

Celebrating 25 years of briefings in bioinformatics: a comprehensive bibliometric analysis

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Abstract

Over the past 25 years, Briefings in Bioinformatics (BIB) has been the leading journal in the bioinformatics field. To commemorate this milestone and trace the journal's academic trajectory, we conducted a comprehensive bibliometric analysis of 4185 BIB publications published between 2000 and 2024. The publications were retrieved from Elsevier's Scopus. Since 2021, the annual number of citations has increased prominently, peaking in 2024 ($n = 30\,729$). These publications have accumulated a total of 183 911 citations, including 364 publications that have received more than 100 citations. The most cited article was published by Kumar et al. (2004) and it has received 10 750 citations. The 4185 publications were contributed by 4140 authors from 79 countries/regions, reflecting BIB's international characteristics. In terms of the total number of publications (TP) and the total number of citations (TC), China (TP = 2085; TC = 58 851), the United States (TP = 1120; TC = 67 000), and the United Kingdom (TP = 329; TC = 16 581) were the leading countries. The Chinese Academy of Sciences (TP = 216; TC = 6200), Central South University (TP = 112; TC = 3079), and Zhejiang University (TP = 105; TC = 3503) were the leading affiliations. Zou, Quan (TP = 64; TC = 3023), Song, Jiangning (TP = 58; TC = 2652), and Wu, Rongling (TP = 35; TC = 633) were the leading authors. Collaboration has intensified over time, with the median number of authors per publication rising from two in 2000–2004 to five in 2020–2024. The research focus of BIB has shifted from foundational bioinformatics and database development to integrative multi-omics analysis and AI-driven biomedical research. As BIB develops, its international impact will continue to grow, solidifying its pivotal role in shaping the future of bioinformatics research.

Keywords bioinformatics, bibliometrics, visualized analysis, co-occurrence analysis

Introduction

From the 1990s to the early 21st century, the rapid advancement of molecular biology and medical informatics, together with the rise of the big data era, contributed to the gradual emergence of bioinformatics as an independent field of research, playing a pivotal role in the life sciences [1, 2]. The international interdisciplinary journal *Briefings in Bioinformatics (BIB)* was founded in 2000 and is regarded as an authoritative platform for the dissemination and exchange of comprehensive reviews, new methods, case studies, and opinion articles in the field of bioinformatics [3]. Focusing on the convergence of biology, mathematics, statistics, computer science, and clinical medicine, the journal consistently publishes high-quality research findings, thereby providing essential academic references and inspiration for researchers in

related fields. The current Editor-in-Chief, Shuangge Ma, has held the position since 2023. According to the 2024 Journal Citation Reports (JCR), BIB achieved a Journal Impact Factor (JIF) of 7.7, ranking second in the category of *Mathematical & Computational Biology* and third in *Biochemical Research Methods*.

Bibliometric analysis is a systematic and rigorous methodology used to analyze large volumes of scientific data. It enables researchers to uncover insights from data, characterize research subjects, and identify future trends. In recent years, bibliometrics has been increasingly applied to research on journal development, with a focus on publication and citation trends, as well as thematic evolution. At the present time, exploratory work has been conducted on the subject of bibliometric studies of a single journal in the field of bioinformatics and in related disciplines [4].

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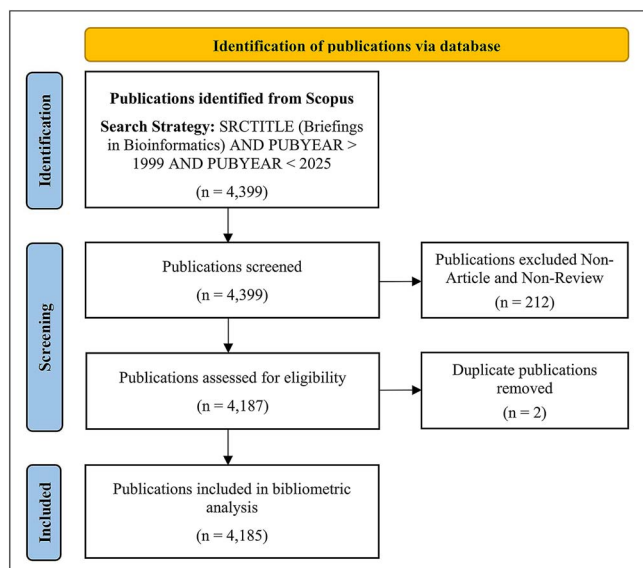


Figure 1 Flowchart of the BIB publications acquisition process.

In 2025, BIB celebrated its 25th anniversary. Both the form and content of publications in BIB have changed over the last 25 years. This study conducts a comprehensive bibliometric analysis of BIB, covering its publication history from 2000 to 2024. It is the first to provide a detailed examination across five time periods based on keywords, countries/regions, and affiliations, supplemented by a co-occurrence analysis of keyword evolution. We delineate the journal's evolving research priorities, shifting patterns of international collaboration, and growing scholarly influence. Our findings demonstrate a clear thematic transition—from early publications centered on foundational bioinformatics methods to its current prominence as a forum for integrative multi-omics analyses and artificial intelligence-driven biomedical discoveries. The current study also guides research institutions and scholars dedicated to advancing the field's future evolution.

Materials and methods

Data sources and retrieval strategy

With a huge collection of publications, Elsevier's Scopus is the largest abstract and citation database in the world. It contains extensive bibliographic metadata, and numerous large-scale bibliometric analyses have employed it as a primary data source [5]. Compared with other databases, Scopus provides a more comprehensive coverage of BIB publications since its inception. Therefore, the data used in this study were retrieved from Scopus. Figure 1 shows the process of publication identification, screening, and inclusion. Publications appearing in BIB during the publication window from 2000 to 2024 were collected using the following retrieval strategy: SRCTITLE (Briefings in Bioinformatics) AND PUBYEAR > 1999 AND PUBYEAR < 2025. A total of 4399 publications were initially identified. The dataset was subsequently refined to include only articles and reviews, yielding 4187 publications [6, 7]. After the removal of two duplicates, 4185 publications were retained for analysis, consisting of 3476 articles and 709 reviews [8]. Metadata for each publication was exported in CSV format for bibliometric analysis. The citation metrics here are based on citations that accumulated from publication until July 18, 2025, which is consistent with the date of data retrieval and download.

