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Review

Artificial intelligence and microbiome research: Evolution of hotspots, research trends, and thematic-based narrative review

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Abstract

Artificial intelligence (AI) and microbiome have emerged in recent years as transformative fields with far-reaching implications for various biomedical domains. This paper presents a comprehensive bibliometric analysis examining the intersection of AI and the microbiome (AIM). The study aims to provide information on this interdisciplinary field's research landscape, trends, and emerging topics. Using a systematic approach, data-driven studies were extracted from the Scopus database on 23 November 2023 and analyzed using the VOS-viewer and Bibliometrix applications. The regression coefficient of 0.94 and the yearly growth rate of 7.46% in AIM production indicate a consistent increase over time. Identification of essential contributors, organizations, and nations illuminated cooperative networks and research hotspots. The trend themes are the gut microbiome, disease prediction, machine learning, transfer learning, categorization, big data, artificial neural networks, chronic rhinosinusitis, epidemiology, COPD, and bronchoalveolar lavage. These hot issues in AIM reflect the present emphasis on research and developments in our knowledge of the microbiome's function in health, sickness, and individualized treatment. The findings give researchers, policymakers, and industry experts a thorough picture of the research environment and guide future paths in AIM's fascinating and promising subject.

Keywords: Artificial intelligence (AI), Bibliometric analysis, Data sharing, Interdisciplinary collaboration, Microbiome.

1. Introduction

Recently, artificial intelligence and microbiome (AIM) have become transformational fields with far-reaching ramifications [1]. AI's capacity to analyze enormous volumes of data and find detailed patterns has transformed healthcare, banking, and transportation [2, 3]. The microbiome is the broad microbial population that includes bacteria, viruses, fungi, and archaea and is essential to many physiological functions [4]. It affects the immune system, digestion, metabolism, and even brain functions. Many illnesses, including autoimmune diseases, gastrointestinal problems, mental health issues, and obesity, have been linked to imbalances or disturbances in the microbiome. As such, deciphering the complexities of the microbiome has lately attracted a lot of attention in studies [1, 5, 6].

Rapid developments in AI methods have simultaneously given scientists strong instruments for analyzing intricate biological data, including the enormous volumes of data produced by microbiome research. AI techniques, like deep learning and machine learning, have shown to be effective in deriving important information from microbiome datasets, enabling scientists to find microbial biomarkers, find hidden patterns, and forecast disease states [1, 5-7]. There is growing interest in using machine learning methods in AIM. Computer algorithms are being used by researchers to examine intricate microbiome data, spot trends, and forecast. Based on microbial profiles, machine learning helps to identify biomarkers, disease subtypes, and individualized treatment strategies [2, 8, 9]. Furthermore, computer models motivated by the operation of the human brain are known as artificial neural networks (ANNs). In AIM, ANNs are applied to simulate micro-

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bial interactions, interpret complicated microbiome data, and forecast illness results. ANN-based methods advance knowledge of the interactions between the host and the microbiome and help to classify and predict diseases [10].

Researchers, practitioners, and legislators alike must grasp the state of AIM today. It could help to develop new approaches, point up knowledge gaps, promote teamwork, and direct further studies. This paper attempts to investigate the junction of AIM by means of a bibliographic study, which is quantitative examination and assessment of publications on a certain topic. We may obtain important understanding of the development of this multidisciplinary subject, important research issues, prominent works, and possible future directions by looking at trends and patterns in the academic literature on AIM. Furthermore, this research may clarify the revolutionary possibilities of artificial intelligence in advancing our knowledge of the microbiome and its consequences for human health.

2. Materials and Methods

2.1. Selection of databases

Because it covers so much scientific literature in many fields, including biomedical research, Scopus was selected as the database for this bibliographic study. Scopus was the chosen resource for this study even though PubMed, Web of Science, and Google Scholar are excellent sources because of its extensive coverage, conference proceedings, strong citation metrics, sophisticated search features, and dedication to data quality. Strong Scopus citation measures made it easier to examine citation trends and find significant research [11]. The sophisticated search features and stringent quality control procedures of Scopus guaranteed a targeted and trustworthy examination of the academic literature related to the AIM.

2.2. Search strategy

The search strategy involved extracting search terms from the MeSH (Medical Subject Headings) database [12] and combining them to retrieve relevant articles. The search query used in Scopus was as follows:(TITLE-ABS-KEY ("AI" OR "Artificial intelligence" OR "Deep learning" OR "machine learning" OR "Computational "Intelligence" OR "Computer Reasoning" OR "Bayesian network" OR "Bayesian learning" OR "neural networks" OR "Random forest" OR "Advanced imaging" OR "Machine Intelligence" OR "Computer-assisted" OR "Data learning" OR "Computer vision" OR "Artificial neural network" OR "Radiomics" OR "Automated screening" OR "Convolutional neural network" OR "Hierarchical Learning" OR "Feature learning" OR "Computer-aided detection" OR "Computer-aided diagnosis" OR "Computer-aided" OR "Reinforcement learning" OR "Big data" OR "Image segmentation" OR "Hybrid intelligent system" OR "Autonomous robotics" OR "Robotics" OR "Natural language processing") AND TITLE-ABS-KEY (microbiota OR microbiome)) AND (LIMIT-TO (LANGUAGE, "English")) AND (LIMIT-TO (DOCTYPE, "ar")). This query combined terms related to AI, including different AI techniques and applications, with terms related to the microbiota or microbiome. The search was limited to articles written in English and restricted to the type of article document. Using this search strategy, relevant articles that explore the AIM were retrieved from the Scopus database for further analysis in the bibliographic study.

