Exploring AI Trends in Molecular and Cell Biology: A 10-Year Bibliometric Analysis (2015-2024)

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Abstract

This study examines the evolution of artificial intelligence (AI) applications in molecular and cell biology from 2015 to 2024, utilizing bibliometric analysis compliant with PRISMA guidelines. An analysis of 1,779 open-access articles highlighted significant growth in AI-related publications, increasing from 39 in 2015 to 418 in 2024, with the U.S. leading in total publications. Key applications identified include genome analysis, drug discovery, and personalized medicine. The research underscores the importance of AI in fostering interdisciplinary collaboration and advancing global genomic initiatives. Recommendations are provided to guide scientists, policymakers, and funders in addressing knowledge gaps and forming new research avenues.

Keywords
Bibliometric Analysis; Artificial Intelligence; Molecular Biology; Cell Biology; Dimensions; PRISMA

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1. Introduction

Intelligent retrieval is also known as artificial intelligence. Combining machine learning and artificial intelligence is fundamental to modern scientific databases. The molecular and cellular biology disciplines use neural networks with knowledge engineering as their leading innovative approaches. Scientists use artificial intelligence, combined with molecular and cell biology research methods, to improve complex biological assessment and primary life science inquiries. Over the last 10 years, machine learning, deep learning, and neural network technology have advanced genomic, proteomic, and cellular dynamics research. The surge in biological data enables neural networks to develop tools that extract knowledge from the data and accelerate discovery. A functional evaluation system needs to monitor the development of changes in molecular and cell biology engineering applications during this quickly changing period. Intelligent retrieval research development and molecular and cell biology intellectual structure analysis were done through bibliometrics from 2015 to 2024. The Dimensions database provided the necessary information to complete the broad-scale analysis of this subject. The research sought to uncover primary patterns, establish new trends, and provide research guidance for this evolving field.

2. Literature Review

Academic analyses utilizing the Dimensions database and analysis techniques to interpret smart technology research activities in molecular and cell biology remain insufficient despite their achievements in the field. Research validity is crucial because documented gaps urge researchers to develop bibliometric research that encompasses diverse scholarship outputs to uncover disciplinary patterns and intellectual trends.

The advancement of artificial intelligence research within molecular and cellular biology requires proper analysis to determine research directions, inspire team collaboration, and support budgeting decisions. A thorough research perspective results from an evaluation using the dimension database, which maintains a wide range of academic literature. The results will assist researchers, policymakers, and interested parties in navigating the swiftly changing landscape of AI-driven biological research.
How do dimension database records reflect the evolution, themes, and consequences of artificial

intelligence studies in the fields of molecular and cellular biology between 2015 and 2024?

The central objective of this investigation was to conduct a bibliometric assessment of artificial intelligence research in molecular and cellular biology, spanning 2015 to 2024, using the Dimensions database as the primary data source. Precise goals comprise:

- Recognising patterns in research output, citation impact, and collaboration.
- Analyzing the field's framework through co-citation and keyword examination.
- Evaluating the impact of prominent organizations, nations, and researchers. Future developments and research fields were evaluated for identification purposes.

This hypothesis posits that artificial intelligence research in molecular and cellular biology has experienced rapid growth from 2015 to 2024. Three components explain the exponential growth of artificial intelligence research in molecular and cellular biology: advances in computational capability, improvements in data accessibility, and growth in interdisciplinary teamwork. Drug development assistance from AI systems, along with single-cell investigation techniques, will become the most significant topic because they provide essential biological solutions.

