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Exploring the Trends in Multiomics Research: A Comprehensive Bibliometric Analysis with Interactive Visualization Tools (BiblioMaps)

Multiomik Araştırmalarındaki Eğilimlerin İncelenmesi: Etkileşimli Görselleştirme Araçları (BiblioMaps) ile Kapsamlı bir Bibliyometrik Analiz Çalışması



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Abstract

Objective: This study introduces BiblioMaps, a web-based platform designed to facilitate the bibliometric analysis of multiomics research. It enables the visual exploration of the field's thematic and structural development, global publication trends, key research topics, leading authors and institutions, and patterns of international collaboration.

Material and Methods: A total of 5,835 articles were retrieved from the Web of Science database and analyzed in terms of publication year, country of origin, authorship, keywords, and subject categories. Thematic and structural visualisations were created using the BiblioMaps platform, which offers an interactive mapping interface accessible at <http://ankara.baskent.edu.tr/~muratkocak/>

Results: The highest number of publications was recorded in 2024 (31.57%), followed by 2023 (19.95%) and 2022 (17.36%). China emerged as the leading contributor, accounting for 50.78% of the total output, while the United States (23.67%) and the United Kingdom (5.98%) ranked second and third, respectively. Approximately 26.21% of the studies involved international collaborations.

The most prolific authors were Wang Y, Zhang Y, and Li Y. Keyword analysis revealed that terms such as “expression” (18.63%), “gene expression” (6.96%), and “cancer” were among the most frequently used, indicating a strong emphasis on biological processes and disease-oriented studies. The most active journals publishing in this domain were Scientific Reports, Nature Communications, and the International Journal of Molecular Sciences.

Öz

Amaç: Bu çalışmanın amacı, BiblioMaps adlı etkileşimli haritalama aracı kullanılarak kapsamlı bir bibliyometrik analiz yoluyla multiomik araştırmalarının tematik ve yapısal eğilimlerini incelemektir. Bu doğrultuda, alandaki küresel eğilimler, öne çıkan konular, etkili yazarlar, kurumlar ve uluslararası iş birliği ağları analiz edilmiştir.

Gereç ve Yöntemler: Web of Science veri tabanından toplanan 5.835 makale, yayın yılı, ülke, yazar, anahtar kelime ve konu kategorilerine göre analiz edilmiştir. Tematik ve yapısal görselleştirmeler BiblioMaps platformu üzerinden sağlanmıştır. Etkileşimli haritaya <http://ankara.baskent.edu.tr/~muratkocak/> bağlantısından ulaşılabilir.

Bulgular: En fazla yayın 2024 yılında gerçekleşmiş (%31,57), bunu sırasıyla 2023 (%19,95) ve 2022 (%17,36) yılları takip etmiştir. Yayınların %50,78'i ile Çin en yüksek katkıyı sunarken; Amerika Birleşik Devletleri (%23,67) ve Birleşik Krallık (%5,98) onu izlemiştir. Çalışmaların yaklaşık %26,21'inde uluslararası iş birliklerine yer verilmiştir. En üretken yazarlar sırasıyla Wang Y, Zhang Y ve Li Y olarak belirlenmiştir. Anahtar kelime analizi; “expression” (%18,63), “gene expression” (%6,96) ve “cancer” gibi baskın terimlerin ön plana çıktığını göstermekte, bu da alanın biyolojik süreçler ve hastalık odaklı temalara yöneldiğini ortaya koymaktadır. En aktif akademik dergiler ise Scientific Reports, Nature Communications ve International Journal of Molecular Sciences olarak öne çıkmaktadır.

Sonuç: Multiomik alanı hızlı bir gelişim içinde olup küresel ölçekte önemli bir araştırma alanıdır. BiblioMaps gibi etkileşimli araçlar, bilimsel eğilimlerin yapısal ve tematik analizine değerli katkılar



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Conclusion: The field of multiomics is rapidly evolving and has become a significant area of research on a global scale. BiblioMaps provides valuable support for researchers, educators, and policy-makers by helping to identify emerging trends, knowledge gaps, and opportunities for collaboration.

Keywords Multiomics • bibliometric analysis • science mapping • bibliomaps • interactive visualization • research collaboration

sunmaktadır. Araştırmacılar, eğitimciler ve politika yapıcılar için ortaya çıkan eğilimlerin, bilgi boşluklarının ve potansiyel iş birliklerinin belirlenmesinde değerli bir kaynak sunmaktadır.

Anahtar Kelimeler Multiomik • bibliyometrik analiz • bilim haritalaması • bibliomaps • etkileşimli görselleştirme • araştırma iş birliği

INTRODUCTION

Multiomics research is a rapidly changing field that combines different types of biological data, such as genomics, transcriptomics, proteomics, and metabolomics, to provide a complete picture of complex biological systems and diseases. The growing number of large-scale datasets and improvements in computational biology have made multiomics one of the most important areas in biomedical and life sciences. To track of how this research area has changed in terms of structure and themes, you need advanced visualisation tools and comprehensive bibliometric methods.

Multiomics also refers to the integrative analysis of multiple omics data layers, including genomics, transcriptomics, proteomics, metabolomics, and epigenomics. By combining these complementary datasets, researchers can obtain a holistic understanding of the biological systems, disease mechanisms, and therapeutic responses. Unlike single-omics approaches, multiomics provides a systems-level perspective that enables the identification of complex interactions across different molecular levels. This integrative strategy has become particularly important in biomedical sciences, where the complexity of diseases such as cancer, diabetes, and neurodegenerative disorders requires multidimensional datasets to reveal hidden mechanisms and potential biomarkers.

BiblioMaps is an advanced extension of BiblioTools (1), a comprehensive toolkit previously designed to generate static representations of topical fields. However, the earlier tool necessitated the creation of extensive companion documents to establish connections between paper- and topic-level information. In contrast, BiblioMaps is a web-based, interactive platform that facilitates the exploration of large-scale bibliographical datasets and provides a user-friendly interface for a broad audience. BiblioMaps offers a freely accessible toolkit that empowers users with minimal development expertise to process metadata from their chosen publication corpus and generate interactive science maps from any bibliographic data extracted from the Web of Science database. The corpus description and thematic map analysis visualization interfaces were built using the BiblioMaps software and are available online (<http://ankara.baskent.edu.tr/~muratkocak>).

edu.tr/~muratkocak). These interfaces provide an interactive platform for users to operate on the data and analyses.