2.3. Inclusion criteria

The inclusion criteria consisted of articles written in English. On the contrary, articles not related to the AIM intersection, lacking the application of AI techniques in microbiota or microbiome analysis, written in languages other than English, or being conference abstracts, editorials, reviews, or opinion pieces were excluded from the study. The initial search in Scopus yielded a total of 4,125 documents, covering various types and languages. The majority of the documents were articles, representing 73.02% (3,012) of the total. Reviews constituted 15.35% (633) of the documents, while conference papers represented 2.93% (121). Editorials and book chapters accounted for 2.50% (103) and 1.89% (78), respectively. The notes comprised 1.45% (60) of the documents, followed by conference reviews of 0.90% (37). The remaining types of documents, including short surveys, letters, and books, constituted smaller proportions, each contributing less than 1% to the total. A total of 2,956 documents that met the inclusion criteria were found. These documents were retrieved from the Scopus database in CVS and BibTex formats for further analysis and examination of the AIM literature.

2.4. Quality control

To maintain quality, rigorous control measures were implemented (Figure 1). This involved establishing clear selection criteria, selecting a reputable database (such as Scopus), developing a comprehensive search strategy, conducting a systematic screening process, ensuring accurate data extraction, applying robust data analysis techniques and incorporating peer review. These measures aimed to enhance the reliability, precision, and validity of the study findings and ensure the inclusion of relevant articles while excluding irrelevant ones.

2.5. Data analysis

Data analysis in the bibliometric study was performed using two key tools: VOSviewer (01.16.20) [13] and Bibliometrix (4.2.1) [14]. Examining the evolution of publications over time, identifying significant application domains and research subjects, ascertaining influential studies and publishing patterns, analyzing citation

Fig. 1. Search and selection criteria. ar; article; DOCTYPE: type of documents.

networks and researcher cooperation, and investigating keyword co-occurrence to expose main themes and trends were the objectives of the work. Structural dynamics and trends within the AIM bibliometric network were visualized using the Sankey diagram. Lotka's law was applied to analyze the productivity of researchers, finding that a significant portion of the research was single-authored, but the average number of co-authors each document had. By means of VOSviewer and Bibliometrix, a complete study of the AIM literature was made possible, therefore offering a comprehensive knowledge of the field's development, eminent research areas, major studies, and cooperative networks. A corpus of publications was collected, with metadata extracted. Keywords were pre-processed, and a co-occurrence matrix was constructed to calculate co-word metrics. The network evolution was analyzed to identify emerging trends and hot topics, such as clusters of strongly co-occurring keywords and keywords with increasing centrality. Visualization and interpretation of the co-word network were followed by validation through expert input and other analyses [15, 16].

3. Results

3.1. Temporal analysis of AIM

AIM's yearly growth rate of 7.46% shows that the quantity of documents is increasing steadily over time. The average age of the document is found to be 2.35, indicating that the documents in the data set are often somewhat new. An R^2 of 0.9436 polynomial regression fit model was found by statistical study of yearly increase (Figure 2).

3.2. Hotspots

3.2.1. Constituents of top publishing

Knight, R. is among the most notable scholars in this subject; Schloss, P.D.; Nieuwdorp, M.; Lu, W.; and Bucci, V. follow. The Chinese Academy of Sciences is the most prominent affiliation with 119 publications, followed closely by the Ministry of Education of the People's Republic of China with 111 publications. Harvard Medical School has 78 publications, the Chinese Academy of Sciences has 63, and the University of California, San Diego has 57. In terms of countries, the United States leads with 1,070 publications, followed closely by China with 986 publications. The United Kingdom has 229 publications, Germany has 174, and Canada has 154. Countries with a dark blue color are the most productive. Countries outside of the blue category have not made any contribution to research in this particular area (Figure 5A).

In the field of AIM, the data set includes 914 sources. Frontiers in Microbiology has the highest number of publications with 176, followed by Microbiome with 105 publications. Frontiers in Cellular and Infection Microbiology has 103 publications, Scientific Reports has 84, and Science of the Total Environment has 57.

