Review

Artificial intelligence for Microbiota Analysis: Advances and Applications

Abhinandan Patil * and Neha Singh

Posted Date: 27 July 2023

doi: 10.20944/preprints202307.1765.v1

Keywords: Bacteria, Microbiota, Artificial intelligence, microbiome doi:10.20944/preprints202307.1765.v1

Review

Artificial Intelligence for Microbiota Analysis: Advances and Applications

Abhinandan Patil [1,*] and Neha Singh [2]

[1] D. Y. Patil Education Society, (Deemed to be University), Kolhapur
[2] Department of Microbiology, Pt. JNM Medical Raipur
* Correspondence: abhisirdyp@gmail.com

Abstract: The body's billions of bacteria—the microbiota—influence health and illness. The microbiome—the genetic material of these microbes—affects digestion, immunological function, and mental health. Due to bacterial variety, complicated relationships, and research technique constraints, investigating the microbiota is difficult. AI and machine learning have expanded microbiome research. Artificial intelligence (AI) systems can efficiently scan large microbiome datasets to help researchers understand microbial populations and their functions. AI-based predictive algorithms can analyze food impacts on microbial communities and forecast illness risks based on gut microbiota composition. AI helps find microbial biomarkers linked to specific health disorders, enabling early illness identification and targeted therapy. AI-driven medication development platforms also modulate microbiome to treat microbiota-related diseases. Understanding microbial populations' involvement in health and illness requires understanding complicated microbial interactions within the microbiome and between it and the host. AI systems improve human health by comprehending these complex relationships. AI in microbiota study must overcome various obstacles. Data quality and AI model interpretability are essential for accurate findings. Diverse and representative datasets avoid biases and strengthen AI-driven conclusions. AI in microbiota research requires data protection, informed permission, and appropriate use of sensitive data. AI is improving our understanding of the human microbiome and its health effects, changing microbiota research. Overcoming difficulties and adhering to ethical norms will enable the proper use of AI-driven findings, leading to microbiome insights and precision medical breakthroughs.

Keywords: bacteria; microbiota; artificial intelligence; microbiome

---

1. Introduction

The Microbiota and the Microbiome:

There are trillions of bacteria that call the human body their home. These microbes, which are collectively referred to as the microbiota, may be found on numerous bodily surfaces, including as the skin, the mouth, and the gastrointestinal system. The microbiome is the aggregate name given to the genetic material that is contained inside these microbes. The microbiome is an important component in human health, since it may have an effect on digestion, the operation of the immune system, and it can even have an effect on mental health. It is now of major interest to the scientific community to get an understanding of the intricate interactions that take place between these microbial populations and the human host [1].

The Difficulty in Conducting Microbiota Analysis:

It is not an easy undertaking to analyze the microbiota because of the wide variety of bacteria that are there, the extensive genetic variation among them, and the complex interactions that they have with both each other and the host. The capacity of traditional ways of researching microbiota, such as culture-based approaches, to capture the entire complexity of microbial communities is severely constrained. In addition, typical techniques of data analysis are sometimes insufficient for gleaning relevant insights from large-scale microbiome datasets [2].

The Development of Machine Learning and Other Forms of Artificial Intelligence in the Study of Microbiota:

The application of artificial intelligence (AI) in the study of microbiota has led to the opening of new doors for research, and it has become a potent instrument in a number of different subfields of science. AI covers machine learning algorithms, which can learn from data patterns, recognize trends, and make predictions without explicit programming. These algorithms can learn from data, identify trends, and learn. Because of these qualities, artificial intelligence is well-suited for the study of large and complicated microbiome datasets, which paves the path for ground-breaking findings [3].