A few science maps are available online (2-7). Also available is one of the most popular toolsets like the CiteSpace developed by Chen (2006) (8), which helps researchers discover emergent trends and transformative patterns of scientific literature through the visualization of citation bursts over time. The Gephi is a popular open-source network exploration and visualization platform with an interactive user interface that enables us to scrutinize co-authorship, cogitation, and keyword networks (9). To accomplish temporal and structural analyses of research trends, the Sci² Tool (10) offers exhaustive features such as social network analysis and time series visualizations. In the context of the country of Brazil, the Lattes Platform has also been applied to map the scientific production of the nation on the basis of researcher CVs and provides information about the performance of institutions and regions (2). The HistCite™ software developed by Eugene Garfield provides a chronological map of scientific domains through a network of citations (11), while the knowledge domain visualizer (KDV) offers thematic mapping through clustering and cogitation analysis (12, 13). Finally, the Microsoft Academic Graph (MAG) consists of a large-scale open dataset used for tracing scientific trends using embedded vectors for topic classification (14).

Although they have contributed significantly, most of these tools require specific technical knowledge or coding expertise to work efficiently and visualize data. In particular, software such as Gephi and CiteSpace demand intermediate-level proficiency in data manipulation and theory of networks and consequently have limited accessibility to non-expert communities. Moreover, most of the above tools generate static outcomes that remain non-web-friendly and require additional software instrumentation or post-processing procedures. In contrast, BiblioMaps eliminates the above disadvantages with a fully web-friendly and interactive science-mapping environment. In contrast to most standard software tools, BiblioMaps requires neither software instrumentation nor coding expertise and is consequently available to broader communities of people, such as educators, students, and policymakers. It enables



the dynamic navigation of bibliographic datasets with the help of real-time filterable views, navigable topics, and direct salient publication access. In comparison with other software that primarily produces static network maps, BiblioMaps integrates all procedures from data processing to visualization within a common environment, enhancing usability and interpretability. Consequently, BiblioMaps offers a user-friendly, more extensive, and shareable solution for mapping highly interdisciplinary domains, such as the multiomics field. However, such maps typically require information visualization skills to be investigated and interpreted from the information presented. Additionally, Vosviewer software toolkits on the generation of common bibliographic maps (co-authors, co-citations, bibliographic coupling networks, etc.) are available (14). Nevertheless, most of the above tools provide non-web-friendly visualization outcomes that necessitate the download and installation of specific interfaces and also programming skills. BiblioMaps overcomes the above disadvantages with the provision of a user-friendly, web-focused platform on interactive science mapping. A series of tools have been developed to support the visualization and exploration of the scientific knowledge domains on the basis of bibliometric methods. The most popular platform is the CiteSpace announced by Chen, enabling researchers to detect emerging tendencies and transformative patterns on the basis of the scientific literature by visualization of the citation bursts over time (8). Gephi is also a highly influential tool in the information visualization community and is an open-source network and visualization software package that enables the exploration of co-authorship, co-citation, and keyword networks on the basis of a user-friendly interface (9). For the research trend analyses on the temporal and structural research trend analyses, the Sci² Tool (10) offers ample features such as social network analysis and time series visualization. In Brazil, the Lattes Platform has been applied on the visualization of the nation's scientific production on the basis of researcher CVs, offering information on the performance of the regions and institutions (2). HistCite™™ announced by Eugene Garfield, provides the chronologic map of the scientific domains through the citation networks (11), while the knowledge domain visualizer enables the thematic mapping through clustering and co-citation exploration (12). Finally, the Microsoft Academic Graph (MAG) is an open large-scale dataset utilized for tracing scientific trends via embedded vectors for topic classification (13). Being useful as they are, most tools also require particular technical expertise or even programming proficiency to work on and visually represent the data most efficiently. For example, programs such as Gephi

and CiteSpace require intermediate-level data manipulation and network theory proficiency, limiting their accessibility to non-expert communities. Furthermore, most of the resulting software provides for static outcomes that do not take the best advantage of web interaction and often require additional software installs or even manual postprocessing procedures.

Alternatively, BiblioMaps overcomes such limitations via an entire web and interactive science mapping interface. Unlike the vast majority of traditional tools, BiblioMaps does not require installation or coding proficiency and is therefore accessible to a broader range of stakeholders, including educators, students, and policymakers. BiblioMaps also enables the dynamic exploration of bibliographic datasets through the application of real-time filtering and topic navigation with direct access to exemplar publications. Compared with other interfaces that only produce static network diagrams, BiblioMaps integrates all phases—data processing and visualization—of the science mapping process within the same environment and optimizes usability and interpretation. BiblioMaps offers a more user-friendly, integrated, and collaborative solution for mapping trans-, multi-, and interdisciplinary areas such as multiomics research.

MATERIAL AND METHODS

Data retrieval and processing

The primary aim of this study was to perform a comprehensive bibliometric analysis of multiomics research between 2015 and 2024, with the support of the interactive visualization tool BiblioMaps. By systematically examining publication trends, author contributions, subject categories, and collaboration patterns, this research seeks to highlight the structural and thematic evolution of the field. The importance of this study lies in its ability to provide both a macroscopic overview of global scientific activity in multiomics and an accessible visualization platform for researchers, educators, and policymakers. Such an approach not only documents past and current developments but also helps to identify emerging trends, knowledge gaps, and opportunities for interdisciplinary collaboration.

Bibliographical data were systematically retrieved from the Web of Science database. The data were subsequently processed using BiblioMaps software in accordance with the methodology outlined by Grauwin et al. (15). A specifically designed query was employed to curate a corpus representative of research performance in the field of multiomics. The query parameters were as follows: TI=("multi-omics" OR "multiomics" OR "integrated omics" OR