3. Methods

3.1 Data Source

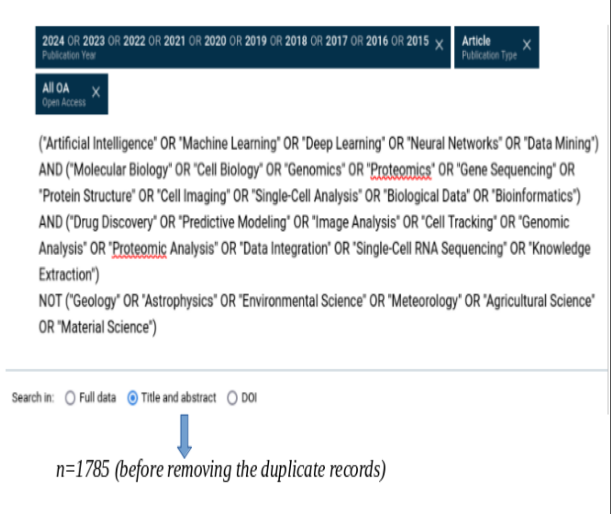
Research data were obtained mainly from Dimensions, a Digital Science research platform. The researchers selected dimensions because they provide access to 146 million research publications along with patents and funding information, and use AI technology for data extraction and trend analysis functionality (Lin et al., 2023). It can utilize this platform as a bibliometric research tool because its functionality reveals citation networks for research development alongside collaborative relationships. Through these dimensions, researchers can perform sophisticated filtering of information, allowing them to explore the use of artificial intelligence in molecular and cellular biology research.

3.2 Timeframe

This study considers a timeframe from 2015 to 2024, which allows researchers to analyze the swift development of artificial intelligence technologies during their increased utilization in molecular and cellular biology. The high-quality bibliometric information available supports the defined period through which this study extends. The chosen time period shows perfect conditions for studying AI trends alongside temporal patterns, because it captures the intensified usage of AI in this interdisciplinary field.

3.3 Search Strategy for Data Collection

A system-based search protocol was used to identify available field research articles that address artificial intelligence applications in molecular and cellular biology. The search implemented Boolean logic to connect artificial intelligence and machine learning with deep learning, molecular biology, and cell biology terminologies. Research articles published between 2015 and 2024 within peer-reviewed English documents formed the basis of the search results. The search used artificial intelligence techniques, such as data mining, deep learning, and machine learning, to identify studies on genomics proteomics and drug discovery. The search engine enabled by Dimensions AI allows the execution of this approach **(Figure 1).**



2024 OR 2023 OR 2022 OR 2021 OR 2020 OR 2019 OR 2018 OR 2017 OR 2016 OR 2015 ×
Publication Year
Article ×
Publication Type
All OA ×
Open Access

("Artificial Intelligence" OR "Machine Learning" OR "Deep Learning" OR "Neural Networks" OR "Data Mining")
AND ("Molecular Biology" OR "Cell Biology" OR "Genomics" OR "Proteomics" OR "Gene Sequencing" OR "Protein Structure" OR "Cell Imaging" OR "Single-Cell Analysis" OR "Biological Data" OR "Bioinformatics")
AND ("Drug Discovery" OR "Predictive Modeling" OR "Image Analysis" OR "Cell Tracking" OR "Genomic Analysis" OR "Proteomic Analysis" OR "Data Integration" OR "Single-Cell RNA Sequencing" OR "Knowledge Extraction")
NOT ("Geology" OR "Astrophysics" OR "Environmental Science" OR "Meteorology" OR "Agricultural Science" OR "Material Science")

Search in: ○ Full data ● Title and abstract ○ DOI

n=1785 (before removing the duplicate records)

Figure 1 : Search strategy for collecting data in the Dimensions AI
(Source: https://app.dimensions.ai/discover/publication)

3.4 PRISMA Flow Diagram

The study has used the PRISMA 2020 guidelines to ensure the systematic selection of all the documents for this bibliometric study. To ensure the data was transparent, relevant, and met quality standards, the Identification, Screening, Eligibility and Final Selection, and Data Cleaning steps were carried out (Haddaway et al., 2022; Tricco et al., 2018). This method is suitable for beginners since it explains everything step by step.

Identification Stage

The initial search was conducted in the Dimensions AI database on November 13, 2024, yielding 4,957 documents across various types, including research articles, conference papers, reviews, and other scholarly outputs. This stage served to collect a broad base of potentially relevant literature without applying restrictive filters.

Screening Process

Publications published from 2015 to 2024 were used to focus on current research. Therefore, we rejected 776 records that exceeded the time limit, leaving 4,181 papers for further exploration. During this process, the study thoroughly reviewed titles and abstracts to identify articles classified as original research publications. After removing 726 less relevant articles, the total number of studies decreased to 2,511.

Eligibility Assessment

At this point, the selected articles were evaluated for open access availability, a necessary criterion for inclusion in the bibliometric analysis. Of the remaining documents, 1,785 research articles were found to be openly accessible. These articles were considered eligible for the study based on access, content type, and subject alignment.