The Importance of AI in the Progress of Microbiome Research:

Artificial intelligence systems are able to analyze huge volumes of raw sequencing data acquired from microbiome research in an effective manner. Researchers are now able to acquire a thorough grasp of microbial communities and their possible functional applications because to the ability of these algorithms to recognize and categorize microbial species and genes. Researchers may use predictive models based on AI to assist them better understand how changes in the microbiome may have an effect on human health. For instance, these models may analyze the impact of particular dietary treatments on microbial communities or forecast the likelihood of developing a disease based on the make-up of the microbiota found in the gut. Artificial intelligence can help in the process of identifying microbiological biomarkers that are related with particular illnesses or disorders. These biomarkers have the potential to act as indications of the presence of a disease, the severity of the condition, or the patient's reaction to therapy. This will allow for earlier diagnosis and more tailored therapeutic methods. The Development of New Drugs and the Therapeutic Use of Microbiota: Platforms for drug development that are driven by AI can be used to investigate the possibility of treating microbiota-related conditions. AI may be used to help create innovative medications that successfully cure a variety of diseases by modulating the microbiota. This is accomplished by examining the interactions that occur between host and microbiome systems. A Better Understanding of Microbial Interactions: The use of AI algorithms enables a better understanding of the complex interactions that occur between microbes within the microbiome as well as between the microbiome and the host. This information is essential for gaining an understanding of the function that microbial populations play in both health and illness. Ensuring that the data is of a high quality and that the AI models are able to be interpreted is vital in order to draw trustworthy conclusions and steer clear of erroneous results. The level of success achieved by AI algorithms is directly proportional to the quantity and variety of the dataset. To prevent the results from being skewed in any way, it is imperative that various people be included in the study. The use of AI to the study of microbiota involves a number of ethical concerns relating to data privacy, permission, and the possibility of inappropriate use of sensitive information [4,21–23].

2. Machine Learning Techniques for Microbiota Profiling:

In the field of microbiota profiling, Machine Learning (ML) approaches have emerged as essential tools to have at one's disposal. Researchers are able to acquire insights into the structure and function of microbial communities by analyzing massive and complicated microbiome datasets using these algorithms controlled by artificial intelligence (AI). In this part, we will examine a variety of ML approaches that are utilized for microbiota profiling. Some of these techniques include clustering, classification, and network analysis [5].

Clustering using the K-Means Algorithm:

In the field of microbiome research, K-Means is a common unsupervised machine learning approach that is used to group comparable samples or microbial taxa on the basis of their abundance profiles. On the basis of their degree of similarity, the algorithm repeatedly places data points (microbial taxa) in the cluster center that is geographically closest to them. Within a given dataset, the K-Means clustering method can assist in the identification of various microbial community types or patterns, hence revealing insight on the structure and variety of microbial communities. Hierarchical Clustering is another unsupervised machine learning approach that builds a tree-like structure (dendrogram) to describe the associations between microbiological taxa or samples. It does this by grouping the samples into hierarchical clusters. It groups together samples or taxa that are quite similar to form clusters at a variety of different granularities. Researchers are able to better visualize the hierarchical order of microbial communities by using hierarchical clustering, and they can also more easily identify subgroups with comparable taxonomic characteristics. The supervised machine learning technique known as Random Forest is extensively utilized because of its ability to categorize data into predetermined groups or predict certain events. In the process of microbiota profiling, Random Forest can categorize samples according to the microorganisms that they contain and discover the major microbial taxa that contribute to the accuracy of the classification. In addition to this, it may be utilized for the categorization of diseases according to the microbiome, which is helpful for diagnostics and individualized medication [6,26,27].

Support Vector Machines (often referred to as SVM):

SVM is a robust supervised machine learning technique that can perform binary classification as well as jobs involving the classification of several classes. SVM may be utilized in the field of microbiota profiling to categorize samples into diseased or healthy states based on the information contained within their microbiomes. Because of its capacity to process high-dimensional data, support vector machines (SVM) are well-suited for the analysis of complicated microbiological datasets [7,23–25].

Networks Based on Co-Occurrence:

Researching the ways in which microbes interact within a community might benefit greatly from using network analysis tools. Co-occurrence networks are used to describe the associations between different microbial taxa based on the co-occurrence patterns of those taxa across different samples. These networks have the ability to provide light on the possible ecological connections and mutualistic relationships that exist between different microorganisms. In these networks, the identification of keystone taxa or hub species can provide vital insights into the stability and operation of microbial communities [8].