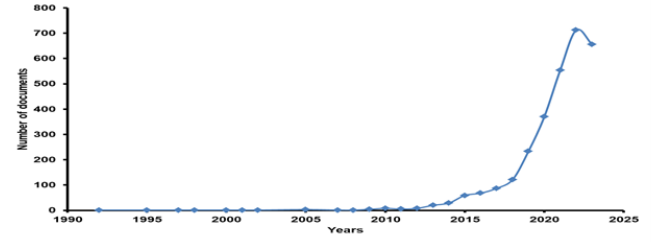

Fig. 2. AIM Annual Publishing Trends. Y-axis: the number of articles published. X-axis: the years since the first article was published on the topic of this paper.

3.2.2. Differential authorship

The several relationships and interactions of bibliometric analysis are shown in the Sankey diagram (Figure 3). By using this visualization, analysts and researchers may examine the structural dynamics and trends of bibliometric networks [17]. The diagram uses varying-thickness lines for connections and rectangles. Whereas the line width indicates the number of co-authored articles between authors from different countries and the papers published in different sources by each country, the rectangle size indicates the importance of the nodes [17]. Chinese academics controlled the top 10 journals, as this Sankey graphic illustrates.

3.2.3. Lotka's law

In their productivity study, the authors applied Lotka's rule using Biblioshiny. The empirical concept known as Lotka's rule, sometimes referred to as the law of scientific production, describes the distribution of scientific output among researchers in a certain subject. American mathematician and statistician Alfred J. Lotka invented it in the early 1900s. Many times, the distribution of scientific publications is modeled using Lotka's rule [18]. In Figure 4, the proportion of authors is shown on the Y-axis and the

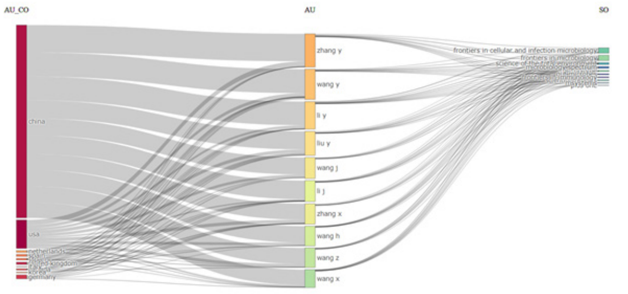

Fig. 3. An author, country, and source relationship Sankey diagram. Through the thickness of the connecting lines, the graphic illustrates the relationships between scholars from various nations according to the number of co-authored publications. Comparably, the number of papers published from each nation in each source is shown by the thickness of the lines separating them. A node in the diagram is represented by a rectangle, whose size indicates how important the node is in the network. This Figure was produced with the BibTex data file and the Bibliometrix program.

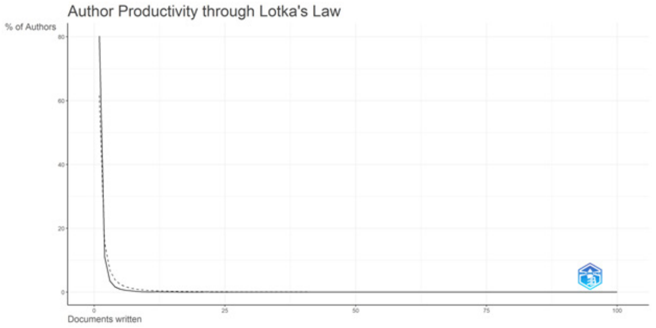

Fig. 4. The analysis of author productivity was conducted using Lotka's law, which is a principle used to understand the distribution of scientific productivity among researchers. In the analysis, a shaded line was used to represent the expected values based on Lotka's law.

number of articles on the X-axis. The graph makes it quite evident that most AIM writers have only published one paper.

3.3. Collaborative research

The authors' cooperation analysis found 56 single-authored documents, indicating that much of the study was collaborative. On average, each document had 8.96 coauthors, demonstrating field collaboration. Additionally, 31.4% of coauthorships were international, highlighting the relevance of global cooperation in research and complicated problem-solving. Figure 5A shows the nations with the strongest collaborative links, while Figure 5B colors single- and multi-country articles. The yellow nodes in Figure 5C show China, South Korea, and India emerging in international research initiatives from AIM's collaborative research temporal analysis.

3.4. Impact analysis

The countries mentioned in AIM represent the substantial contributions and influence of several nations in the sector (Figure 6). The leads with the greatest citation count constitute 31.791% of the total citations. China ranks second with a citation share of 11.155%. With 6.104%, 5.012%, 4.060%, and 3.826% of the citations, respectively, the United Kingdom, Australia, Germany, and Canada all have notable counts.

Table 1 lists the most referenced AIM papers. The first three documents have the most influence and citations. The first article, "Optimizing taxonomic classification of marker gene amplicon sequences with QIIME 2's q2-feature classifier plugin", appeared in Microbiome in 2018. It has 2,372 citations, averaging 395.33 per year. This work employs the QIIME 2 q2-feature classifier plugin to improve marker gene amplicon sequence taxonomic categorization for more accurate and efficient microbiome data processing [19]. Published in Cell in 2015, the second study is titled "Personalized Nutrition by Prediction of Glycemic Responses." Citations for it total 1,545, or 171.67 years. This work allows for nutritional customisation based on glycemic profiles by predicting the glycemic reactions to tailored nutrition [20]. The third study, "Persistent intestinal microbiota immaturity in malnourished Bangladeshi children," was reported in Nature in 2014. Citations total 825, or 82.50 years. This investigation reveals the long-term immaturity of the gut microbiota of underprivileged Bangladeshi children, therefore illuminating the relationship between malnutrition and microbiome development [21].