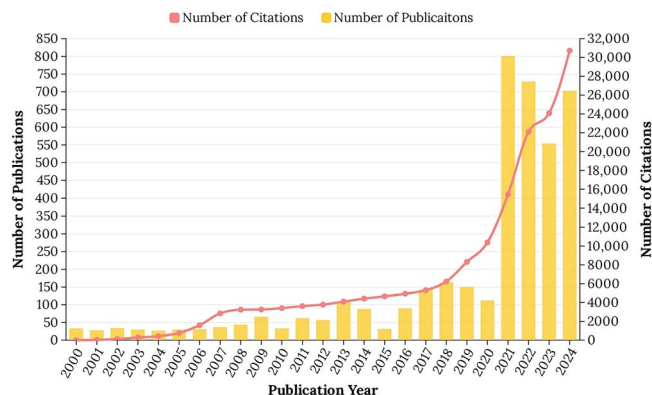


Figure 2 The trend of publications and citations of BIB.

Data analysis tools and methods

VOSviewer is a widely used software tool for creating bibliometric visualization maps that display the network structure of bibliometric data [9]. Methodologically, the following analyses were conducted: (i) an examination of publication and citation metrics for BIB articles and reviews over the past 25 years, identifying the most-cited works; (ii) an identification of key contributors and influencers (countries/regions, affiliations, authors) across periods, alongside an exploration of co-authorship networks; and (iii) an analysis of high-frequency author keywords to trace the evolution of research topics. This study encompasses 4185 articles and reviews, collectively referred to as 'publications.'

The specific threshold and parameter settings utilized for network analysis conducted by VOSviewer are as follows: In the context of countries/regions and affiliations, the display is limited to their respective maximum collaboration networks, with the exclusion of nodes devoid of connections (those lacking in collaborative relationships). The collaboration network analysis for countries/regions does not set a publication volume threshold; all countries/regions that have participated in international collaborations are shown in the network map to capture the overall landscape of international collaboration. The collaboration network analysis for affiliations employs a publication volume threshold of 20. Furthermore, the collaboration network analysis for authors employs a publication volume threshold of 10. All authors meeting this threshold are displayed in the network, irrespective of whether they have collaborated with other authors within the threshold range. In the context of co-occurrence analysis of author keywords, the frequency threshold is set to 10. It is important to note that all analyses conducted using VOSviewer employ the 'Full Counting' counting method and the 'LinLog/modularity' normalization approach. Furthermore, the layout parameters are uniformly set to 'attraction = 2' and 'repulsion = -1.'

Results

Dynamic changes in the number of publications and citations

BIB began publication in 2000 as a quarterly journal (four issues per year) and adopted a bimonthly schedule (six issues per year) in 2007, which remains in place today [10]. From 2000 to 2024, BIB published a total of 4185 articles and reviews. The bar chart in Fig. 2 shows the trend in the annual number of publications. The

Table 1 Most-cited BIB publication per publication year (2000–2024).

PY	FA	Title	Type	TC	CPY	NC
2000	Stevens, R.	Ontology-based knowledge representation for bioinformatics	Review	265	10.60	10.81
2001	Kaplan, W.	Swiss-PDB Viewer (Deep View)	Article	431	17.96	8.94
2002	Sigrist, C. J. A.	PROSITE: A documented database using patterns and profiles as motif descriptors	Article	736	32.00	6.58
2003	Kim S.Y.	Inferring gene networks from time series microarray data using dynamic Bayesian networks	Article	255	11.59	8.10
2004	Kumar, S.	MEGA3: Integrated software for molecular evolutionary genetics analysis and sequence alignment	Article	10,750	511.90	22.83
2005	Cohen A.M.	A survey of current work in biomedical text mining	Review	597	29.85	8.11
2006	Larrañaga, P.	Machine learning in bioinformatics	Review	652	34.32	5.71
2007	Boulesteix A.-L.	Partial least squares: A versatile tool for the analysis of high-dimensional genomic data	Article	660	36.67	8.18
2008	Katoh K.	Recent developments in the MAFFT multiple sequence alignment program	Article	3183	187.23	14.74
2009	Karp P.D.	Pathway Tools version 13.0: Integrated software for pathway/genome informatics and systems biology	Article	397	24.81	4.73
2010	Li H.	A survey of sequence alignment algorithms for next-generation sequencing	Review	684	45.60	10.35
2011	Gaudet P.	Phylogenetic-based propagation of functional annotations within the Gene Ontology consortium	Article	693	49.50	8.52
2012	Li W.	Ultrafast clustering algorithms for metagenomic sequence analysis	Article	392	30.15	6.10
2013	Thorvaldsdóttir H.	Integrative Genomics Viewer (IGV): High-performance genomics data visualization and exploration	Article	6426	535.50	47.15
2014	Liu B.	Identifying miRNAs, targets and functions	Article	470	42.73	9.06
2015	Pahikkala T.	Toward more realistic drug-target interaction predictions	Article	422	42.20	7.33
2016	Ferrè F.	Revealing protein-lncRNA interaction	Article	568	63.11	8.30
2017	Miotto R.	Deep learning for healthcare: Review, opportunities and challenges	Article	2043	255.38	27.28
2018	Katoh K.	MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization	Article	6108	872.57	55.34
2019	Chen L.	Trends in the development of miRNA bioinformatics tools	Review	492	82.00	8.82
2020	Dziak J.J.	Sensitivity and specificity of information criteria	Review	369	73.80	6.62
2021	Maeser D.	oncoPredict: An R package for predicting in vivo or cancer patient drug response and biomarkers from cell line screening data	Article	1065	266.25	28.12
2022	Luo R.	BioGPT: Generative pre-trained transformer for biomedical text generation and mining	Article	584	194.67	24.17
2023	Liu C.-J.	GSCA: An integrated platform for gene set cancer analysis at genomic, pharmacogenomic and immunogenomic levels	Article	292	146.00	21.79
2024	Zhang P.	Network pharmacology: Towards the artificial intelligence-based precision traditional Chinese medicine	Review	229	229.00	43.91

Abbreviations: PY, publication year; FA, first name; TC, total number of citations; CPY, citations per year; NC, normalized citations.

annual number of publications has exhibited three distinct periods. From 2000 to 2012, it remained stable at fewer than 70 publications. From 2013 to 2020, it increased but did not exceed 170 publications. Since 2021, it has fluctuated between 554 and 801 publications [11]. Publications from BIB over the past 25 years have accumulated 183 911 citations as recorded through July 18, 2025. The line graph in Fig. 2 shows the trend in the annual number of citations for publications from 2000 to 2024. Specifically, the annual number of citations was calculated as the number of citations received in a given year by all publications published from the inception year of the journal to that year. The annual number of citations has consistently exhibited an upward trend. From 2000 to 2005, growth was modest, remaining below 1000 citations. A marked surge occurred in 2006 and 2007, with the 2006 count rising by 1.09 times compared with 2005, followed by a further 0.79-fold increase in 2007 over 2006. This trend highlights BIB's growing influence in the bioinformatics field and the establishment of its initial academic impact. From 2006 to 2018, the annual number of citations experienced a period of steady and sustained growth, increasing from 1593 in 2006 to 6224 in 2018. Since 2019, the annual number of citations has entered a new period of rapid growth. Especially after 2021, the annual number of citations

surged markedly, increasing from 8316 in 2019 to 30 729 in 2024, alongside the explosive growth of the annual number of publications. During this period, BIB demonstrated a pronounced academic impact.