Networks Based on Correlation:

The relationships that exist between microbial taxa and host phenotypes or environmental variables can be investigated using correlation networks. Researchers are able to uncover taxa that have the potential to be connected to particular health disorders or environmental exposures by conducting an analysis of correlations between the abundance of microbes and clinical information. The development of biomarkers and a knowledge of the part played by the microbiome in a variety of illnesses can both benefit from the use of correlation networks. In order to reach an all-encompassing comprehension of the microbiome, several research employ a mix of distinct analytical approaches, such as clustering, classification, and network analysis. Integrative methods have the ability to shed light on the intricate interactions that exist between microbial populations and host health, as well as open the door to the discovery of new therapeutic targets and intervention strategies [9,11].

3. Predictive Modeling in Microbiota Research:

The application of predictive modeling, an essential component of artificial intelligence (AI), has transformed the study of microbiota. This has given researchers the ability to generate predictions regarding microbial relationships, functional pathways, and disease connections based on empirical evidence. Researchers have the ability to create tailored medical applications and enhance human health by utilizing the large amounts of microbiome data available to them thanks to the use of AI methods. In this part of the article, we will discuss how predictive modeling is changing the field of microbiota research as well as the possible uses of this field in personalized medicine [12–15].

An Analysis of the Co-occurrence and Mutual Exclusion of Events:

Predictive modeling that is powered by AI can discover microbial taxa that have a tendency to co-occur within a microbial community or that tend to mutually exclude one another. The analysis of big datasets by machine learning algorithms enables them to identify patterns of co-occurrence, which in turn provides insights into the ecological interactions between microorganisms. For a full comprehension of the stability and operation of microbial communities, it is essential to get an understanding of these interactions [16].

The Ability to Anticipate Keystone Species:

The identification of keystone species, which are microorganisms that are essential to the structure and function of microbial communities, may be accomplished through the use of predictive models. These major actors have a considerable impact on the entire dynamics of the community and have the potential to act as therapeutic intervention targets in order to rebalance microbiomes [17,28].

The Prediction of the Metagenomic:

Using data from metagenomics, AI systems are able to make predictions about the functional potential of communities of microbes. The process of inferring the functional gene content of a microbial community based on the taxonomic composition of that community is known as metagenomic prediction. This method yields extremely helpful insights on the metabolic capacities of the microbiome as well as the possible effects that the microbiome may have on the host [18,21].

Annotation of Functional Interactions and Pathway Analysis:

Annotating genes in microorganisms and locating the functional pathways that are connected with particular host phenotypes or environmental conditions can be helped along by predictive modeling. It is vital to have an understanding of the functional characteristics of the microbiome in order to investigate possible treatment targets and evaluate the role that the microbiota plays in a variety of disorders [19,24].

4. Anticipating the Associations of Diseases:

On the basis of the microbiome profiles of the samples, predictive modeling powered by AI may categorize the samples as either healthy or diseased. Machine learning algorithms are able to build reliable disease classifiers when microbiome data is combined with clinical information. These classifiers can be helpful in the early diagnosis of disease, in the stratification of patients according to risk, and in the guidance of individualized treatment options. It is possible to uncover microbial biomarkers that are connected to certain illnesses or situations by using predictive modeling. AI algorithms, by performing an analysis of the discriminatory capacity of microbial taxa, can identify possible biomarkers that have the potential to act as indications of the existence of disease, the severity of disease, or a patient's response to therapy [20–24].

Anticipating the Patient's Reaction to Treatment:

The make-up of the patient's microbiota may be used by models powered by AI to make predictions about individual reactions to therapy. This paves the way for customized medicine methods, in which physicians may adapt medicines based on the patient's individual microbial composition. This has the potential to improve treatment efficacy while simultaneously minimizing unwanted effects [1,26].

Applications in Individualized Medical Treatment:

The development of microbiota-based medicines has been made possible because to predictive modeling in the field of microbiome research. Researchers are able to modify the microbiome and improve health by designing tailored therapies, such as probiotics, prebiotics, or fecal microbiota transplantation, when they have a knowledge of how distinct microbial populations impact illness outcomes [27].