The remaining AIM investigations in Table 1 gave excellent insights and conclusions. The research examined age, region, and lifestyle to reveal the human microbiome's vast variety. Another study linked breast milk bacterial populations to newborn gut microbiomes. Additionally, a gut microbiome-based metagenomic signature was created for noninvasive diagnosis of progressive fibrosis in nonalcoholic fatty liver disease. A further notable study showed that faecal microbiota transplantation (FMT) might potentially overcome the resistance of melanoma patients to anti-PD-1 therapy. Furthermore, the research focused on developing methodologies to quantify the prevalence of different species in metagenomics data. A supplementary investigation examined the influence of the Zebrafish's microbiota on the absorption and metabolism of fat. Finally, a complete Bioconductor pipeline from raw readings to community-level analyses was demonstrated for the processing of microbiome data. All of this research advances our knowledge of the influence of the microbiome in several circumstances, from human health to treatment response and analytical techniques [7, 22-27].

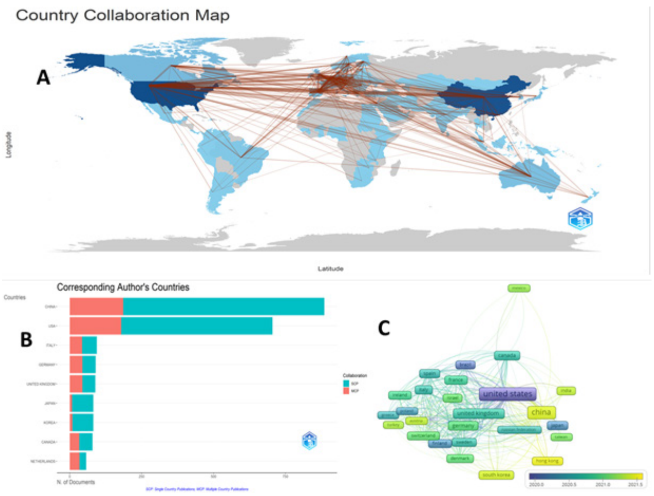

Fig. 5. A: Global production and co-authorship network analysis. Lines show joint research initiatives. Blue countries were new to AIM joint research. The Bibliometrix program and BibTex data file created this Figure. B: Multi-country publications. Green signifies multi-country publishing. C: VOSviewer was used to investigate the country co-authorship network, with nations as nodes and collaborations as linkages. Yellow nodes symbolize these nations.

Fig. 6. Highly cited countries in AIM. Nodes represent the number of total citations. This Figure was generated using the VOSviewer application and the CVS data file.

3.5. Conceptual structure

3.5.1. *Keyword analysis*

18,502 Keywords Plus (ID) and 6,580 Author's Keywords (DE) were detected. Keywords Plus (ID) has more occurrences and proposes a wider range of keywords from diverse sources, whereas Author's Keywords represents authors' selected keywords. These data establish the variety and importance of both sorts of keywords in collecting research information. AIM study highlights various keywords. The term "microbiome" appears 420 times, indicating the focus on microbial communities and their interactions in individual environments. AIM studies use computational techniques and statistical models to examine complicated datasets, therefore "machine learning"

Table 1. Top-cited documents in AIM.

Rank	Title	Source	Year	Citations	Citation average
1st	10.1186/s40168-018-0470-z [19]	Microbiome	2018	2372	395.33
2nd	10.1016/j.cell.2015.11.001[20]	Cell	2015	1545	171.67
3rd	10.1038/nature13421[21]	Nature	2014	825	82.50
4th	10.1016/j.cell.2019.01.001[26].	Cell	2019	740	148.00
5th	10.1001/jamapediatrics.2017.0378[25]	JAMA Pediatrics	2017	638	91.14
6th	10.1016/j.cmet.2017.04.001[23].	Cell Metabolism	2017	616	88.00
7th	10.1126/science.abf3363[22]	Science	2021	596	198.67
8th	10.7717/peerj-cs.104. [24]	PeerJ Computer Science	2017	591	84.43
9th	10.1016/j.chom.2012.08.003[27]	Cell Host and Microbe 2012	2012	591	49.25
10th	10.12688/F1000RESEARCH.8986.1[7]	F1000Research	2016	546	68.25

(374 times) is another popular keyword. The "gut microbiota" appeared 301 times. Metagenomics (178 times), which studies microbial genomes, has become popular for understanding microbial populations. The terms "gut microbiome" (173 times) and "microbiota" (172 times) emphasize the study of gut microbes and their effects on health and disease. The term "16S rRNA" (164 times) shows that this genetic marker is widely used to identify and classify bacteria in microbial communities. Metabolomics (101 times) and other biomarker research methods are vital for discovering health or disease markers. Machine learning technique "random forest" algorithms (77 times) are used to analyze AIM data. Colorectal cancer (66 times), inflammatory bowel disease (42 times), obesity (41) and type 2 diabetes (19 times) are also represented. Also being studied are the effects of nutrition (28 times), antibiotics (25 times), and probiotics (34 times) on the microbiota. AIM's transdisciplinary research focuses on complex microbial ecosystems and their effects on human health.