Final Selection and Data Cleaning

A final selection was made after a duplicate removal process using Microsoft Excel. Following a thorough check, six duplicates were removed, leading to a final count of 1,779 publications for detailed bibliometric analysis. This step not only increases data quality but also ensures that each study is represented only once for accurate evaluation. The illustration below (Figure 2) presents a PRISMA flow diagram that details the document-selection process.

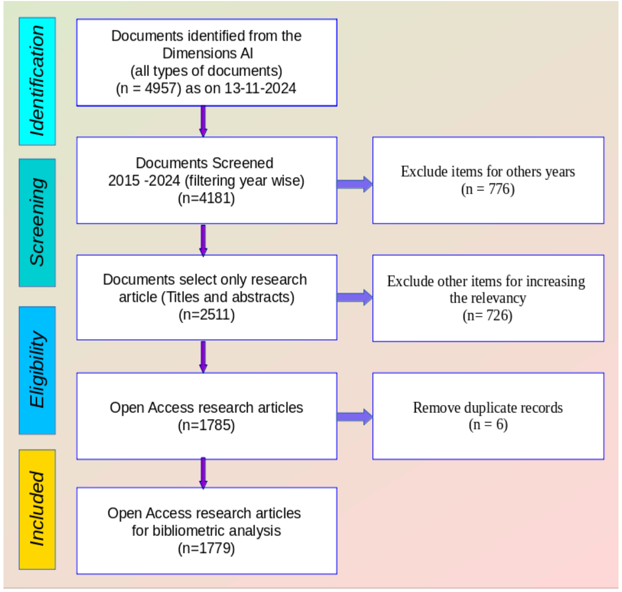


Figure 2: Flow diagram of PRISMA for document selections
(*It was meticulously developed in accordance with the PRISMA 2020 guidelines, as outlined at https://www.prisma-statement.org/prisma-2020*)

With this approach, the analysis used many studies, all of which were widely available, relevant, and of high quality. Because all steps in PRISMA were carefully carried out, from beginning to end, any bias was overcome and the results became more reliable. This means that the final set of 1,779 open-access research articles gives us a robust basis for researching AI use in molecular and cell biology.

3.5 Metrics Analyzed

This academic work utilized bibliometric indicators to evaluate the significance and dissemination of artificial intelligence applications in molecular and cellular biology. This study employed citation metrics to assess scholarly impact and examined publication productivity to identify temporal patterns in output. This study mapped the contributions of leading countries and institutions, recognized influential researchers, and explored the distribution of publications across journals and sources. These metrics provide an understanding of the research landscape and highlight salient contributors, trends, and primary channels of knowledge dissemination within the discipline.

3.6 Tools for Data Analysis and Visualisation

Analytical and visualization instruments were used in this study. Artificial intelligence facilitates data collection and bibliometric assessment, and extracts and analyzes research information. The network analysis software VOSViewer elucidates collaboration and citation patterns and highlights significant research themes. Data management, statistical analysis, and duplicate removal were performed using Microsoft Excel software. ChatGPT generated insights and refined the interpretation of results (Bulut, 2024). These tools were selected for their synergistic capabilities, enabling comprehensive analysis of artificial intelligence applications in molecular and cellular biology.

4. Results and Discussions

Over the last decade, the study has meticulously analyzed the development, expansion, and main topics of AI applied to molecular and cellular biology. An analysis of 1,779 academic papers using Dimensions reveals main challenges in publishing, authors' regions, academic citations, and researcher collaborations.. Here, it brings together the results to explain how publications are made, by whom, and on which main research subjects. The purpose is to uncover how AI has impacted and continues to influence studies in the life sciences, such as those related to genomics, proteomics, and personalized medicine. The results and discussions are explained as follows:

4.1 Publications, Citations, and Global Contributions

Scientific advancements in molecular and cell biology have been notably enhanced by artificial intelligence, as evidenced by the changing patterns in research publications, citations and world wide contributions in recent years. Based on the data in Table 1, an analysis can be conducted on publications, citations, and global contributions to artificial intelligence research in molecular and cell biology over 10 years. Research has shown that publication numbers expanded considerably between 2015 and 2024, when they grew from 39 to 418, indicating rapid growth. A considerable number of published studies reached their peak in 2019, and once again in 2021. According to global contributions, the United States issued 628 publications, whereas China authored 454. The research identifies the United Kingdom, Germany, and Canada as the leading participants in this field.