Accurate Nutritional Measurement:

The microbiota profile of an individual can serve as the basis for individualized dietary recommendations that are guided by AI-driven predictive modeling. Data from the microbiome may be combined with information about a person's diet in order to create individualized meal plans that improve both gut health and general well-being [3,24].

Evaluation of the Dangers of Disease and Prevention:

The individual's microbiome makeup, their genetics, and the lifestyle variables that contribute to their risk of illness may all be taken into account through predictive modeling. Because of this knowledge, medical practitioners are able to take preventative actions and make changes to their lifestyles in order to reduce patients' chances of acquiring specific diseases [2,28].

5. Conclusion

Our understanding of microbial interactions, functional pathways, and illness connections has been fundamentally altered as a result of the application of predictive modeling in microbiota research. Researchers have been able to tap into the potential of data from the microbiome and develop applications for customized treatment as a result of algorithms driven by AI. via the identification of illness connections and biomarkers, as well as via the prediction of microbial interactions and functional pathways, artificial intelligence is opening up new doors for focused therapies and precision healthcare. It is anticipated that the incorporation of predictive modeling into personalized medicine will completely transform the healthcare industry and lead to significant improvements in patient outcomes on a global scale as AI technologies continue to advance. In order to ensure the appropriate and successful implementation of AI in microbiota research and personalized treatment, it is essential to solve problems relating to data quality, interpretability, and ethical considerations.

Reference

1. Toju H, Peay KG, Yamamichi M, Narisawa K, Hiruma K, Naito K, et al. Core microbiomes for sustainable agroecosystems. Nat Plants. 2018;4:247–57.
2. Labbate M, Seymour JR, Lauro F, Brown MV. Editorial: anthropogenic impacts on the microbial ecology and function of aquatic environments. Front Microbiol. 2016;7:1044.
3. Lozupone CA, Stombaugh JI, Gordon JI, Jansson JK, Knight R. Diversity, stability and resilience of the human gut microbiota. Nature. 2012;489:220–30.
4. Müller DB, Vogel C, Bai Y, Vorholt JA. The plant microbiota: systems-level insights and perspectives. Annu Rev Genet. 2016;50:211–34.
5. Pita L, Rix L, Slaby BM, Franke A, Hentschel U. The sponge holobiont in a changing ocean: from microbes to ecosystems. Microbiome. 2018;6:46.
6. Alberdi A, Andersen SB, Limborg MT, Dunn RR, Gilbert MTP. Disentangling host–microbiota complexity through hologenomics. Nat Rev Genet. 2021;1–17.
7. Berg G, Rybakova D, Fischer D, Cernava T, Vergès M-CC, Charles T, et al. Microbiome definition re-visited: old concepts and new challenges. Microbiome. 2020;8:1–22.
8. Sessitsch A, Mitter B. 21st century agriculture: integration of plant microbiomes for improved crop production and food security. Microb Biotechnol. 2015;8:32–3.
9. Marcos-Zambrano LJ, Karaduzovic-Hadziabdic K, Loncar Turukalo T, Przymus P, Trajkovik V, Aasmets O, et al. Applications of machine learning in human microbiome studies: a review on feature selection, biomarker identification, disease prediction and treatment. Front Microbiol. 2021;0:313.
10. Gupta MM, Gupta A. Survey of artificial intelligence approaches in the study of anthropogenic impacts on symbiotic organisms – a holistic view. Symbiosis. 2021;84:271–83.
11. Albright MBN, Louca S, Winkler DE, Feeser KL, Haig S-J, Whiteson KL, et al. Solutions in microbiome engineering: prioritizing barriers to organism establishment. ISME J. 2022;16:331–8.
12. Lewis WH, Tahon G, Geesink P, Sousa DZ, Ettema TJG. Innovations to culturing the uncultured microbial majority. Nat Rev Microbiol. 2021;19:225–40.
13. Malla, M. A., Dubey, A., Kumar, A., Patil, A., Ahmad, S., Kothari, R., Yadav, S. (2021). Using RSM and GC-MS-based metabolomics, the organophosphorus and pyrethroid degradation pathways of a new bacterial group called C3 were figured out and made better. The Taiwan Institute of Chemical Engineers publishes this journal, 144, 104744.
14. Munot, N., Kandekar, U., Rikame, C., Patil, A., Sengupta, P., Urooj, S., Bilal, A. (2022). A systematic study called Improved Mucoadhesion, Permeation, and In Vitro Anticancer Potential of Synthesised Thiolated Acacia and Karaya Gum Combination. Molecules, 27(20), 6829.
15. Munot, N., Kandekar, U., Giram, P. S., Khot, K., Patil, A., Cavalu, S. (2022). A Study of Quercetin-Loaded Nanocochleates and Liposomes: Formulation, Characterization, Assessment of Degradation, and In Vitro Anticancer Potential. Pharmaceutics, 14(8), 1601.
16. Manikyam, H. K., Tripathi, P., Patil, S. B., Lamichhane, J., Chaitanya, M., et al. (2020). Hesperidin from the unripe Citrus grandis/maxima fruit Nepal variety was taken out, cleaned up, and measured. Asian Journal of Biochemistry of Natural Products, 20(1).
17. Patil, A., Munot, N., Patwekar, M., Patwekar, F., Ahmad, I., Alraey, Y., Alghamdi, S., et al. (2022). Encapsulation of lactic acid bacteria by lyophilization and its effects on the bacteria's ability to live and stick together. Complementary and alternative medicine based on evidence, 2022.