3.5.2. Thematic evolution

AIM research themes evolve throughout time (Figure 7). From 1992 until 2020, AIM focused on diagnosis studies. However, from 2021 to 2024, research on gut microbiota, health, and disease has increased. At the same time, fecal microbiota transplantation has given way to microbiome research. In 2021–2024, the COVID-19 pandemic inspired AIM research. Understanding of the gut-brain axis has also changed, with a focus on the gut microbiota's function in bidirectional communication. Researchers intensively explored the human microbiome from 1992 to 2020, but from 2021 to 2024, they are focusing on specific bacterial species or strains. Microbiome research has evolved from exogenous infections to include a wide range of health problems and diseases. Between 2021 and 2024, the intersection between the gut microbiome and irritable bowel syndrome will gain attention. Research developments in this field have included the study of the vaginal flora, probiotics in the intestinal flora, and the coronavirus (COVID-19) have also received well-deserved attention. In the evolution of AIM, quorum sensing has gained recent interest. Between 1992 and 2020, the microbiome analysis random forest algorithm rose to prominence and continues to garner attention in 2021–2024.

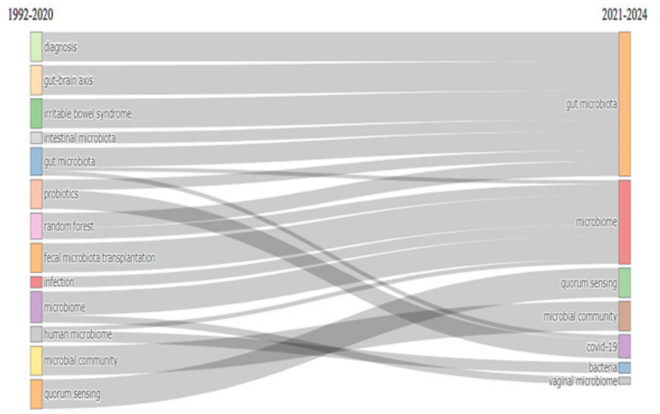

Fig. 7. Thematic evolution of MBR research in OC. 2021 was a crucial point for the transformation of the main topics. This Figure was generated using the Bibliometrix application and the BibTex data file.

Fig. 8. Thematic map of the AIM. Thematic maps are divided into four quadrants based on centrality and density, which represent the importance and development of research topics. The values of the x and y axes are shown in Table 2. This Figure was generated using the Bibliometrix application and the BibTex data file.

3.5.3. Conceptual structure of AIM: Thematic-based review

Table 2 and Figure 8 showed field topic clusters. The gut microbiota group was a central, dense motor topic. It included gut microbiota, 16s rRNA, and associated terms. The niche themes in AIM include vaginal microbiome and fecal microbiota transplantation. Machine learning, metagenomics, and gut microbiota are the major topics in the microbiome cluster. Finally, the quorum sensing cluster, which studies microorganism communication, was an emerging topic in AIM. This thematic mapping revealed AIM's numerous topics and their relevance, identifying

Table 2. Themes of AIM and their densities, centralities, terms, and classification.

