eMicrobe
https://www.sciltp.com/journals/eMicrobe

Editorial

In Silico Technologies Advancing Microbial Science: A Visionary Review

Lutfun Nahar [1,2]

[1] Centre for Natural Products Discovery, School of Pharmacy and Biomolecular Sciences, Liverpool John Moores University, Byrom Street, Liverpool L3 3AF, UK; profnahar@outlook.com
[2] Laboratory of Growth Regulators, Palacký University and Institute of Experimental Botany, The Czech Academy of Sciences, Šlechtitelů 27, 783 71 Olomouc, Czech Republic

Received: 2 December 2025; Accepted: 16 December 2025; 5 January 2026

How To Cite: Nahar, L. *In Silico* Technologies Advancing Microbial Science: A Visionary Review. *eMicrobe* **2026**, *2*(1), 4. https://doi.org/10.53941/emicrobe.2026.100004

The transformative impact of *in silico* methodologies on microbiology and infectious disease research has been authoritatively articulated in the inaugural editorial of *eMicrobe* [1]. The present commentary reflects upon this vision and illustrates its realisation through recent exemplary studies.

1. The Computational Redefinition of Microbiology

High-throughput sequencing, pangenomic analysis, machine-learning-enabled surveillance systems, and multi-omics convergence have rendered traditional reductionist approaches insufficient. These technologies are now regarded as foundational rather than supplementary to microbial discovery and clinical translation [1].

2. Integrated Bioinformatics Pipelines

A fully containerised, modular pipeline (MIntO) that performs paired metagenomic-metatranscriptomic analysis while preserving sample identity has been developed. This approach enables simultaneous taxonomic profiling, functional potential assessment, and active gene-expression quantification, yielding biologically coherent insights unattainable through separate analyses [2].

3. Machine Learning for Precision Diagnostics and Risk Stratification

Harmonised multi-cohort frameworks employing recursive feature elimination and ensemble learning have achieved area-under-the-curve values consistently exceeding 0.90 in predicting inflammatory bowel disease from gut microbiome data [3]. Similarly, gradient-boosting and recurrent neural network models applied directly to raw genome assemblies have attained >98% accuracy in identifying carbapenemase-producing Enterobacterales from clinical isolates [4].

4. Artificial Intelligence and Deep Learning in Biomarker Discovery

Deep-learning architectures, particularly graph neural networks and transformers, have been demonstrated to substantially outperform classical statistical methods in identifying robust gut microbiota biomarkers across metabolic, oncological, and neuropsychiatric disorders [5]. Multimodal neural networks integrating amplicon, shotgun, and host phenotypic data have further enabled personalised dietary interventions that significantly improve postprandial glycaemic control [6].

5. The Gut Microbiome as a Systems-Level Metabolic Entity

The gut microbiota is increasingly conceptualised as a dynamic metabolic organ whose myriad small-molecule effectors orchestrate systemic immunological, neurological, and xenobiotic responses. Contemporary *in silico* reconstruction of community-wide metabolic networks now permits prospective identification of taxa driving short-chain fatty acid synthesis, tryptophan catabolism, and secondary bile-acid biotransformation [7].

6. Clinical Translation and Persisting Barriers

Although 87% of surveyed European infectious-disease clinicians anticipate genomic methods becoming routine within five years, critical deficits in bioinformatics standardisation, workforce training, and reimbursement mechanisms remain [8]. Clinical metagenomic next-generation sequencing currently delivers diagnostic yields of 30–70% in culture-negative infections; however, widespread adoption continues to be impeded by high costs, prolonged turnaround times, and interpretative complexity [9].

7. Reproducibility, Openness, and Data Sovereignty

Irreproducible findings stemming from opaque preprocessing and non-deposited code are now recognised as a profound threat to microbiome science. Universal adoption of FAIR-compliant repositories, immutable containerised workflows, and standardised metadata schemas has therefore become imperative [10].

8. Predictive Modelling in the Post-Pandemic Era

Nationwide primary-care cohorts encompassing >4 million patients have been utilised to develop externally validated models revealing sustained 18–34% increases in antimicrobial-resistant community-onset infections attributable to pandemic-related disruptions in care delivery [11].

9. Global Equity and Open Science

Low- and middle-income countries, despite bearing >80% of the global infectious-disease burden, contribute <5% of microbiome publications. Open-access publishing, cloud-native analysis platforms, and distributed training initiatives are thus ethical and scientific imperatives [12].