The most-cited publications

BIB has published a substantial number of influential publications in the field of bioinformatics. The total number of citations (TC) serves as a widely accepted indicator of the impact and importance of scientific publications. Table 1 presents, for each year during the past 25 years, the publication that has received the highest number of citations to date. In addition, Supplementary Table 1 presents the top 10 journals that most frequently cite BIB's publications. These publications can be regarded as the most representative and influential research of their respective publication years. Notably, while highly cited publications reflect considerable impact, some highly cited publications were published earlier and thus have accumulated more citations. Therefore, we conducted a more balanced assessment by using the indicator of citations per year (CPY). Furthermore, the normalized citation (NC) function of VOSviewer was employed to evaluate the relative impact of publications from the same year.

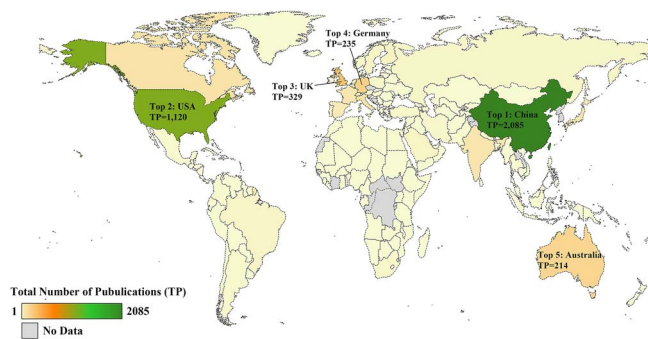


Figure 3 The global distribution of publications of BIB.

Among these 25 publications, the most-cited 2004 publication, ‘MEGA3: Integrated software for molecular evolutionary genetics analysis and sequence alignment’ [12], also ranked first in TC among all publications (TC=10 750; CPY=511.90). While its NC (n=22.83) is lower than some recent publications, it significantly exceeds the average citation level of publications from the same year, demonstrating its sustained and outstanding academic impact. The most-cited 2018 publication, ‘MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization’ [13], recorded the highest CPY and NC among all publications (TC=6108; CPY=872.57; NC=55.34). Although it ranked third in TC among all publications, the high CPY and NC, respectively, highlight its growing academic impact in recent years and its outstanding relative impact among contemporaneous publications. In early publications (2000–2015), except for those in 2004, 2008, and 2013, which exhibited relatively high CPY, the CPY of the most-cited publications in other years fluctuated between 10 and 50. In contrast, recent publications (2016–2024) have shown a substantial rise in CPY. NC also exhibited a trend similar to CPY, with recent publications (mostly above 20) generally showing higher NC than early publications (mostly below 10).

The most contributing and influential countries/regions

A total of 79 countries/regions contributed publications to BIB. Figure 3 shows the global distribution of these publications in the form of a world map, where the color gradient from pale yellow to dark green indicates an increase in the total number of publications (TP) [14]. China was the leading contributor with 2085 publications, accounting for 49.82% of the total. The United States ranked second with 1120 publications (26.76%), followed by the United Kingdom (329 publications, 7.86%), Germany (235 publications, 5.62%), and Australia (214 publications, 5.11%).

Table 2 lists the top 10 contributing countries/regions over five-year periods. From 2000 to 2004, a total of 18 countries were published in BIB. The main contributors were the United Kingdom (TP=57) and the United States (TP=38). The United States ranked first in terms of average number of citations per publication (ACP), with an ACP of 329.45, highlighting its long-standing leadership in bioinformatics research. Switzerland ranked second in ACP (n=224.60), distinguishing itself among countries with relatively low publication counts. From 2005 to 2009, a total of 34 countries were published in BIB. The United States rose to the top of the TP rankings and sustained

its leading position in the following periods. During this period, European countries, including Germany, Italy, and France, experienced an increase in TP rankings, concomitant with further expansion of BIB’s author base across Europe. Additionally, Canada, the Netherlands, China, and Spain made their first entry into the top 10. From 2010 to 2014, a total of 43 countries were published in the BIB. The top 10 member remained consistent in composition, although their relative rankings have changed. Notably, China advanced to second place with 77 publications, reflecting a substantial increase in publication contribution during this period. From 2015 to 2019, a total of 53 countries have published in BIB. China’s TP continued to increase significantly, approaching that of the United States. Japan reached the highest ACP in this period (n=364.75). From 2020 to 2024, a total of 76 countries have published in BIB. China ranked first in TP (n=1802), followed by the United States (n=662). India and South Korea entered the top 10 for the first time.

To examine international collaborations, we constructed a visualization map depicting collaborative links among 77 of the 79 countries/regions that contributed to BIB (Fig. 4). The network consists of four clusters. The largest is the red cluster centered around the United Kingdom, comprising 33 countries, mainly European nations. The second largest is the green cluster centered around China, including 24 countries, primarily Asian nations. The remaining two clusters each contain 10 countries. The blue cluster is centered around Canada and mainly consists of American nations. The yellow cluster is centered around South Africa, with all its members being African nations. In this network, node size reflects the number of publications, the number of edges indicates the breadth of collaborative partnerships, and edge thickness denotes the strength of collaboration. The collaboration within the cluster is closer than that between the clusters. [15] The strongest collaboration ties were observed between China and the United States (375 co-authored publications), China and the United Kingdom (93 co-authored publications), and China and Australia (57 co-authored publications) [16].