The quantity of published literature related to deep learning technology integration in molecular and cell biology has shown substantial growth from 2015 to 2024. An expansion occurred because of greater data availability alongside better machine learning techniques and expanding recognition of cognitive computing abilities in tackling complex biological matters. Changes in citations throughout the years stem from both the late adoption of novel research findings and the different stages at which specific scientific developments have achieved global recognition. Research on highly cited articles reveals important scientific opportunities that have moved the field forward. Publications by the United States and China likely dominate the field because they spend generously on R&D activities. Machine learning research in molecular and cell biology demonstrates a global collaborative character because of significant country participation from the United Kingdom, Germany, and Canada.

Table 1: Publications and Citations Over the Years and Countries Publications

Years	Publications	Citations		Country	Publications
2015	39	8385		United States	628
2016	56	6452		China	454
2017	48	1983		United Kingdom	172
2018	83	9414		Germany	104
2019	139	12912		Canada	79
2020	167	8929		India	68
2021	225	14657		Japan	61
2022	269	6390		Italy	60
2023	334	3542		South Korea	58
2024	418	766		Spain	54

4.2 Top Cited Articles

Analysis of the top-cited neural networks Research articles in molecular and cell biology (Table 2) revealed significant trends. The most-cited paper, Radiomics: Images Are More than Pictures, They Are Data (2015), with 6,272 citations, highlights AI-driven imaging in medical diagnostics. A Review of Deep Learning (2021) with 3,834 citations shows rapid advancements and widespread adoption of deep learning. Highly cited works also focus on machine learning in cellular analysis, such as Digital Cytometry for Cell Type Abundance (2019) with 2,811 citations and computational techniques for uncertainty quantification (A Review of Uncertainty in Deep Learning, 2021). The Harmonizome dataset integration platform (2016) demonstrated the impact of AI on gene and protein research.

AI-powered precision medicine is also well represented, with studies on SVM in Cancer Genomics (2018), DeepDTA for Drug-Target Binding Prediction (2018), and Circulating Tumor DNA Detection (2018), all exceeding 750 citations. Single-cell RNA-Seq in AML (2019) in the top ten emphasizes AI's role of AI in single-cell transcriptomics.

These discoveries confirmed that machine learning-driven innovations in imaging, computational biology, and personalized medicine have significantly influenced molecular and cellular biology research.

Table 2: Top cited articles

Rank	Title	Journal	Year	Citations	References
1	Radiomics: Images Are More than Pictures, They Are Data	Radiology	2015	6272	Gillies et al., 2015
2	Review of deep learning: concepts, CNN architectures, challenges, applications, future directions	Journal of Big Data	2021	3834	Alzubaidi et al., 2021
3	Determining cell type abundance and expression from bulk tissues with digital cytometry	Nature Biotechnology	2019	2811	Newman et al., 2019
4	A review of uncertainty quantification in deep learning: Techniques, applications and challenges	Information Fusion	2021	1440	Abdar et al., 2021
5	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins	Database	2016	1267	Rouillard et al., 2016
6	Applications of Support Vector Machine (SVM) Learning in Cancer Genomics	Cancer Genomics & Proteomics	2018	1130	Huang et al., 2018
7	DeepDTA: deep drugâ€“target binding affinity prediction	Bioinformatics	2018	982	Hakime et al., 2018
8	Image analysis and machine learning in digital pathology: Challenges and opportunities	Medical Image Analysis	2016	811	Madabhushi & Lee, 2016
9	Enhanced detection of circulating tumor DNA by fragment size analysis	Science Translational Medicine	2018	783	Mouliere et al., 2018
10	Single-Cell RNA-Seq Reveals AML Hierarchies Relevant to Disease Progression and Immunity	Cell	2019	763	van Galen et al., 2019

4.3 Influential Authors

Exceptional authors have presented a hierarchical form (Table 3) for the AI-driven Molecular and Cell Biology field. The authors' position in the list depended on the influence their research had on citations within the selected research domain.