10. Strategic Priorities for the Decade Ahead

Immediate priorities include seamless multi-omics integration with electronic health records, regulatory acceptance of explainable artificial-intelligence frameworks, internationally harmonised benchmarking standards, and systematic incorporation of computational literacy into microbiology curricula [1].

11. Conclusions

A compelling vision has been articulated in which computational rigour is fused with clinical relevance, openness with disciplined innovation, and global equity with scientific excellence [1]. By serving as the premier international platform for advancing this integration, *eMicrobe* invites researchers, clinicians, bioinformaticians, and data scientists worldwide to shape the next epoch of microbial scholarship.

Funding

Lutfun Nahar gratefully acknowledges the support from the European Regional Development Fund (Project ENOCH #CZ.02.1.01/0.0/0.0/ 16_019/0000868) and the Czech Science Foundation (Project #23-05474S).

Conflicts of Interest

The author declares no conflict of interest.

Use of AI and AI-Assisted Technologies

No AI tools were utilized for this paper.

References

1. Woo, P.C.Y. Rigorous Analysis of Microbes and Infectious Diseases Using an Expanding Range of Robust *in Silico* Technologies. *eMicrobe* **2025**, *1*, 1. https://doi.org/10.53941/emicrobe.2025.100001.

2. Saenz, C.; Nigro, E.; Gunalan, V.; et al. MIntO: A Modular and Scalable Pipeline for Microbiome Metagenomic and Metatranscriptomic Data Integration. *Front. Bioinform.* **2022**, *2*, 846922. https://doi.org/10.3389/fbinf.2022.846922.
3. Peng, Y.; Liu, Y.; Liu, Y.; et al. Comprehensive Data Optimisation and Risk Prediction Framework: Machine Learning Methods for Inflammatory Bowel Disease Prediction Based on the Human Gut Microbiome Data. *Front. Microbiol.* **2024**, *15*, 1483084. https://doi.org/10.3389/fmicb.2024.1483084.
4. Gao, Y.; Liu, M. Application of Machine Learning Based Genome Sequence Analysis in Pathogen Identification. *Front. Microbiol.* **2024**, *15*, 1474078. https://doi.org/10.3389/fmicb.2024.1474078.
5. Dakal, T.C.; Xu, C.; Kumar, A. Advanced Computational Tools, Artificial Intelligence and Machine Learning Approaches in Gut Microbiota and Biomarker Identification. *Front. Med. Technol.* **2025**, *6*, 1434799. https://doi.org/10.3389/fmedt.2024.1434799.
6. Liu, Y.Y. Deep Learning for Microbiome-Informed Precision Nutrition. *Natl. Sci. Rev.* **2025**, *12*, nwaf148. https://doi.org/10.1093/nsr/nwaf148.
7. Nahar, L. Gut Feeling: What Gut Microbes Do and Why They Matter. *J. Med. Nat. Prod.* **2025**, *2*, 100022. https://doi.org/10.53941/jmnp.2025.100022.
8. Michel, C.; Martin, C.; Smeesters, P.; et al. Next-Generation Sequencing: What Are the Needs in Routine Clinical Microbiology? A Survey Among Clinicians Involved in Infectious-Diseases Practice. *Front. Med.* **2023**, *10*, 1225408. https://doi.org/10.3389/fmed.2023.1225408.
9. Elbehiry, A.; Abalkhail, A. Metagenomic Next-Generation Sequencing in Infectious Diseases: Clinical Applications, Translational Challenges, and Future Directions. *Diagnostics* **2025**, *15*, 1991. https://doi.org/10.3390/diagnostics15161991.
10. Huttenhower, C.; Finn, R.D.; McHardy, A.C. Challenges and Opportunities in Sharing Microbiome Data and Analyses. *Nat. Microbiol.* **2023**, *8*, 1960–1970. https://doi.org/10.1038/s41564-023-01484-x.
11. Fahmi, A.; Palin, V.; Zhong, X.; et al. Evaluation of the Impact of COVID-19 Pandemic on Hospital Admission Related to Common Infections: Risk Prediction Models to Tackle Antimicrobial Resistance in Primary Care. *PLoS ONE* **2025**, *20*, e0321408. https://doi.org/10.1371/journal.pone.0321408.
12. Newton, C.R. Research and Open Access from Low- and Middle-Income Countries. *Dev. Med. Child Neurol.* **2020**, *62*, 537. https://doi.org/10.1111/dmcn.14513.