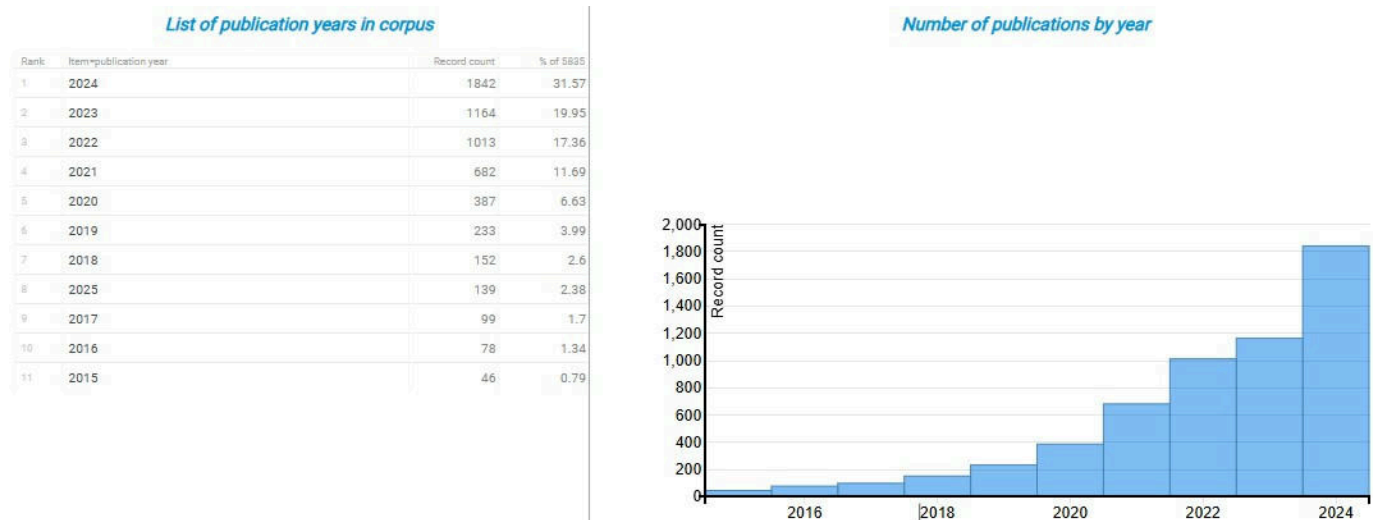


Figure 1. Publication trends in multiomics research: A decade overview (2015–2024)

"multi omics" OR "multi-modal omics" OR "multi-dimensional omics" OR "multi-scale omics" OR "multi-source omics" OR ("multi" AND ("omics" OR "omic" OR "omic data" OR "omic integration")) AND PY=2015-2024 AND DT=Article

This query combination facilitated the collection of publications pertinent to multiomics. To ensure that the selected papers had a substantial focus on both multiomics and design, the terms "user experience" and "design" were incorporated into a complementary query. The use of a query based solely on "user experience" yielded an excessive number of results outside the scope of interest. The resultant multiomics-design corpus comprised 12,220 publication records.

Clustering and analysis

Publications were aggregated into relevant topical clusters via a standard bibliographic coupling (BC) analysis, as described in Grauwin et al. (15). BC is a suitable technique for representing research fronts and emerging topics, such as multiomics design, as it considers all publications, including those not yet cited (16).

BiblioTools is a set of Python scripts designed to generate science maps from bibliographic data. The software enables the user to perform the following main tasks:

1. **Data Mining:** Process bibliographic records exported from the Web of Science efficiently.
2. **Processing of Data:** The raw data are filtered and parsed beforehand.
3. **Analyzing Data:** Define a specified corpus; create co-occurrence networks (co-words, co-authors, co-citations, etc.); create bibliographic coupling networks and clusters.

4. **Data Visualization:** Visualize and export results in BiblioMaps, a dedicated web-based interface; export networks in a standard visualization-tool-compatible format, e.g., Gephi.

5. **Data Reporting:** Produces automatically comprehensive reports in LaTeX.

RESULTS

Corpus description

Figure 1 presents the distribution of publications over the various years within a multiomics dataset. This shows that the number of publications has tended to increase over the years with a specific sharp increase exemplified in 2020 and above. The highest number of publications was in 2024, accounting for 31.57% (1,842 records) of the aggregate dataset. This is followed by the years 2023 and 2022 with 19.95% and 17.36%, respectively. The statistics show an expanding trend in the annual production of publications with an embracing increasing trend of interest or activity on the topic area in the recent past.

Figure 2 shows the geographical distribution of the dataset publications and the contributions of the countries. The left table shows the number of records per country and finds that the largest contributor is China with 2,963 records (50.78%), followed by the United States with 1,381 records (23.67%), and the UK with 349 records (5.98%). Also, notable but much smaller compared to the contributions of China and the U.S. are Germany, France, Canada, and South Korea. The world map on the right offers a graphic support to this distribution with the U.S. and China being the darker shades and thus the highest concentration of research production. Overall, the results show a prevalent Western and Eastern Asia dominance

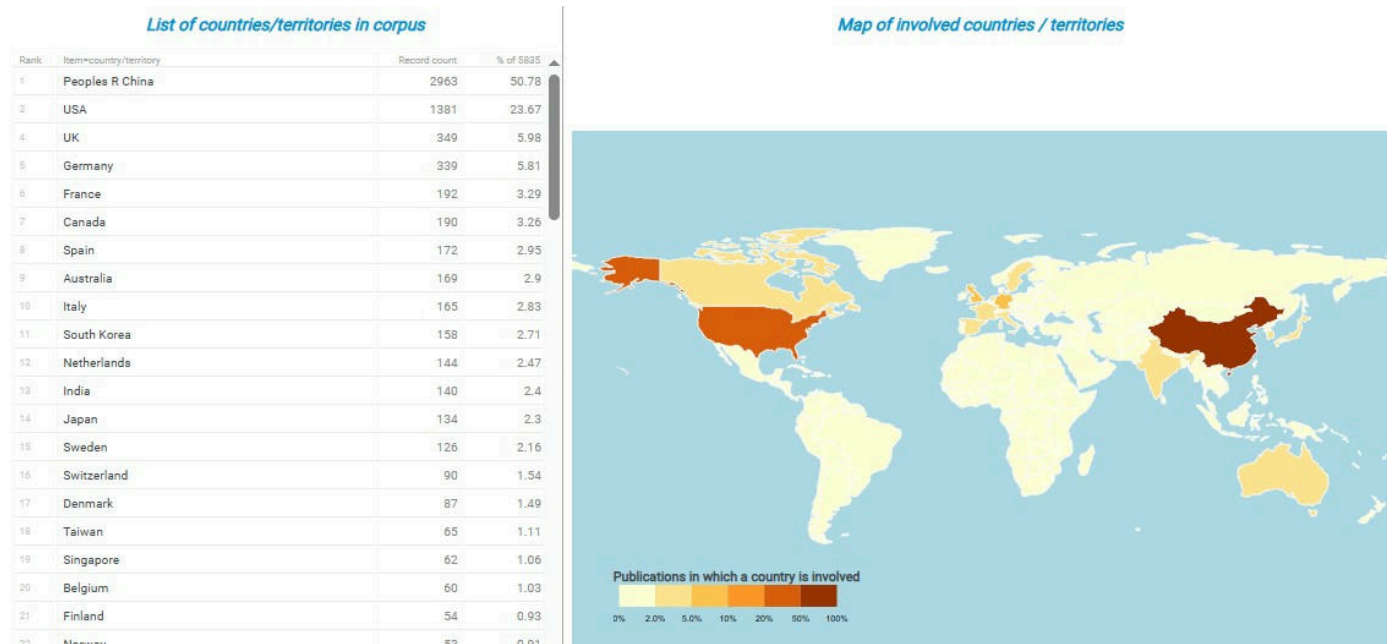


Figure 2. Country contributions to multiomics studies in the dataset (2015–2024)

in the production and publication of multiomics research from the dataset.