Cluster	Callon Centrality*	Callon Density*	Terms and frequency	Classification
Gut microbiota	0.2963	5.3782	Gut microbiota (301), gut microbiome (172), microbiota (172), 16s rrna (72), colorectal cancer (66), biomarker (58), biomarkers (52), dysbiosis (47), obesity (41), inflammation (37), 16s rrna gene sequencing (36), metabolome (35), covid-19 (34), probiotics (34), metagenome (32), diet (28), 16s rrna sequencing (25), antibiotics (25), diagnosis (23), meta-analysis (23), oral microbiome (22), sars-cov-2 (22), children (21), saliva (21), lactobacillus (19), type 2 diabetes (19), intestinal microbiota (18), microbial communities (18), nutrition (18), immunotherapy (17), gut-brain axis (16), hypertension (16), metabolites (16), metagenomic sequencing (15), oral microbiota (15), short-chain fatty acids (15), fecal microbiota (14), hepatocellular carcinoma (14), irritable bowel syndrome (14), periodontitis (14)	Motor
Bacteria	0.0389	4.1762	Bacteria (38) and fungi (23),	Basic
Vaginal microbiome	0.0045	6.6964	vaginal microbiome (16), high-throughput sequencing (14)	Niche
Fecal microbiota transplantation	0.0256	5.1042	Fecal microbiota transplantation (30), clostridium difficile (16)	Niche
Microbial community	0.0307	5.0537	Microbial community (42), co-occurrence network (17), bacterial community (16)	Basic
Microbiome	0.2163	5.6355	microbiome (420), machine learning (374), gut microbiota (301), metagenomics (178), gut microbiome (173), microbiota (172), 16s rrna (164), biomarker (110), metabolomics (101), random forest (77), colorectal cancer (66), deep learning (55), dysbiosis (47), inflammatory bowel disease (42), microbial community (42), artificial intelligence (41), obesity (41), bacteria (38), inflammation (37), covid-19 (34), probiotics (34), human microbiome (32), fecal microbiota transplantation (30), bioinformatics (29), microbial ecology (29), classification (28), diet (28), prediction (28), antibiotics (25), multi-omics (25), diagnosis (23), fungi (23), meta-analysis (23), oral microbiome (22), quorum sensing (22), sars-cov-2 (22), children (21), saliva (21), crohn's disease (20), feature selection (20), precision medicine (20), lactobacillus (19), type 2 diabetes (19), intestinal microbiota (18),	Motor
Quorum sensing	0.0076	4.5455	Quorum sensing (22)	Emerging

*Callon centrality can be read as the importance of the topic in the whole collection, while Callon density can be read as a measure of the topic's development.

study areas and possible trends.

3.5.4. Trend topics

Gut microbiome, disease prediction using 16S rRNA data with machine learning, and personalized medicine are trending topics (Figure 9) in AIM.

3.6. Co-citation analysis

Within the field of AIM, a total of 228,490 authors were co-cited. Thirteen of these authors have been co-cited 750 times, as shown in Figure 10. Two distinct clusters were identified among these influential authors. Knight, R. is the most co-cited author in AIM and anchors the green cluster. The second-most cocited author is Wang, Y., who leads the red cluster.

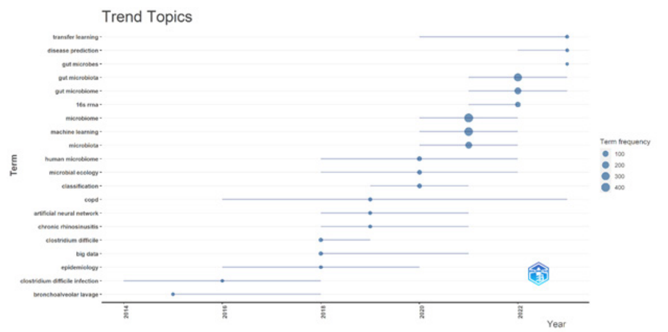

Fig. 9. Trend Topics in AIM. The graph depicts the research topic's time span, with horizontal lines indicating the duration and blue circles representing the frequency of the term. This Figure was generated using Bibliometrix and BibTex data files.

4. Discussion

This article presents a comprehensive bibliometric analysis examining the intersection of AI and the microbiome (AIM). The study aims to provide information on the research landscape, trends, and emerging topics within this interdisciplinary field. Using a systematic approach,

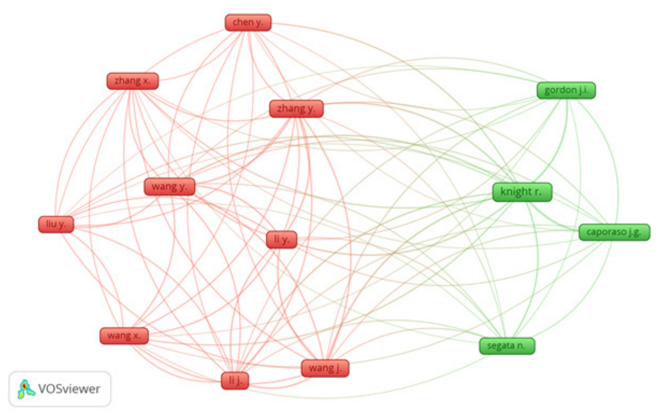

Fig. 10. VOSviewer analysis of co-citation of authors. Two clusters were detected. A total of 228490 of the authors were co-cited in AIM. Thirteen of them have been cocited 750 times.

data-driven studies were extracted from the Scopus database and analyzed using the VOSviewer and Bibliometrix platforms. AIM's yearly growth rate of 7.46% shows that the quantity of documents is increasing steadily over time. This rate of increase points to a dynamic and changing research environment where fresh studies are released often and help to increase the body of knowledge on the subject. Previous research has indicated a substantial increase in the development of AI in the field of biomedicine, such as neurodegenerative disease [8], medical imaging [9], onco-haematology [28], and drug discovery [29].

Determining hotspots in AIM through bibliometric analysis is crucial for gaining a comprehensive understanding of the field's research landscape. It helps identify leading authors and prominent affiliations. This information helps researchers navigate the area and possible joint ventures. Institutions and funding organizations may also make strategic decisions and efficiently distribute resources by using this research. Comparisons of contributions to the found hotspots make benchmarking and assessment of research performance feasible [30-32]. Generally speaking, bibliometric study of AIM hotspots offers institutions, funding organizations, and researchers important information.