The most contributing and influential affiliations

Table 3 lists the top 10 contributing affiliations over five-year periods. From 2000 to 2004, BIB publications were primarily published by Europe’s leading bioinformatics affiliations. The European Molecular Biology Laboratory-European Bioinformatics Institute (EMBL-EBI), based in the United Kingdom, led with 12 publications and an ACP of 69.75. The Swiss Institute of Bioinformatics (TP=4; ACP=278.25) also exhibited a strong academic impact despite its relatively low publication counts. From 2005 to 2009, several universities entered the top 10, mainly from Europe and North America. The University of Queensland was the only Australian affiliation among the top 10 (TP=5; ACP=43.00), and the National University of Singapore was the sole representative from Asia (TP=4; ACP=99.75). Notably, Stanford University (TP=5; ACP=679.40), based in the United States, exhibited exceptional academic impact during this period. From 2010 to 2014, the publication structure of BIB experienced significant changes, with the top 10 affiliations featuring contributions from China, the United Kingdom, and the United States. Pennsylvania State University (TP=22; ACP=11.73) ranked first. Chinese affiliations entered the top 10 for the first time, marked by the rapid rise of five Chinese universities, with Beijing Forestry University (TP=20; ACP=9.55) as a representative example. From 2015 to 2019, Harbin Medical University (TP=27; ACP=35.48) and the Chinese Academy of Sciences

Table 2 Top 10 countries/regions in terms of total number of publications across 25 years of BIB.

Country/Region (2000–2004)	TP	TC	ACP	Country/Region (2005–2009)	TP	TC	ACP	Country/Region (2010–2014)	TP	TC	ACP
UK	57	2866	50.28	US	81	9709	119.86	US	132	15 828	119.91
US	38	12 519	329.45	UK	45	2558	56.84	China	77	3993	51.86
Germany	14	489	34.93	Germany	25	2835	113.40	UK	38	2851	75.03
Switzerland	5	1123	224.60	Italy	17	993	58.41	Germany	36	1400	38.89
Australia	5	679	135.80	France	14	1680	120.00	Italy	22	1294	58.82
Italy	4	182	45.50	Canada	13	878	67.54	Canada	19	982	51.68
France	4	53	13.25	Netherlands	11	922	83.82	Netherlands	15	786	52.40
Japan	3	269	89.67	Australia	8	759	94.88	Spain	15	689	45.93
Singapore	3	103	34.33	China	8	551	68.88	Australia	14	1134	102.93
Russia	3	75	25.00	Spain	6	1102	183.67	France	14	1441	81.00
Country/Region (2015–2019)	TP	TC	ACP	Country/Region (2020–2024)	TP	TC	ACP				
US	207	13 926	67.28	China	1802	41 450	23.00				
China	198	12 857	64.93	US	662	15 018	22.69				
UK	62	5248	84.65	Australia	145	3888	26.81				
Germany	55	2552	46.40	UK	127	3058	24.08				
Australia	42	2195	52.26	Germany	105	2663	25.36				
Italy	27	1986	73.56	India	89	2275	25.56				
France	26	1110	42.69	Japan	78	2476	31.74				
Canada	25	2370	94.80	Canada	77	2101	27.29				
Japan	20	7295	364.75	Italy	76	1652	21.74				
Netherlands	20	1679	83.95	South Korea	72	1779	24.71				

Abbreviations: TP, total number of publications; TC, total number of citations; ACP, average number of citations per publication.

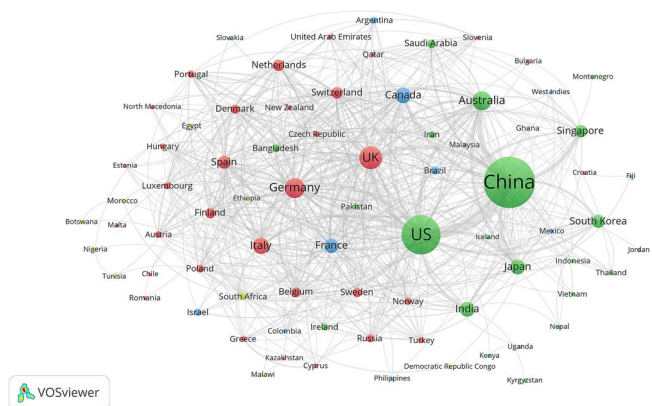


Figure 4 Co-authorship map among 77 countries/regions with collaborative links.

(TP = 23; ACP = 93.52), both based in China, have become the two most representative contributors. Concurrently, Australia’s Monash University (TP = 17; ACP = 53.29) and Japan’s Kyoto University (TP = 13; ACP = 61.62) entered the top 10 for the first time. From 2020 to 2024, Chinese affiliations exhibited remarkable growth in publications, emerging as the dominant force in BIB. All top 10 affiliations were based in China, with the Chinese Academy of Sciences (TP = 189; ACP = 18.93) ascending to the first place, substantially surpassing other affiliations. However, during this period, the academic impact of these affiliations remained in an accumulation phase, resulting in relatively lower ACP compared to previous periods.

To examine collaboration among highly contributing affiliations, we selected 70 affiliations with at least 20 publications to construct a visualization map of their collaborative relationships. [Figure 5](#)

shows the collaborative relationships (edges) among the 70 affiliations (nodes). The network was divided into four clusters. The strongest collaboration ties were identified between Beijing Forestry University (China) and Pennsylvania State University (United States), between Zhejiang University (China) and Central South University (China), and between Monash University (Australia) and the University of Melbourne (Australia). These three pairs of closely collaborating affiliations produced 28, 21, and 17 co-authored publications, respectively.

The most contributing and influential authors

A total of 4140 authors have contributed to BIB. [Table 4](#) shows the top 10 most contributing authors. Authors with an equal total number of publications were ranked by total number of citations. At the top of the list was Zou, Quan (TP = 64; TC = 3023), a member of the BIB editorial board, from the University of Electronic Science and Technology of China. Zou has long been engaged in interdisciplinary research at the intersection of bioinformatics and artificial intelligence, with primary research interests in biological sequence analysis, disease-associated molecular prediction, and the development of machine learning algorithms [17–19]. His publications in BIB span from 2014 to 2024, with no publications in 2015 and 2017. Research output occurred in all other years, with 2021 being the most prolific year, yielding 23 publications. The second-ranked author was Song, Jiangning (TP = 58; TC = 2652), from Monash University in Australia. Song, Jiangning, mainly focused on cancer genomics, infection and immunity, the integration of multi-omics data, and the development of computational tools [20–23]. He has published in BIB from 2013 to 2024, with the highest number of publications occurring in 2021, totaling 18. Both Zou and Song contributed significantly more than other authors.

Table 3 Top 10 affiliations in terms of total number of publications across 25 years of BIB.