As illustrated in Figure 3, this analysis offers a comprehensive overview of the author contributions within the corpus, emphasising both quantitative and qualitative insights. The left-hand table provides a ranking of the most prolific authors based on their publication records. The table shows Wang Y as the leader with a count of 122 publications (2.09% of the total), followed by Zhang Y with 112 publications (1.92%), Li Y with 103 publications (1.77%), and others. The right-hand side of the screen displays a word cloud, which is a visual representation of the most commonly occurring words in a given text or corpus. This word cloud features the top 100 authors, thereby highlighting the frequency of names based on their prominence in the corpus. It is evident that prominent names such as Wang Y, Zhang Y, Li Y, and Wang J are given greater font prominence, thereby underscoring their substantial contributions to the subject matter. This dual representation serves to highlight the fact that a relatively small number of authors produce most research output, thus suggesting the existence of potential collaboration networks or prominent researchers in the field.

Figure 4 shows the most common words and how they are used together in the multiomics dataset. It also shows how often these words are used and how they are connected. On the left, a table lists the top keywords ranked by their record count, with "EXPRESSION" leading with 1,087 instances (18.63% of the total), followed by "IDENTIFICATION" (423 instances, 7.25%), "GENE-EXPRESSION" (406 instances, 6.96%), and others

such as "CANCER," "CELLS," "METABOLISM," and "PROTEIN." The right-hand side features a network visualisation of the top 100 keywords, illustrating their co-occurrence relationships. Key terms such as "EXPRESSION," "GENE-EXPRESSION," "IDENTIFICATION," and "CANCER" are pivotal nodes with high connectivity, suggesting their regular connection with other terms. The presence of two different types of representation in this text highlights the importance of biological processes, molecular mechanisms and disease-related topics in the collection of research material. This provides valuable insights into the thematic focus and interconnectedness of research in this area.

Figure 3 shows a comprehensive overview of the author contributions within the corpus, emphasising both quantitative and qualitative insights. In the left-hand table, the authors with the highest number of publications are listed according to their record count. Wang Y is in the first position, having published 122 works, which constitutes 2.09% of the total. He is followed by Zhang Y, who has published 112 works, making up 1.92% of the total. Li Y is third, with 103 publications, which makes up 1.77% of the total. The other authors are listed below. On the right-hand side of the screen, a word cloud has been incorporated to provide a visual representation of the most prevalent authors in the corpus, with the frequency of each name indicated by its size. It is evident that prominent names such as Wang Y, Zhang Y, Li Y, and Wang J are given greater font prominence, thereby underscoring their substantial contributions to the subject matter. This dual representation serves to highlight the fact that a relatively

small number of authors produce most research output, thus suggesting the existence of potential collaboration networks or prominent researchers in the field.

Figure 5 indicates that the distribution of publication sources within the analyzed corpus of 5,835 articles is concentrated within a specific set of scholarly journals. The left panel provides a quantitative ranking, identifying Scientific Reports (SCI REP-UK) as the most frequent publication

source, comprising 186 articles or 3.19% of the total corpus. Following closely are Nature Communications (NAT COMMUN) and the International Journal of Molecular Sciences (INT J MOL SCI), with 118 (2.02%) and 117 (2.01%) articles, respectively. The word cloud on the right panel offers a qualitative, visual corroboration of this data, where the font size of each journal title is proportional to its publication frequency. In this visualization, the same leading journals, along with others

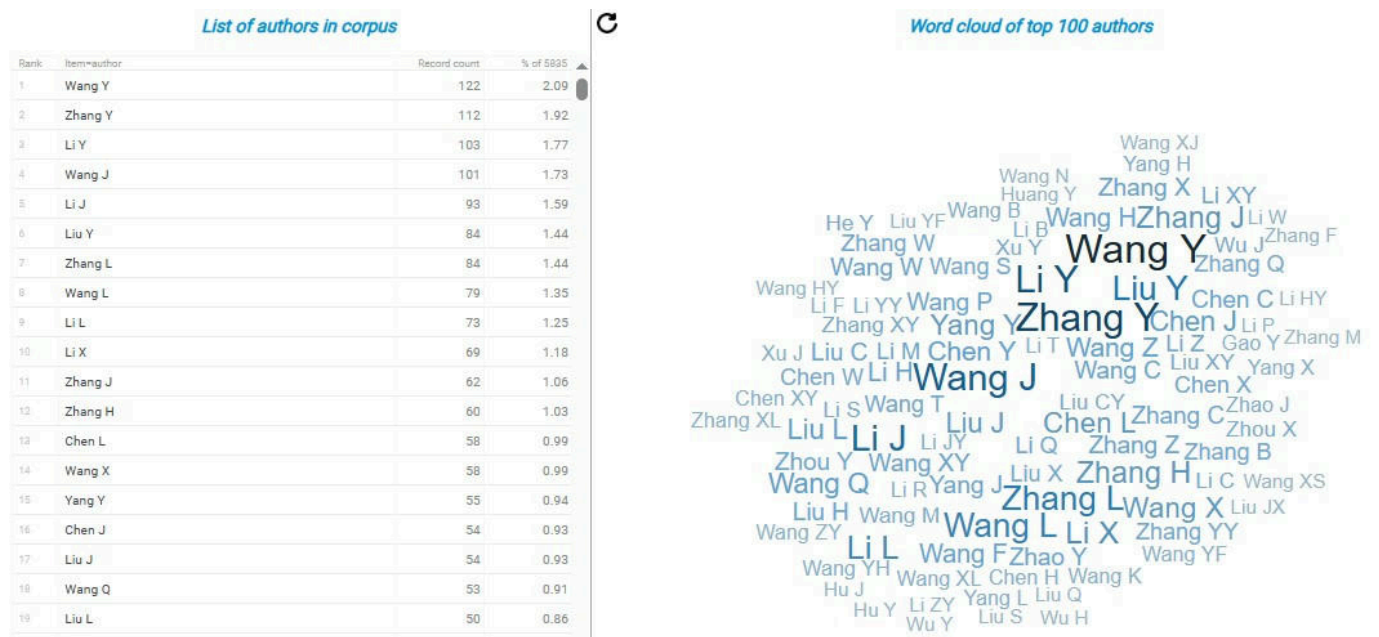


Figure 3. Author contributions in multiomics research: Lists of authors and word clouds of the top 100 authors