Knight, R. is among the most notable scholars in this subject. Knight, R. is a computational and microbiologist who has significantly advanced the domains of AIM. His work has concentrated on creating computer tools and techniques for microbiome data analysis and interpretation, which has enabled scientists to learn more about the intricate microbial communities that live in different settings [5, 33-35]. Among his many accomplishments are his co-development of the QIIME software package, a popular tool for microbial sequence data analysis, and his groundbreaking work in the field of machine learning and artificial intelligence applied to microbiome research [6, 36]. His studies have clarified how the microbiome affects obesity, inflammatory bowel disease, antibiotic resistance, and cancer among other facets of human health [5, 33-35].

Chinese academics controlled the top 10 journals. AIM research has drawn in more Chinese academics because of government support, data availability, a growing pool of talent, and teamwork. The Chinese government has made significant investments in AIM technologies as they can address problems with healthcare, agriculture, and the environment. The funding has been used to build research facilities, create state-of-the-art technologies, and educate upcoming scientists and engineers. China offers a wealth of microbiome and artificial intelligence data for creating and evaluating new models and algorithms. These data are supplied by agricultural sensors, environmental monitoring systems, and electronic health records. Chinese scientists and engineers abound in AIM experience. This results in part from the government giving scientific innovation and STEM education top priority. China collaborates highly with AIM. This is partially due to government sponsorship of industry-university-research institute collaboration [37, 38].

AMIR grows by collaboration, and bibliometric mapping facilitates it and promotes this. Bibliometric data may be analyzed by researchers and legislators to comprehend important participants, cooperation patterns, research progress, and impact. This data can enhance development, collaboration, and financing for research in these important fields [17, 18, 32, 39]. Most of the work was collaborative, as the cooperation analysis uncovered 56 single-authored items. Each document averaged 8.96 coauthors, suggesting field collaboration. 31.4% of coauthorships were international, emphasizing the importance of worldwide collaboration in research and complex problem-solving. These data reflect the changing environment of international collaboration in AIM and the expanding number of nations participating in joint research.

Citation analysis is an invaluable technique for obtaining a deeper understanding of the effect and influence of research. This data can serve several functions, such as assessing the influence of research, appraising academic achievements, monitoring the progress of research areas, and recognizing patterns of collaboration [39]. The countries mentioned in AIM represent the substantial contributions and influence of several nations in the sector (Figure 6). The high citation counts of these countries highlight their major influences too. The United States is at the forefront of AIM research. The reasons for this may be attributed to several variables, such as generous financial support for research, prestigious institutions, a thriving commercial sector, a legacy of groundbreaking ideas, a vast and varied population, a robust entrepreneurial culture, and a prominent open scientific movement [40, 41].

Bibliometrix thematic mapping of AIM categorizes topics by study domain centrality and density. Traditional categories include basic, core, niche, and emerging or declining topics. Basic themes reflect essential concepts and processes, whereas motor themes are influential and field-central [42]. Niche topics serve unique AIM research objectives. Rising themes imply new study fields, whereas falling themes indicate diminishing research areas. Researchers may grasp the AIM field's structure, identify key topics, and follow research trends utilizing thematic mapping [17, 18, 32]. The major theme is the "Microbiome," which has a Callon Centrality of 0.2163 and a Callon Density of 5.6355. This theme encompasses a wide range of topics related to the microbiome, including machine learning (374), gut microbiota (301), metagenomics (178), gut microbiome (173), and microbiota (172). Classified as a "Motor," this group represents a central and highly interconnected area of research that drives advancements in understanding the microbiome and its impact on various aspects of human health. Researchers in this topic employ machine learning techniques to analyze microbiome data and identify patterns and associations between microbial communities and health outcomes [2, 37]. For example, studies use machine learning algorithms such as random forest and deep learning to analyze microbiome data and identify biomarkers associated with conditions such COVID-19 [43]. Metagenomics, a key component of microbiome research, involves sequencing and analyzing the genetic material of microbial communities. This approach plays a crucial role in the investigation of the microbial composition, functional potential, and its correlation with diseases and conditions [44]. At the same time, scientists explore dysbiosis, an imbalance in the gut microbial community, and its association with inflammation and conditions such as inflammatory bowel disease [45]. Researchers also examine the composition and diversity of the gut microbiota and its impact on human health. They investigate the effects of diet, antibiotics, and probiotics on the gut microbiota, as well as the role of the gut microbiota in conditions such as type 2 diabetes and intestinal disorders [46]. Example studies within this theme demonstrate the practical applications of these research areas. For example, a study applies machine learning algorithms to the data of the gut microbiome to develop a predictive model of colorectal cancer, in order to enhance early detection [47]. Another research uses metagenomic sequencing to analyze the gut microbiome in patients with inflammatory bowel disease, seeking potential targets for therapeutic interventions [48]. Furthermore, investigations explore the effects of diet and probiotics on the diversity of the gut microbiota in obese individuals, contributing to a better understanding of the role of the gut microbiota in obesity management [49]. Lastly, a study employs deep learning techniques to analyze microbiome data from COVID-19 patients, aiming to identify microbial signatures associated with disease severity and gain insight into the potential role of the microbiome in COVID-19 outcomes [50]. These studies highlight the diverse range of research within the microbiome theme. By integrating machine learning and metagenomic analysis, researchers aim to uncover associations between the microbiome and various health conditions. Through understanding the complex interactions within the microbiome and its implications for human health, they strive to develop personalized approaches for the diagnosis, treatment, and prevention of diseases.