Affiliation (2000–2004)	TP	TC	ACP	Affiliation (2005–2009)	TP	TC	ACP	Affiliation (2010–2014)	TP	TC	ACP
EMBL-EBI	12	837	69.75	Univ. Manchester	10	933	93.30	Penn State Univ.	22	258	11.73
Hum. Genome Map. Res. Cent.	10	56	5.60	EMBL-EBI	8	287	35.88	Beijing For. Univ.	20	191	9.55
Indiana Univ.	6	195	32.50	NIH	6	676	112.67	Yale Univ.	10	349	34.90
Univ. Manchester	5	435	87.00	CNR	6	362	60.33	EMBL-EBI	10	280	28.00
Swiss Inst. Bioinform.	4	1113	278.25	Stanford Univ.	5	3397	679.40	Dalian Univ. Tech.	7	384	54.86
Sanger Inst.	3	172	57.33	Univ. Queensland	5	215	43.00	Nanjing For. Univ.	7	103	14.71
GSF Res. Cent. Environm. Hlth	3	160	53.33	Natl. Univ. Singapore	4	399	99.75	Peking Univ.	6	548	91.33
NIH	3	77	25.67	Univ. Glasgow	4	250	62.50	Univ. Oxford	6	314	52.33
Entigen Pty Ltd	2	505	252.50	Univ. Groningen	4	176	44.00	Univ. Florida	6	201	33.50
Celera Genomics	2	178	89.00	Univ. Cambridge	4	79	19.75	Fudan Univ.	5	520	104.00

Affiliation (2015–2019)	TP	TC	ACP	Affiliation (2020–2024)	TP	TC	ACP
Harbin Med. Univ.	27	958	35.48	Chinese Acad. Sci.	189	3578	18.93
Chinese Acad. Sci.	23	2151	93.52	Cent. South Univ.	110	2955	26.86
Monash Univ.	17	906	53.29	Zhejiang Univ.	91	2709	29.77
Kyoto Univ.	13	801	61.62	Univ. Elect. Sci. Tech.	89	3468	38.97
Univ. Cambridge	13	520	40.00	Shanghai Jiao Tong Univ.	77	1878	24.39
Univ. Elect. Sci. Tech.	11	1058	96.18	Sun Yat-Sen Univ.	75	2067	27.56
Peking Univ.	11	471	42.82	Fudan Univ.	71	1161	16.35
Penn State Univ.	11	375	34.09	Hunan Univ.	69	2487	36.04
Beijing For. Univ.	11	359	32.64	Peking Univ.	64	1560	24.38
UT Health Houston	10	582	58.20	Tsinghua Univ.	61	1898	31.11

Abbreviations: TP, total number of publications; TC, total number of citations; ACP, average number of citations per publication.

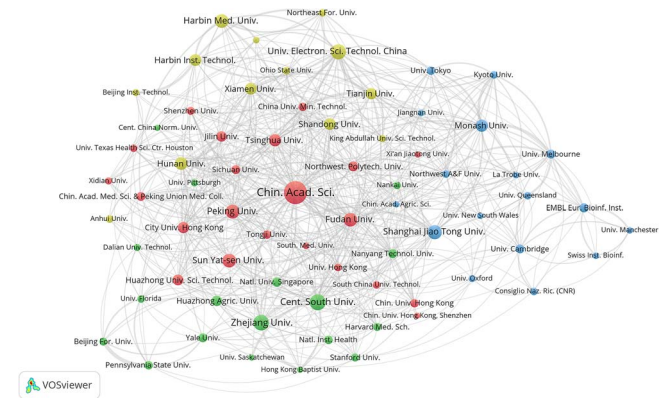


Figure 5 Co-authorship map of the most contributing 70 affiliations with at least 20 publications.

The third-ranked author, Wu, Rongling (TP = 35; TC = 633), was from the Pennsylvania State University in the United States. Among the 10 authors, the author with the highest ACP was Zeng, Xiangxiang (TP = 30; TC = 2053; ACP = 159.87), from Hunan University in China. Zeng, Xiangxiang, focused on the application of machine learning and deep learning techniques to predict and analyze drug interactions, molecular properties, and protein functions [24–26].

Figure 6 illustrates the collaboration network among 85 highly contributing authors, each having published at least 10 publications, forming a total of nine collaboration networks. The largest network comprises 57 authors, while 16 authors are isolated, with no collaborative links to other highly contributing authors depicted in the figure. The two largest clusters are the red and green clusters, consisting of 21

and 19 authors, respectively. Within the red cluster, the two authors with the closest collaboration were Song, Jiangning, and Li, Fuyi (31 co-authored publications), both from Monash University. Their research primarily focuses on the application of machine learning and deep learning for feature extraction and functional prediction of DNA, RNA, and protein sequences [27–29].

A growing trend of author collaboration was evident in BIB. The increase in collaboration indicated the journal’s expanding influence and the maturation of its scholarly network [30]. The bar-line composite graph in Fig. 7 illustrates this upward trend. The median number of authors per publication increased from 2 (2000–2004) to 5 (2020–2024) [31]. The two publications with the maximum number of authors (n = 59) were ‘Computational Pan-Genomics: Status, Promises and Challenges’ and ‘Interoperability with Moby 1.0 - It’s Better Than Sharing Your Toothbrush,’ published in 2016 and 2018, respectively [32, 33]. The petal pie chart in Fig. 7 illustrates the distribution of publications across different periods and varying author group sizes. The proportion of single-authored publications declined markedly, from 44% to 1%. The proportion of publications co-authored by two to four authors initially increased and then declined, whereas the proportion of publications with five or more co-authors showed a pronounced upward trend. [34]

Analysis of primary author keywords

Author keywords are critical metadata provided by authors, serving to accurately summarize the research themes of publications [35]. In order to address potential inconsistencies in keywords with identical meanings provided by different authors, the author keywords were first standardized manually in accordance with the MeSH vocabulary

Table 4 Top 10 authors in terms of the total number of publications published in BIB.

R	Author	Country/Region	Affiliation	TP	TC	ACP
1	Zou, Quan	China	Univ. Elect. Sci. Tech.	64	3023	47.23
2	Song, Jiangning	Australia	Monash Univ.	58	2652	45.72
3	Wu, Rongling	US	Penn State Univ.	35	633	18.09
4	Li, Fuyi	Australia	Monash Univ.	34	1874	55.12
5	Hou, Tingjun	China	Zhejiang Univ.	32	968	30.25
6	Zeng, Xiangxiang	China	Hunan Univ.	31	2065	66.61
7	Wang, Jianxin	China	Cent. South Univ.	30	774	25.80
8	Cao, Dongsheng	China	Cent. South Univ.	29	955	32.93
9	Zhu, Feng	China	Shanghai Jiao Tong Univ.	28	1574	56.21
10	Wang, Guohua	China	Northeast For. Univ.	27	379	14.04

Abbreviations: R, rank; TP, total number of publications; TC, total number of citations; ACP, average citations per publication.