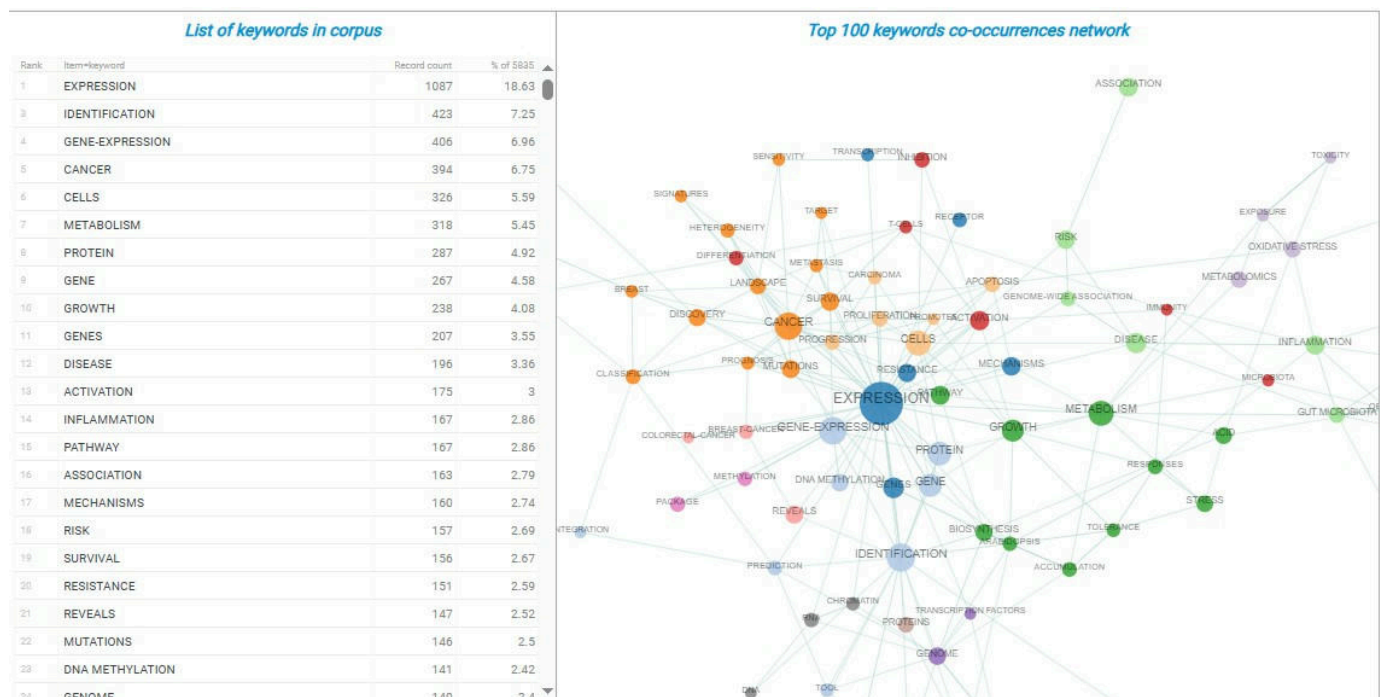


Figure 4. Lists of keywords and the top 100 keywords in the co-occurrence network

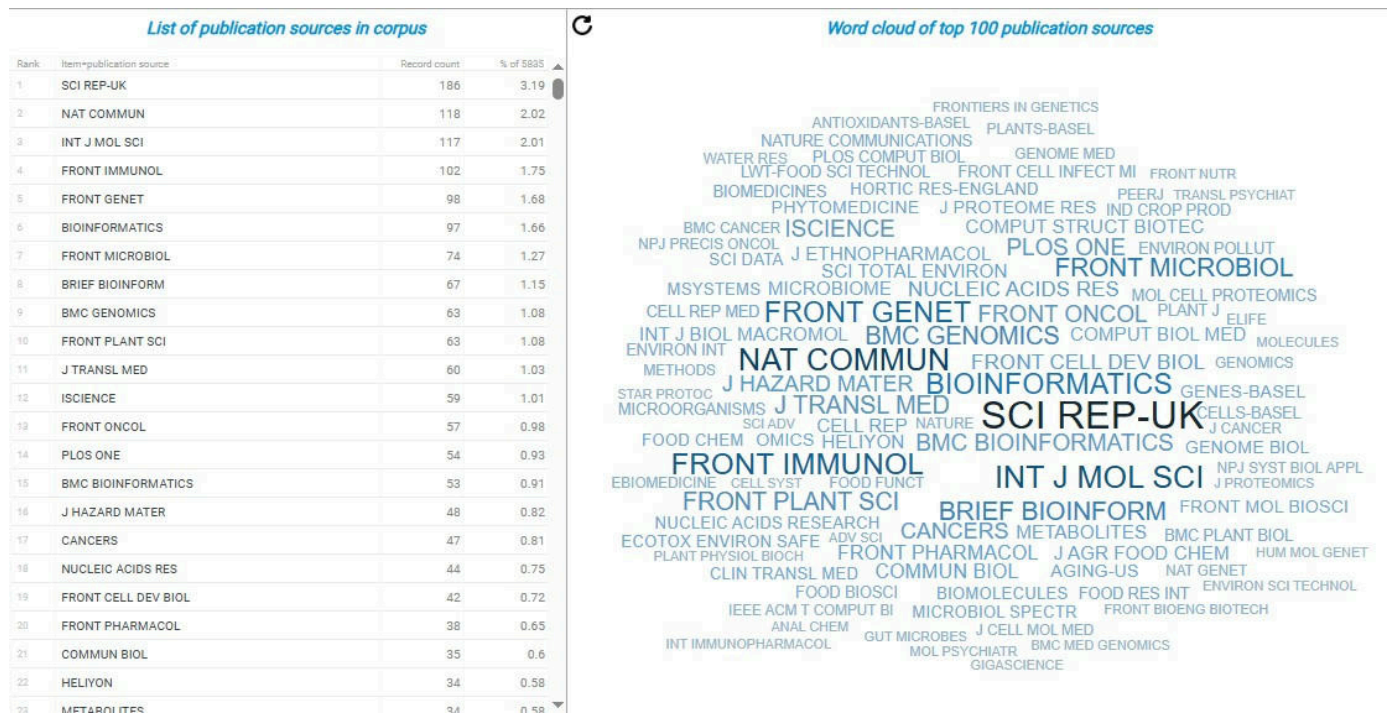


Figure 5. Journal contributions in multiomics research: lists of journals and word clouds of the top 100 authors

such as Bioinformatics, Frontiers in Immunology, and Frontiers in Genetics, are prominently displayed, thereby visually confirming their significance as primary dissemination venues for the research field represented by this corpus