Ruth Nussinov emerges as prominent, accumulating 826 citations across seven publications, averaging 118 citations per article. This demonstrates her substantial influence on the AI-driven molecular studies. Similarly, Feixiong Cheng and Hyunbum Jang exhibited significant citation impacts (496 and 383 citations, respectively), underscoring their importance. Researchers with higher publication counts, such as Lei Xie and Jie Zheng (each with eight papers), demonstrate consistent output, albeit with lower citation averages (28.0 and 16.75, respectively). Kun Huang and Xin Gao also display considerable research visibility, accumulating 263 and 206 citations, respectively. These analyses have elucidated the complex relationship between publication quantity and citation impact. While some scientists produce substantial work volumes, their publications' influence, measured by citations, varies considerably. This pattern underscores the dual significance of productivity and impact in advancing AI applications in molecular and cell biology.

Table 3: Most influential authors

Rank	**Author**	**Publications**	**Citations**	**Average Citation per Article**
1	Lei Xie	8	224	28.00
2	Jie Zheng	8	134	16.75
3	Xin Gao	7	206	29.43
4	Kun Huang	7	263	37.57
5	Ruth Nussinov	7	826	118.00
6	Yang Liu	6	91	15.17
7	Feixiong Cheng	5	496	99.20
8	Dohyun Han	5	23	4.60
9	Hyunbum Jang	5	383	76.60
10	Yong Liu	5	94	18.80

4.4 Top Ten Organizations

The top ten organizations in AI Research in Molecular and Cell Biology (Table 4) demonstrate significant contributions from leading global institutions. Stanford University exhibited a substantial citation impact, with 5,400 citations across 37 publications, yielding an average of 145.95 citations per article, followed by the University of Cambridge (3,120 citations, 130.00 per article). Harvard University ranks third in citation impact (80.93 per article) despite having the highest publication count (41). Additional high-impact contributors include the University of Oxford (51.28 citations per article) and University of Michigan–Ann Arbor (51.08), which demonstrate robust AI-driven research output. Conversely, Shanghai Jiao Tong University and Sun Yat-sen University, despite comparable publication counts (25 each), exhibited lower citation averages (10.20 and 9.92, respectively), indicating disparate research influence. These studies underscore the predominance of elite Western institutions in high-impact AI research, while Chinese universities contribute consistently, albeit with lower citation influence.

Table 4: Top ten organisations

Rank	**Organization**	**Publications**	**Citations**	**Average Citation per Article**
1	Harvard University	41	3318	80.93
2	Stanford University	37	5400	145.95
3	University of Pennsylvania	28	1357	48.46
4	University of Toronto	26	1283	49.35
5	Shanghai Jiao Tong University	25	255	10.20
6	Sun Yat-sen University	25	248	9.92
7	University of Oxford	25	1282	51.28
8	University of Cambridge	24	3120	130.00
9	University of Michigan–ann Arbor	24	1226	51.08
10	Fudan University	23	653	28.39

4.5 Top Ten Journals

Investigation of leading deep learning Research journals in Molecular and Cell Biology (Table 5) reveals bioinformatics as a preeminent, with 160 articles and 7,527 citations, averaging 47.04 citations per paper. Nature Communications has the highest citation impact, averaging 67.61 citations per article, underscoring its significance in AI-related biological studies. Briefings in Bioinformatics and PLOS Computational Biology also contributed substantially, with 25.38 and 46.91 average citations respectively, both of which were recognized for their focus on computational and AI-driven biological research. The prominence of open-access platforms, such as Scientific Reports, BMC Bioinformatics, and PLOS One, emphasizes their importance in disseminating intelligent retrieval research insights. Research results show that machine learning platforms in molecular and cell biology primarily appear in bioinformatics journals and receive important co-publication support from open-access platforms.