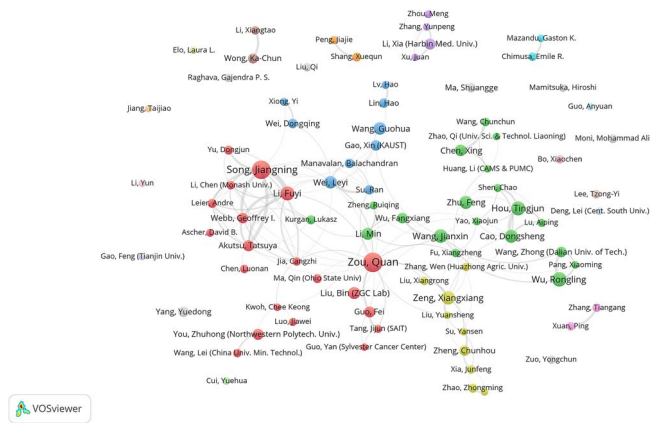


Figure 6 Co-authorship map of 85 contributing authors (≥10 publications).

before analysis. This process ensured that synonyms were uniformly mapped to their corresponding controlled vocabulary terms. Figure 8 presents both the cluster visualization (Fig. 8A) and overlay visualization (Fig. 8B) of author keyword co-occurrence for 244 keywords with a minimum frequency of 10. Node size represents author keyword frequency. In the cluster visualization, different node colors denote distinct clusters. A total of six clusters encompassing different research themes are identified, corresponding to AI-driven computational biology and drug discovery, disease-oriented multi-omics and precision medicine studies, bioinformatics tools and data infrastructure development, sequence analysis and foundational bioinformatics research, statistical genetics and genotype–phenotype association analysis, as well as protein function prediction and anti-infection. Additionally, the node colors in the overlay visualization reflect the average year of publication; earlier appearances are shown in deep blue, while more recent ones are represented in red.

We also analyze the evolution of the research themes from a micro perspective. The data was divided into five-year intervals, and author keywords were extracted for each interval to analyze research themes over time [36]. Table 5 presents the top 10 author keywords with the highest frequency across different periods. ‘Computational biology’ consistently ranked among the top three most frequently used keywords across all five periods and ranked first from the second period to the fourth period (2005–2019). From 2000 to 2004, keywords related to computational science, such as ‘computational biology,’

‘software,’ ‘databases,’ ‘internet,’ and ‘algorithms,’ were frequently used. In addition, traditional biological concepts like ‘biology,’ ‘genetics,’ ‘genome,’ and ‘proteins’ also ranked among the most common keywords. Notably, ‘biology’ (n = 93), ‘computational biology’ (n = 93), and ‘software’ (n = 71) were the most prominent, highlighting the research focus of this period on integrating fundamental biology with computational tools. This characteristic accurately reflects BIB’s disciplinary scope during its early establishment. From 2005 to 2009, the rise of high-frequency keywords such as ‘systems biology’ (n = 22), ‘data integration’ (n = 17), and ‘semantic web’ (n = 15) indicated BIB’s increasing emphasis on interdisciplinary and data integration research. From 2010 to 2014, the prominence of keywords such as ‘high-throughput nucleotide sequencing’ (n = 32), ‘gene expression’ (n = 18), and ‘metagenomics’ (n = 14) reflects the close alignment of BIB publications with the rapid advancements in high-throughput sequencing technologies and genomics research. From 2015 to 2019, ‘machine learning’ (n = 44) and ‘precision medicine’ (n = 20) emerged as prominent keywords, signaling the integration of artificial intelligence with biomedical fields. From 2020 to 2024, the frequency of ‘deep learning’ (n = 427) and ‘machine learning’ (n = 350) increased significantly, far surpassing all previous keywords and emerging as the dominant themes of this period. Meanwhile, the high-frequency use of ‘sars-cov-2’ (n = 107) and ‘covid-19’ (n = 103) reflected BIB’s proactive response and heightened attention to public health crises amid the global pandemic. Additionally, the prominence of ‘graph neural networks’ (n = 81), ‘benchmarking’ (n = 66), ‘drug repositioning’ (n = 58), and ‘drug discovery’ (n = 57) indicated notable progress in computational methods and pharmaceutical research during this phase [37].

Discussion

The bibliometric profile of BIB over the past 25 years outlines the evolution of its academic impact, collaborative contributions from countries/regions, institutions, and authors, as well as key research themes. This analysis shows that BIB’s consistent scholarly influence, interdisciplinary focus, and strong editorial leadership are all propelled by active global collaboration and the sustained evolution of research themes.

The annual number of citations of BIB publications has shown a markedly rapid growth trend since 2019. This trend reflects the growing academic influence of BIB in the field of bioinformatics. The JCR report indicates that over the past decade, BIB has consistently

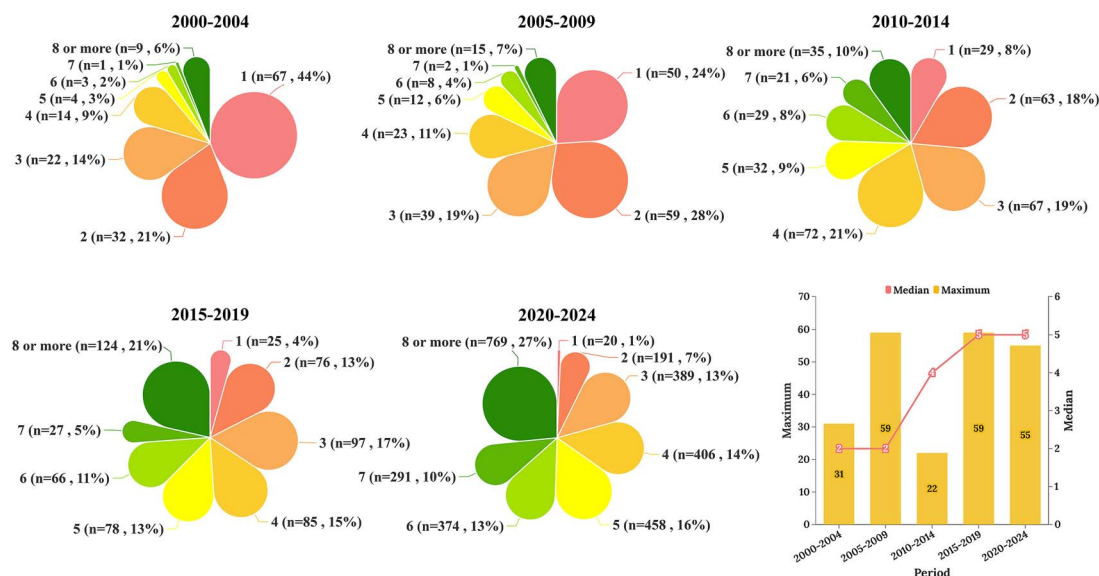


Figure 7 The increasing number and proportions of multi-authored publications in BIB.