The theme of "Quorum Sensing" emerges within this cluster, characterized by a callon centrality of 0.0076 and a callon density of 4.5455. Quorum detection is a social cue that allows bacterial communities to regulate genetic expression based on population density. It plays an important role in the interactions between the human gut and food microbiomes, influencing the taxonomical composition and functional capacity of the resident gut microbiome. Quorum detection has emerged as an attractive target for therapeutic intervention, offering the potential to modulate microbial communities without the negative effects of traditional antimicrobial approaches. By interfering with quorum sensing mechanisms, such as quorum quenching or the application of inhibitory compounds, it is possible to manipulate the microbial composition and potentially impact health and disease outcomes [51].

Gut microbiome, disease prediction using 16S rRNA data with machine learning, and personalized medicine are trending topics (Figure 9) in AIM [52]. This highlights the efficiency of AI in analyzing large data and provides predictive models, with studies achieving high accuracy in predicting diseases like colorectal cancer and inflammatory bowel disease using machine learning. Transfer learning allows scholars to study current knowledge from other studies to enhance prediction in AIM, while AI excels in big data analysis for the microbiome, enabling tasks like data cleaning, pattern recognition, and personalized interventions [4, 23, 25, 35, 41].

Cocitation analysis of authors offers valuable insights into the intellectual framework of a research field by revealing relationships between scholars based on the cooccurrence of their works in cited references. Analyzing cocitation patterns enables researchers to identify influential authors, emerging research themes, and potential collaborations. VOSviewer employs various clustering algorithms, such as Louvain or Leiden, to identify groups of authors with strong cocitation links [53]. These clusters represent distinct research themes or subfields within the broader discipline. Larger nodes represent more influential and frequently cited authors. These prominent authors play a pivotal role in shaping the field and influencing other researchers. Knight, R. is the most co-cited author in AIM and anchors the green cluster. The second-most cocited author is Wang, Y., who leads the red cluster.

Using data-driven studies that exclusively rely on Scopus and English articles in bibliometric analysis has limitations. This approach introduces language bias, potentially excluding non-English publications and limiting the representation of global research output. Sorely relying on Scopus can overlook relevant studies from other databases and disciplines, reducing the scope and inclusivity of the analysis. Furthermore, focusing solely on data-driven approaches can overlook qualitative insights from other types of documents such as reviews, short communications, book chapters, and editorials. Acknowledging these limitations is crucial, and incorporating additional data sources, languages, and research approaches is necessary for a more comprehensive and robust bibliometric study.

5. Conclusions

Bibliometric analysis exploring the intersection of AI and the microbiome provides valuable insights into the research landscape and trends within this interdisciplinary field. The study reveals growth and publication patterns, key contributors, collaboration networks, and emerging research topics at the intersection of AI and the microbiome. It highlights the growing interest in applying artificial intelligence techniques to microbiome studies, with a steady increase in the number of publications over time. The analysis identifies prominent researchers, institutions, and countries, providing an understanding of key players and their collaborations. In addition, it sheds light on specific applications of AI, such as data analysis and integration, microbiome profiling, predictive modeling, drug discovery, and personalized interventions. The findings of this bibliographic analysis help researchers and practitioners understand current trends, potential future directions, and areas that require further investigation within the field of AI and the microbiome. Key recommendations to advance AI-microbiome research include fostering interdisciplinary collaboration, promoting data sharing and standardization, developing robust and tailored AI algorithms, embracing multi-omics approaches, validating findings through experiments, addressing ethical considerations, encouraging diverse research perspectives, and strengthening industry-academia partnerships - all of which can help guide future research endeavors and drive advancements in this interdisciplinary field, leading to valuable scientific insights and practical applications across healthcare, agriculture, and environmental sciences.. The bibliometric analysis on AI and the microbiome highlights key implications for future research, including fostering interdisciplinary collaboration, advancing AI techniques, embracing multi-omics, validating findings, addressing ethics, and strengthening industry-academia partnerships.

Ethics approval and consent to participate

There is no form of human subject involved in this manuscript; therefore, ethics approval is not required.

Consent for publication

Not applicable.

Availability of data and material

The data sets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising, or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be responsible for all aspects of the work.

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