18. Nalawade, A. S., Gurav, R. V., Patil, A. R., Patwekar, M., Patwekar, F. (2022). A full review of the studies of the genus Chlorophytum Ker Gawl's morphological, genetic, and phytochemical variety, breeding, and bioprospecting. made in India. Trends in the study of phytochemicals, 6(1), 19-45.
19. Patil, K. G., Balkundhi, S., Joshi, H., Ghewade, G. (2011). International Journal of Pharmacy and Pharmaceutical Research: MEHSANA BUFFALO MILK AS PREBIOTICS FOR GROWTH OF LACTOBACILLUS, 1(1), 114-117.
20. Das, N., Ray, A. R. Patil, S. S. Saini, B. Waghmode, C. Ghosh, P. B. Patil, and others. By causing apoptosis and going after the -catenin/Wnt pathway, chosen Indian honey stops the growth of colon cancer cells. Food and work, 13(15), 8283-8303.
21. Patil, M. J., Mali, V. (2021). Different Tests of the Cytotoxicity of Lactobacillus Found in Sheep Milk. Acta Scientific Pharmaceutical Sciences, 5(12), 69-70.
22. Abhinandan, P. S. P., John, D. (2020). With its ability to stick to cells, Lactobacillus plantarum has probiotic promise. Global Pharma Technology Journal, 10(12), 1-6.
23. Patil, A., Mali, V., Patil, R. (2019). A 6-month-old baby's banana fibres looked like a gut worm. Iberoamerican Medical Journal, 2(3), 245-247.
24. Munot, N. M., Shinde, Y. D., Shah, P., Patil, A., Patil, S. B., and Bhinge, S. D. (2021). Formulation and Evaluation of Chitosan-PLGA Biocomposite Scaffolds Incorporated with Quercetin Liposomes Made by QbD Approach for Better Healing of Oral Lesions. PharmSciTech, AAPS, 24(6), 147.
25. Patil, A. (2023). Psychology in a time when people are dependent on technology and the Mobile Dilemma. Preprints.org, 2023070101.
26. Patil, A., Kotekar, D., Chavan, G. (2023). How probiotics affect the development and spread of cancer and how to figure out how they work. Preprints.org, 2023070243.
27. Vijaykumar Pawar, Abhinandan Patil, Firoj Tamboli, Dinanath Gaikwad, Dipak Mali, Anilkumar Shinde. (2021). A complete look at how AI can be used in pharmacokinetics and pharmacodynamics. PharmSciTech, AAPS, 14(2), 426-439.