Table 5: Top Ten Journals

Rank	**Journal**	**Publications**	**Citations**	**Average Citation per Article**	**Publisher**	**Impact Factor**	**H-index**
1	Bioinformatics	160	7527	47.04	Oxford University Press	4.4	462
2	Scientific Reports	59	1153	19.54	Nature Publishing Group	3.8	315
3	BMC Bioinformatics	50	1007	20.14	BioMed Central Ltd	7.1	242
4	Briefings in Bioinformatics	50	1269	25.38	Oxford University Press	13.99	142
5	Nature Communications	49	3313	67.61	Nature Publishing Group	14.7	522
6	International Journal of Molecular Sciences	37	856	23.14	Multidisciplinary Digital Publishing Institute (MDPI)	4.9	269
7	Frontiers in Immunology	31	899	29.00	Frontiers Media SA	5.7	225
8	BMC Genomics	24	405	16.88	BioMed Central Ltd	3.5	199
9	PLOS One	24	620	25.83	Public Library of Science	2.9	435
10	PLOS Computational Biology	23	1079	46.91	Public Library of Science	3.8	217

5. Visualisation

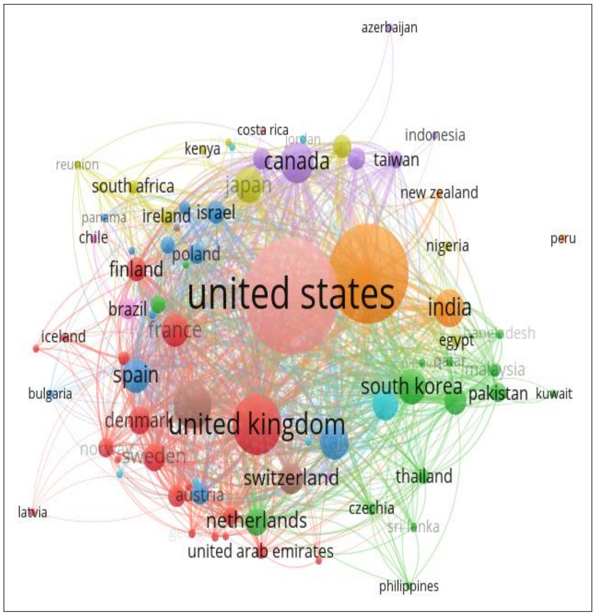
In this study, VOSviewer was used as a tool to analyze scholarly publications on AI applications in molecular and cell biology research (Ulupui et al., 2023). This analysis evaluated data from 10,547 authors working at 2,868 institutions and publishing in 659 journals to identify the main research contributors and their collaborative networks. Global research collaboration is strongest between the United States and the United Kingdom because both countries rank among the leading research institutions. The research methodology enables scientists to identify compatible research teams and discover scientific patterns that help promote knowledge exchange and facilitate field development. Table 6 shows the visualization of scholarly insights into AI research in molecular and cell biology.

Table 6: Visualisations of scholarly insights

Visualization	**Total**	**Selected**
Network visualization	80 Countries	80 Countries
Authors visualization for the citations counts	10547 Authors	605 Authors (minimum number of documents of an author 2)
Organization visualization	2868 Organizations	461 Organizations (minimum number of documents of an organization 3)
Sources or journal visualization	659 Journals	208 Journals (minimum number of documents of a source 2)

The European cluster, which includes France, Germany, Switzerland, and the Netherlands, forms the most evident regional collaboration network. This study simulated these countries, illustrating the importance of closeness in fostering collaborative research and knowledge exchange. The Asia-Pacific cluster for contributors, such as India, South Korea, and Japan, shows the region's activity in global research. Smaller, connected countries, such as Kenya, Costa Rica, and Azerbaijan, bring innovative perspectives. Organising as part of the internationalisation network demonstrates a democratic contribution to science development, where diverse areas can participate. Countries such as Brazil, South Africa, and Thailand have played a significant role in global research projects. This trend shows that nations see science's importance as developing countries collaborate with developed countries to support scientific work. This network of Europe and America, with larger populations serving as learning and creative hubs, personifies their collective efforts to address complex scholarly questions. This visualization underscores the significance of international cooperation in science advancement and global knowledge cultivation. Figure 3 shows the network visualization for the 80 countries involved in AI molecular and cell biology research.

Figure 3: Network Visualization using VOSviewer



(Source: https://www.vosviewer.com/)

The most concentrated areas of activity are found in the well-established academic centers of the United States, United Kingdom, and Western Europe, showcasing their dominant role in worldwide research networks. Emerging regions, particularly Asia and South America, show increased involvement, signaling a rise in research activities. This evolving landscape suggests that new areas are becoming significant contributors to knowledge creation and influencing scientific advancement.