Figure 6 shows the different categories of subjects in the text and how they are all linked together. On the left of the page, there is a table that shows the top subject areas based on their record count. 'Biochemistry and Molecular Biology' is in first place with 690 occurrences, which is 11.83% of the total. Next was "Multidisciplinary Sciences" with 586

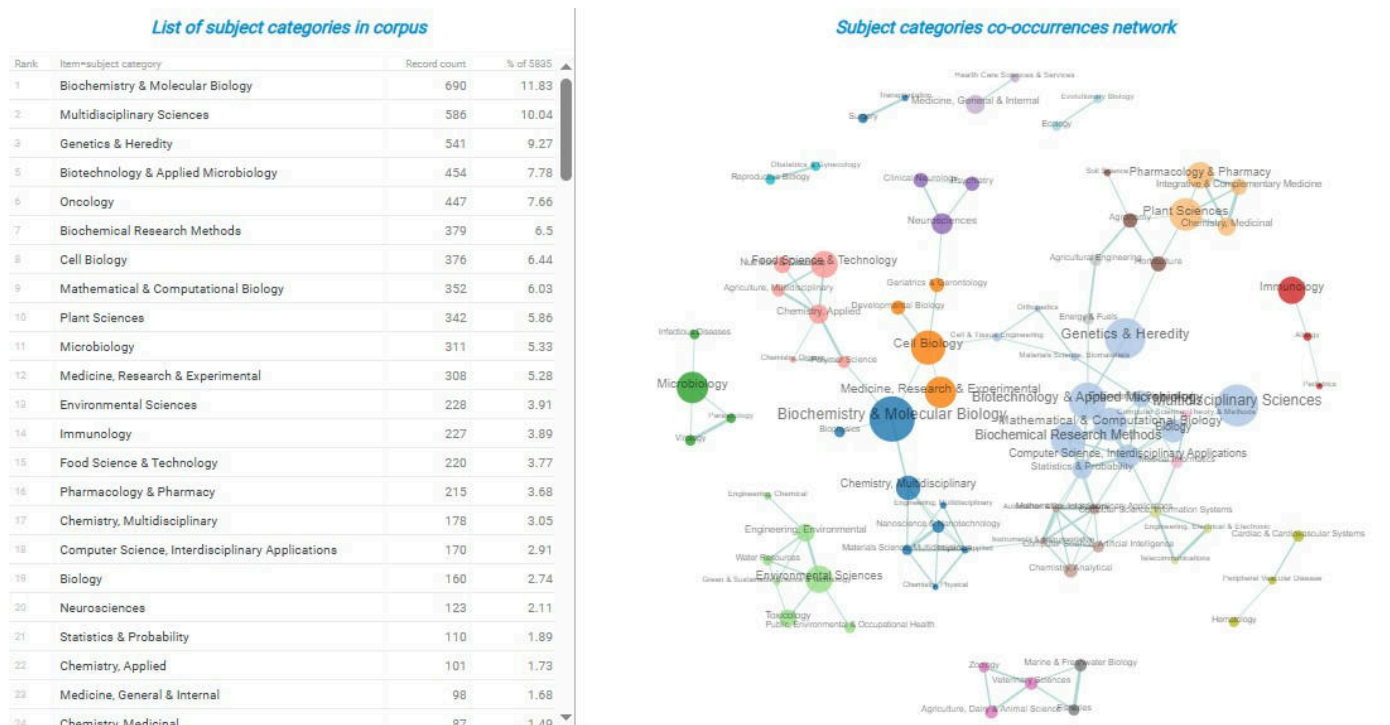


Figure 6. Subject categories co-occurrence network

occurrences, or 10.04%, followed by "Genetics and Heredity" with 541 occurrences, or 9.27%. Other top subject areas include "Biotechnology and Applied Microbiology," "Oncology," and "Biochemical Research Methods." On the right, you can see a picture of the most common subject categories, showing how they are connected. Journals such as "Biochemistry & Molecular Biology," "Cell Biology," "Genetics & Heredity," and "Multidisciplinary Sciences" are important because they are often linked to other subjects. This dual representation shows just how important molecular and genetic research is. It also shows how research in this field is carried out by different experts working together.

Thematic map (Bibliographic coupling)

On the basis of the references they share, 5319 thematically close publications of the studied corpus are gathered into 5 topics (Q=0.307) and 22 subtopics (Q=0.214). Figures 7a and 7b illustrate the complex network of interactions centered around "multiomics," connecting it to various biological and analytical domains such as "BREAST," "PROTEOMICS," "ARABIDOPSIS," and "MENDELIAN RANDOMISATION." The multiomics approach integrates different layers of biological data—potentially genomic, transcriptomic, proteomic and metabolomic information—to reveal how these elements interact within the context of cancer.

Figures 8a and 8b come from a set of data that includes different types of scientific information. They show how different areas of science are connected when studying cancer. The main part of the network is "Oncology," the point around which other areas, including "Biochemistry & Molecular Biology," "Plant Sciences," "Mathematical & Computational Biology," as well as "Multidisciplinary Sciences," are connected. The multiomics approach is the way that