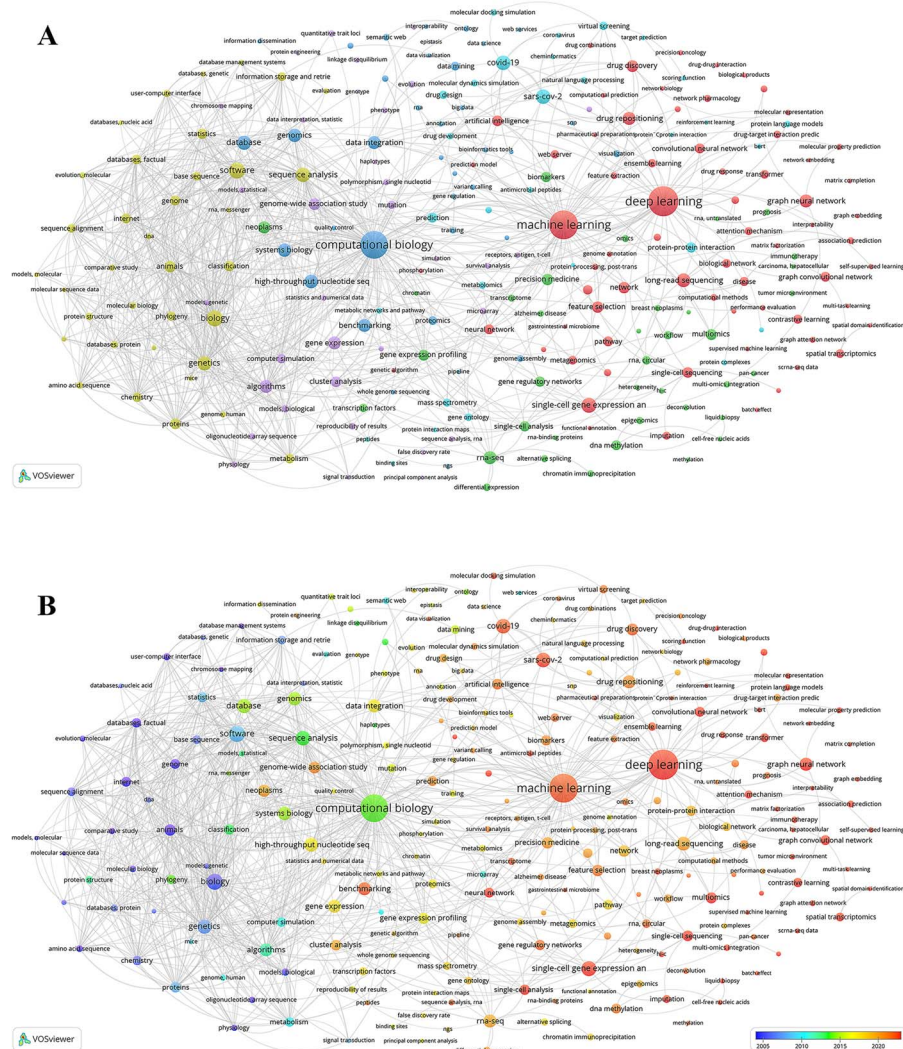


Figure 8 (A) Cluster visualization of the top 244 author keywords. (B) Overlay visualization of the top 244 author keywords.

Table 5 Top 10 author keywords by occurrence across 25 years of BIB.

Top 10 author keywords (2000–2004)		Top 10 author keywords (2005–2009)		Top 10 author keywords (2010–2014)	
biology	93	computational biology	31	computational biology	40
computational biology	93	systems biology	22	high-throughput	32
software	71	data integration	17	nucleotide sequencing	
genetics	63	database	15	gene expression	18
animals	53	semantic web	15	systems biology	18
databases, factual	43	microarray	13	metagenomics	14
internet	42	ontology	12	data integration	13
algorithms	34	genomics	10	quantitative trait loci	10
proteins	34	software	9	genomics	9
genome	33	data mining	9	database	9
				education	9
Top 10 author keywords (2015–2019)		Top 10 author keywords (2020–2024)			
computational biology	53	deep learning	427		
machine learning	44	machine learning	350		
high-throughput nucleotide sequencing	30	computational biology	153		
rna-seq	29	sars-cov-2	107		
genomics	23	single-cell gene	104		
		expression analysis			
precision medicine	20	covid-19	103		
systems biology	19	graph neural network	81		
biology	18	benchmarking	66		
software	18	drug repositioning	58		
database	18	drug discovery	57		

maintained high percentile rankings in both the *Biochemical Research Methods* and *Mathematical & Computational Biology* categories (with average percentiles of 95.84% and 97.15%, respectively), showing an upward trend in most years. The improvement in the journal's rankings has enhanced its visibility within the academic community, which may have fostered cumulative advantages through the Matthew Effect and contributed to increased citation activity [38]. Furthermore, an official announcement on the BIB website states that full open access has been in effect since January 2024, a development that has resulted in a substantial reduction in the barriers that readers face when attempting to access full-text publications. This shift may be one reason for the further surge in the annual number of citations in 2024. Beyond the sustained growth in the annual number of citations, the sources of citations for BIB publications further reflect its influence within the broader academic ecosystem. As shown in [Supplementary Table 1](#), the top 10 journals that cite BIB publications most frequently are listed. These journals are predominantly leading international multidisciplinary or bioinformatics journals, suggesting that research published in BIB has been widely incorporated into scholarly work across related domains and has achieved substantial cross-journal visibility within the bioinformatics research ecosystem.

Our analysis focused particularly on the highly cited publications, as shown in [Table 1](#). It reveals that research focusing on methodological and tool-oriented approaches, as well as studies involving emerging technologies, tends to garner broader citation recognition across both absolute and relative citation advantages. For instance, tools like MEGA3 and MAFFT provide foundational infrastructure for sequence alignment and evolutionary analysis; IGV has emerged as a high-performance tool for genomic data visualization; and emerging technologies and tools, including oncoPredict and BioGPT, enable data-driven drug response prediction and text mining powered by

generative artificial intelligence [12, 13, 39–41]. The CPY of this type of publication is significantly higher than that of other types, reflecting their sustained and intensive citation patterns. Additionally, their notably elevated NC indicates citation potential far exceeding that of other publications from the same year. This evidence underscores the critical role such research plays in the field of bioinformatics. Comparing the citation-related indicators of the most-cited publications across different years reveals variations in the impact of publications between years. The generally higher CPY and NC observed in recent publications (2016–2024), relative to earlier publications (2000–2015). This trend suggests that the academic impact of publications in BIB has transitioned from gradual accumulation to rapid expansion. It can be attributed to two primary factors. First, emerging technologies and tools have served as powerful drivers of cutting-edge advancements in bioinformatics. Second, the advancement of academic social media has substantially amplified the dissemination of BIB publications, thereby enhancing their overall impact. The higher CPY of recent publications reflects the accelerated accumulation of citations, while their elevated NC values indicate enhanced relative citation advantages.