The citation analysis in Figure 4 shows the author's involvement in the field. Subject importance becomes visible through the node-size system, which helps students better understand the academic field. The network core consists of scholars Zheng Jie, Gao Xin and Xie Lei who demonstrate substantial contributions through their large node sizes. Leading contributors show robust collaborative teamwork. Nussinov Ruth alongside Bhattacharya Debswapna operate in the central section of the network to advance field diversity while actively moving research forward. The visualization of the field shows how it evolved to include newer authors, such as Aracri Federica, as smaller nodes that reflect quick recognition of their ideas. The color gradient shows how authors' impact has evolved, while showing emerging scholars who have recently begun to receive acknowledgement. This representation tracks collaborative research development, as it helps users locate important contributors who guide both innovation and present trends in their field.

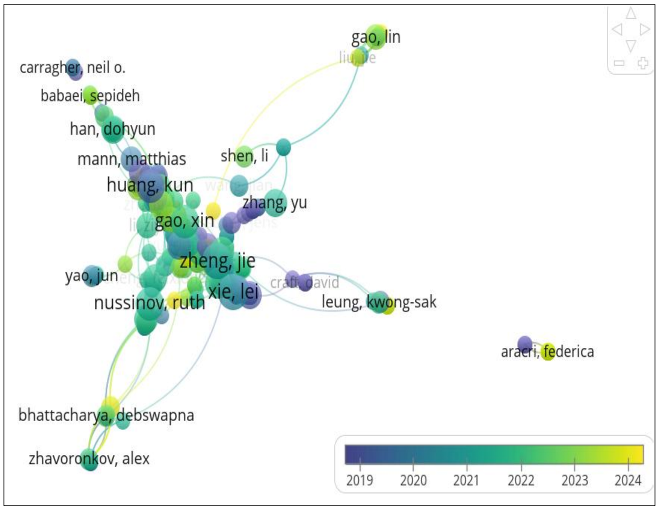


Figure 4: Authors Visualization for citation counts using VOSviewer

(Source: https://www.vosviewer.com/)

Figure 5 illustrates how institutions work together on research endeavors. Each entity receives a representation scale to determine its node size. Significant universities, such as Stanford and Harvard and the University of Pennsylvania, appear as prominent nodes representing their essential positions in the system. Institutions generate innovation while developing global partnerships to effectively advance their research. Several major research institutions such as Imperial College London, the University of California, and the University of Texas Health actively collaborate in well-recognized research areas to enhance knowledge transfer and scientific discoveries. The network presents Ilia State University and Saint Louis University as essential components, even though they are positioned outside the central points. Such research institutions profit from their connections to larger organizations to show how all institutions support the research community. Color coding within the chart identifies both regional sections and thematic organizations that showcase cooperation through specializations and geographic locations. Visual representation displays research centers while displaying knowledge-based institutions, along with the varied characteristics of the research field.

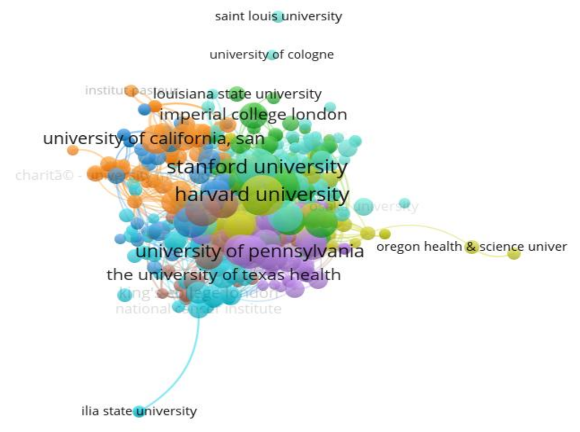


Figure 5 : Organisation Visualisation using VOSviewer

(Source: https://www.vosviewer.com/)