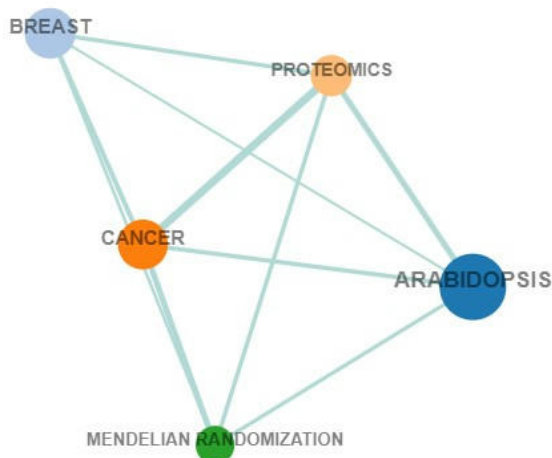


Figure 7. a: Most significant main keywords

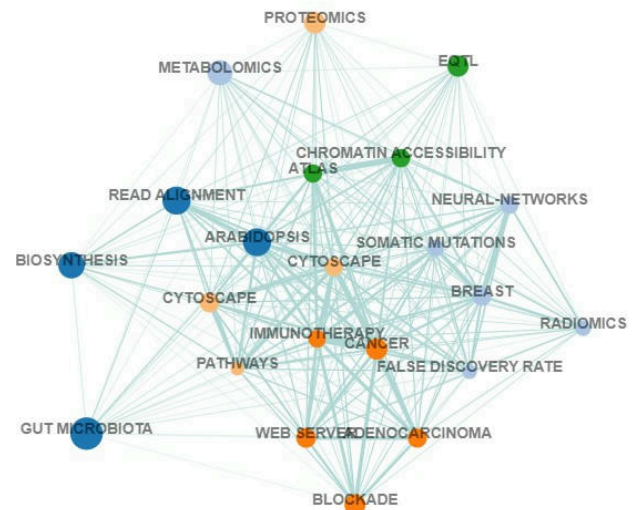


Figure 7. b: Most significant main keywords

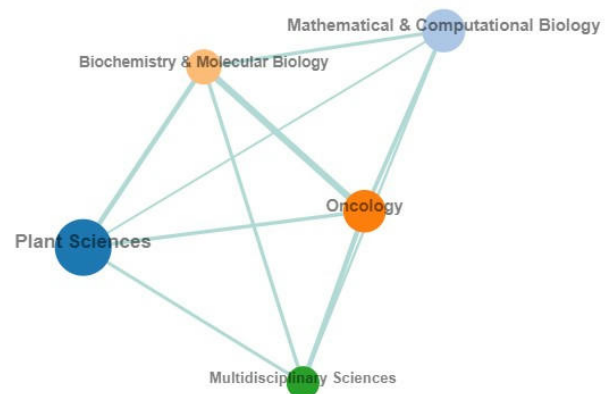


Figure 8. a: Most frequent main subjects

this network works. This approach combines different types of biological data (such as genomics, proteomics, and metabolomics) to provide a full understanding of cancer biology.

Figures 9a and 9b present a visual representation of the intricate interconnections among diverse scientific disciplines and publications within the field of immunology research. The focal point of the network is "FRONT IMMUNOL," which represents *Frontiers in Immunology*, a distinguished journal within the domain of immunology. This central node connects to other key nodes, including "BIOINFORMATICS," "SCI REP-UK" (likely referring to *Scientific Reports* published by Nature Research), and "NAT COMMUN" (short for *Nature Communications*). The connections between these nodes highlight the interdisciplinary nature of modern immunological research, where bioinformatics plays a crucial role in analysing complex biological data, whereas high-impact journals such as *Scientific Reports* and *Nature*

Communications serve as platforms for disseminating cutting-edge findings.

Figures 10a and 10b illustrate the collaborative network among researchers in a specific scientific domain. At the centre of the network are five key nodes representing individual researchers: Zhang J, Li XJ, Wang Y, Wang JD and Zhou GY. The connections between these nodes indicate collaborative relationships or co-authorship, suggesting that these researchers have worked together on studies or projects related to multiomics data.

The use of different colours for the nodes clearly represents various roles, expertise areas or affiliations within the research group. This network proves that multiomics datasets require a multidisciplinary approach, where researchers from diverse backgrounds must come together to analyse complex biological data and derive meaningful insights. The graph

provides a clear visual representation of the collaborative ecosystem that is essential for driving innovation and discovery in modern scientific research (Figure 10b).

DISCUSSION

The findings confirm that multiomics has rapidly evolved into one of the most dynamic and influential research areas in the biomedical and life sciences. The substantial increase in publication volume since 2020, with a peak in 2024, reflects the growing importance of integrative omics approaches in addressing complex biological questions.

