medicine, 24*(11), 1716–1720. https://doi.org/10.1038/s41591-018-0213-5

[22] Char, D. S., Shah, N. H., & Magnus, D. (2018). Implementing machine learning in health care—Addressing ethical challenges. *New England Journal of Medicine, 378*(11), 981–983. https://doi.org/10.1056/NEJMp1714229

[23] Shenoy, A., & Appel, J. M. (2020). Safeguarding against algorithmic bias in healthcare: A proposed regulatory framework. *BMJ Health & Care Informatics, 27*(3), e100154. https://doi.org/10.1136/bmjhci-2020-100154

[24] Gerke, S., Minssen, T., & Cohen, I. G. (2020). Ethical and legal challenges of artificial intelligence-driven healthcare. *Journal of Law and the Biosciences, 7*(1), lsaa002. https://doi.org/10.1093/jlb/lsaa002

[25] Lloyd-Price, J., Mahurkar, A., Rahnavard, G., Crabtree, J., Orvis, J., Hall, A. B., Brady, A., Creasy, H. H., McCracken, C., Giglio, M. G., McDonald, D., Franzosa, E. A., Knight, R., White, O., & Huttenhower, C. (2017). Strains, functions and dynamics in the expanded Human Microbiome Project. *Nature, 550*(7674), 61–66. https://doi.org/10.1038/nature23889

[26] Wang, H., La Russa, M., & Qi, L. S. (2021). CRISPR-based diagnostic tools for infectious diseases and beyond. *Nature Biotechnology, 39*(12), 1450–1459. https://doi.org/10.1038/s41587-021-01028-5

[27] Destoumieux-Garzón, D., Mavingui, P., Boetsch, G., Boissier, J., Darriet, F., Duboz, P., Fritsch, C., Giraudoux, P., Le Roux, F., Morand, S., Paillard, C., Pontier, D., Sueur, C., & Voituron, Y. (2018). The One Health concept: 10 years old and a long road ahead. *One Health, 5*, 1–3. https://doi.org/10.1016/j.onehlt.2017.12.002