This study elucidates the sophisticated relationships among journals in bioinformatics and related disciplines, showcasing their reciprocal influence and interconnectedness. Bioinformatics is at the center of this network, fostering numerous connections and disseminating critical research outcomes. Publications such as BMC Bioinformatics, Scientific Reports, and Nature Communications are clustered around this nucleus. Their interconnections mirror the co-citation index and interdisciplinary nature of the field. Periodicals, such as Molecules and Frontiers in Pharmacology, form distinct subgroups delineating research areas associated with bioinformatics. On the network's outskirts, emerging journals such as Frontiers in Plant Science and Frontiers in Pediatrics have tackled cross-disciplinary applications, bridging bioinformatics with plant science and pediatrics. This network underscores the extensive role of bioinformatics in molecular and computational sciences. Journals such as the International Journal of Molecular Sciences and Computational Biology and Chemistry function as connectors, bridging research domains and facilitating knowledge dissemination. Figure 6 depicts the landscape of scientific publishing in bioinformatics, highlighting the journal's role in disseminating novel ideas and advancing interdisciplinary research.

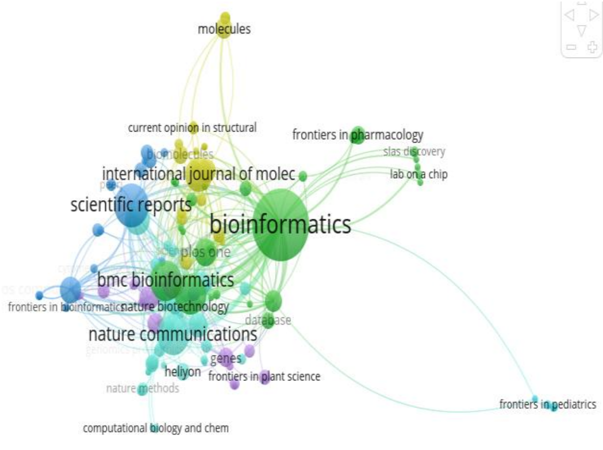


Figure 6: Journal Visualization using VOSviewer

(Source: https://www.vosviewer.com/)

The bibliometric study revealed a rapid increase in publications on artificial intelligence in molecular and cellular biology, with extensive research impacts and global collaborations. These patterns indicate progress in AI analytical tools and the integration of computational intelligence into the biological sciences. Such discoveries highlight the need for cross-disciplinary teams to address the complex challenges associated with microbial structures and the growing significance of AI in advancing molecular and cell biology.

6. Conclusion

Over the last decade, this study investigated the development, influence, and collaborative aspects of machine learning applications in molecular and cellular biology. These findings indicate a significant increase in research productivity, with publications rising from 39 in 2015 to 418 in 2024, underscoring AI's importance for intelligent retrieval when addressing intricate biological issues. Genomics, proteomics, drug development, and single-cell analysis have emerged as central areas, showcasing the potential of neural networks as smart systems to revolutionise life science research.These scientific insights emphasize the dominance of algorithm-driven molecular and cellular biology investigations in the United States and China, contributing to a substantial proportion of global publications. European and Asian institutions have also played pivotal roles in establishing robust international research collaboration. Co-citation analysis reveals a highly interconnected scholarly community, with institutions such as Stanford, Harvard, and the University of Cambridge leading advancements in AI-integrated biological sciences.

The impact of seminal studies on precision medicine, computational biology, and AI-driven methodologies was examined through citation analysis. The field's evolution has been profoundly influenced by notable advancements in radiomics, deep learning applications in cytometry, and deep learning-enhanced drug-target interaction research. Prominent journals, including Bioinformatics, Nature Communications, and Briefings in Bioinformatics, have emerged as crucial venues for the dissemination of innovative cognitive computing applications in the biological sciences.Notwithstanding these advancements, challenges persist regarding the accessibility of high-quality datasets, algorithmic transparency, and ethical considerations for the implementation of knowledge engineering in molecular biology. Confronting these issues requires enhanced international collaboration, interdisciplinary research, and robust regulatory frameworks to ensure the responsible and equitable adoption of intelligent retrieval.

This bibliometric study can serve as a fundamental resource for researchers, policymakers, and funding bodies to navigate the dynamic landscape of expert systems in molecular and cellular biology. As artificial intelligence continues to reshape biological research, future initiatives should focus on refining machine learning methodologies, promoting global knowledge dissemination, and addressing ethical and technical challenges. By capitalising on interdisciplinary collaborations and addressing existing limitations, the scientific community can maximise the transformative capacity of knowledge engineering to catalyse innovation and discoveries in the field of molecular and cellular biology.

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