Based on the analysis of the publication status of countries/regions and affiliations across five periods ([Table 2](#), [Table 3](#)), the evolution of BIB's international impact can be well summarized. During the first and second periods (2000–2009), BIB's research community was primarily composed of scholars from Europe and North America. Although TP was relatively limited, the high quality of research laid a solid foundation for the journal's initial international impact. During the third and fourth periods (2010–2019), the publication structure of BIB became increasingly diversified, with rapid growth in Asian research and progressively closer academic interactions across multiple countries/regions. During the fifth period (2020–2024), the number of countries contributing to BIB rose from 18 in the first period to

76, further underscoring the journal's international scope. This period was marked by a notable expansion of international collaboration, with particularly strong contributions from research communities in China and the United States.

It is noteworthy that China's sustained rise in BIB publication rankings should be understood within the broader context of progress in Chinese bioinformatics research. As shown in [Supplementary Table 2](#), China's publication ranking in BIB's corresponding Web of Science categories *Biochemical Research Methods* and *Mathematical & Computational Biology*—mathematical & a clear and sustained upward trend from 2000 to 2024. Given BIB's status as a leading journal in these categories, China's increasing publication volume in BIB objectively reflects both the overall enhancement of its research capabilities in bioinformatics and its growing international visibility within the field. In addition, this trend may be influenced by research policies and funding environments. However, persistent geographical concentration of contributions may affect the diversity of journals in terms of research perspectives, methods, and themes. Therefore, encouraging broader participation from affiliations worldwide is crucial to maintaining BIB's status as a global platform for dialogue in bioinformatics.

Regarding collaboration, BIB's research has transitioned from predominantly individual-led efforts to team-based approaches. This transformation aligns with the journal's landscape as an interdisciplinary platform. As the complexity of research increases, individual researchers are no longer able to conduct cross-disciplinary studies relying solely on their personal knowledge. The establishment of an academic communication platform for researchers from diverse backgrounds has been shown to foster closer collaboration, thereby promoting integration and innovation across the global bioinformatics community. Overall, the shift in academic focus not only reflects BIB's developmental trajectory but also mirrors the evolving dynamics of global bioinformatics research.

Importantly, the evolution of research themes in BIB publications can be characterized as follows, shown in [Table 5](#) and [Fig. 8](#): During the first and second periods (2000–2009), BIB primarily emphasized a foundational framework for bioinformatics. The journal primarily focused on fundamental methods of bioinformatics, database development and applications, and the creation of computational tools, with the overarching goal of leveraging information technology to advance research in genomics, proteomics, and systems biology [42, 43]. During the third and fourth periods (2010–2019), the author keyword patterns suggest a robust integration of theoretical and practical approaches. The focus appears to have shifted towards high-throughput omics data analysis, network biology, and multi-omics integration [44–46] while computational modeling approaches for biomolecular systems have also garnered increasing attention. Representative studies on structure-informed biomolecular modeling and systems network analysis demonstrate this transitional phase [47, 48]. During the fifth period (2020–2024), author keyword trends indicate a stronger presence of AI-driven biomedical computing, particularly through the application of advanced algorithms, such as deep learning, in disease research and drug development [49, 50]. Simultaneously, during the global pandemic, BIB's proactive response to public health challenges reinforced its position as a leader in cutting-edge bioinformatics [51, 52]. Based on high-frequency author keywords across different periods and terms with relatively recent average publication years, BIB is highly likely to continue deepening its research in AI-driven bioinformatics. It will increasingly emphasize areas centered on molecular modeling, single-cell and spatial omics

analysis, integrative multi-omics inference, and precision medicine centered around graphs and transformers.

The major strength of this study lies in the manual validation and standardization of bibliometric data, which effectively reduced potential inaccuracies in the analysis. Nevertheless, as a retrospective investigation, this study focuses on characterizing the evolution of BIB over the past 25 years rather than forecasting its future development. In addition, the lag of citation may lead to the low citation of high-quality publications published recently. Despite these inherent limitations, the findings provide a comprehensive and reliable overview of the journal's development.

Conclusion

The annual number of citations of BIB publications has shown a discernible upward trend over the past 25 years (especially since 2019). The international character of BIB was demonstrated by the publication status, the citation status, and the collaboration status of countries/regions and affiliations. Global collaboration in BIB publications has become increasingly prominent, with the Chinese and American research communities serving as key contributors. The increasing proportion of multi-authored publications indicated a growing trend toward increased collaboration. The research themes of BIB publications have been enriched and deepened over time, evolving from foundational bioinformatics and database development to integrative multi-omics analysis and AI-driven biomedical research. Overall, BIB continues to stand as a prestigious platform for publishing innovative and high-quality bioinformatics research, and its enduring impact is expected to grow even further in the future [53]. Through the analysis of the characteristics of BIB publications, readers can acquire a comprehensive understanding of the journal's research objectives and scope, while also supporting bioinformatics researchers in identifying current research priorities and emerging issues that warrant further investigation.

Key Points

- BIB has published 4185 publications by 4140 authors from 79 countries, receiving a total of 183 911 citations, reflecting its high impact in bioinformatics.
- The expansion of contributing countries/regions and the rise of multi-authored publications highlight BIB's growing internationalization and collaborative depth.
- The research themes have evolved from foundational bioinformatics and database development to more diverse and sophisticated areas such as integrative omics and AI-driven biomedical research.

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Author contributions

Xin Tian (Information Science): Methodology, Data standardization, Writing original draft; Zheng Li (Library and Information Science): Visualization, Writing original draft; Yufei Tian (Library and Information Science): Data curation; Zhiying Cui (Library and Information

Science): Visualization; Zhongqing Wang (Medical Informatics/Scientometrics): Conceptualization, review & editing, Supervision; Cheng Peng (Clinical Medicine): review & editing, Supervision. Xin Tian, and Zheng Li contributed equally to this work and should be regarded as co-first authors. Zhongqing Wang and Peng Cheng are corresponding authors. All authors read and approved the final manuscript.

Supplementary material

Supplementary material is available at *Briefings in Bioinformatics* online.

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Data availability

Data will be made available on reasonable request.

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