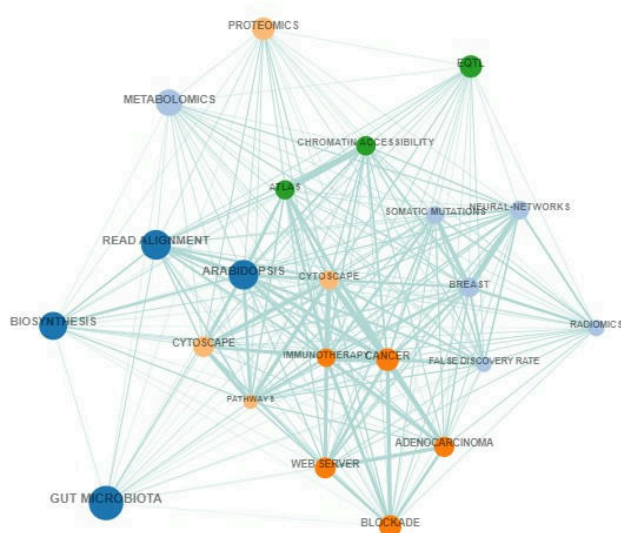


Figure 8. b: Most frequent sub-subjects

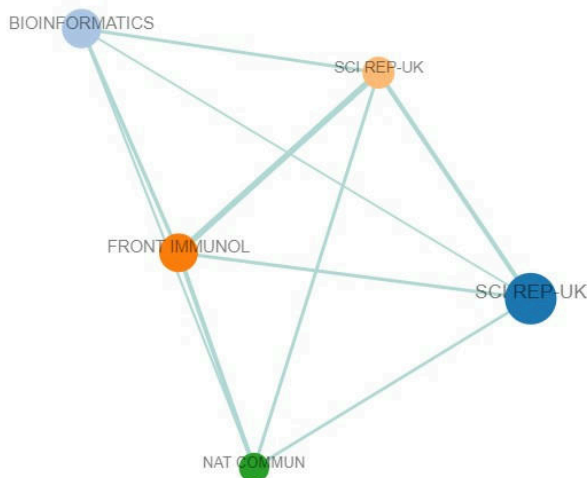


Figure 9. a: Most frequent main journals

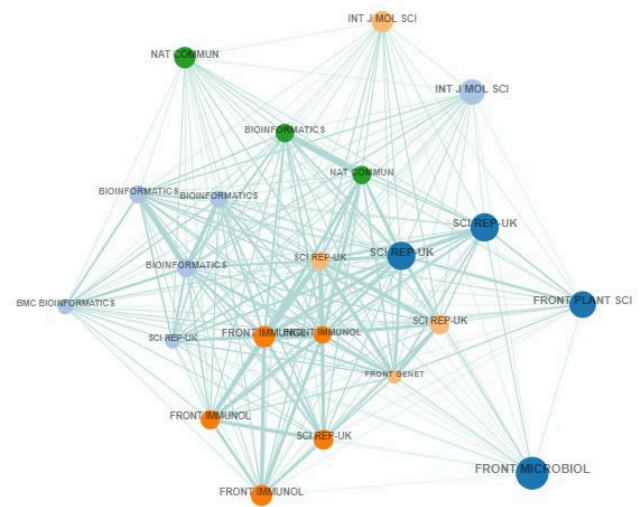


Figure 9. b: Most frequent sub-journals

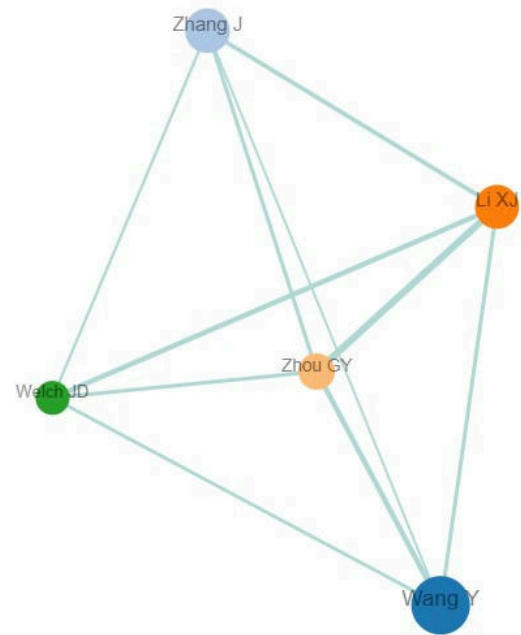


Figure 10. a: Most cited main authors

Our findings are consistent with those of previous bibliometric studies in adjacent scientific domains. For instance, Cobo et al. and Van Eck and Waltman emphasized the growing utility of science mapping tools such as VOSviewer and CiteSpace in identifying thematic clusters and collaboration networks (4, 14). Similarly, Claveau and Gingras demonstrated the role of bibliometric analysis in tracing the historical dynamics of economics research, highlighting how such methods can reveal both thematic continuity and paradigm shifts (3). In the context of biomedical research, studies by Grauwin et al. also underlined the importance of bibliographic coupling for identifying emerging research fronts (1). Compared to these earlier approaches, our use of BiblioMaps adds a web-based, interactive dimension that enhances accessibility for non-expert users and strengthens the visualization of thematic developments in multiomics. This alignment with similar methodological studies confirms both the validity of our approach and the novelty of providing an open, user-friendly interface for the scientific community. In addition, our findings complement earlier domain-specific bibliometric studies such as Koçak et al., who conducted a comprehensive mapping and clustering analysis of the neuroscience literature in Türkiye (17). Their study demonstrated how bibliometric methods can uncover national research trends and collaboration structures, which parallels our approach in highlighting international and thematic dynamics in multiomics research.

From a methodological perspective, the use of BiblioMaps introduced several advantages over traditional bibliometric tools. Unlike static platforms such as Gephi, CiteSpace, or HistCite™, BiblioMaps provides a fully interactive, web-based environment that integrates data processing, visualization, and interpretation. This feature enhances

accessibility for non-expert users, including educators and policymakers, and supports the collaborative exploration of complex bibliographic datasets. Such usability distinguishes BiblioMaps from existing software and underscores its potential contribution to the democratization of science mapping.

This study provides a comprehensive analysis and makes innovative use of interactive science mapping tools, such as BiblioMaps. However, some limitations should be considered. First, the dataset was obtained solely from the Web of Science (WoS) Core Collection. This may not reflect studies published in local or non-indexed journals adequately. Therefore, countries or disciplines that primarily publish their research on local or open-access platforms may be underrepresented.

Second, the search query created to comprehensively identify publications related to multiomics relies on specific keywords such as "multiomics," "integrated omics," and "multidimensional omics." The result may have been the exclusion of some relevant studies due to the diversity of terms used or the lack of standard definitions across fields. Finally, the bibliographic matching method used for clustering relies on common references. It does not rely on direct citations between publications. While the identification of thematic similarities is effective with this approach, there may be a lack of reflection of the most current or rapidly evolving trends in the field.

Additionally, although BiblioMaps provides an intuitive & interactive visualization platform, its current functionality is limited to datasets exported from the Web of Science. Expanding compatibility with other databases, for example, Scopus or PubMed, would increase its utility for broader scientific communities. Finally, the language of analysis and interface is currently available only in English, which may limit accessibility for non-English-speaking researchers and educators who could benefit from using the tool. Future improvements will focus on integrating additional data sources, refining clustering algorithms, and enhancing multilingual support to address these limitations and provide a more inclusive and dynamic representation of multiomics research.

In summary, this discussion situates this study within the broader landscape of bibliometric analyses of multidisciplinary research. By providing an interactive and accessible platform, BiblioMaps enhances the capacity to trace thematic and structural developments in multiomics and complements previous efforts in the related fields. These contributions underscore the value of interactive visualization tools in advancing bibliometric research and supporting knowledge discovery in complex data-driven domains.

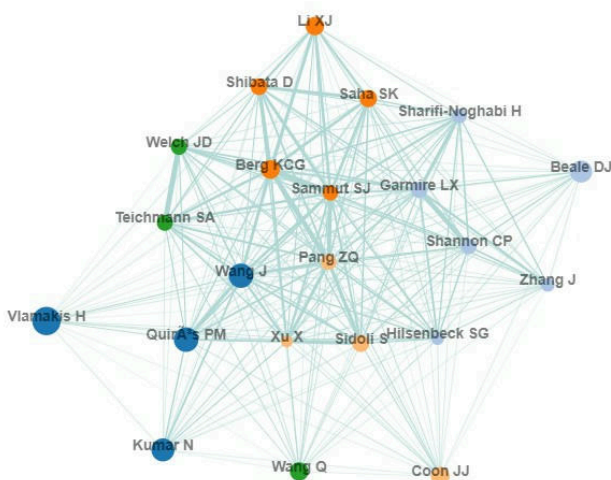


Figure 10. b: Most cited sub-authors

CONCLUSION

This work provides a broad bibliometric analysis of multiomics research from 2015–2024, through the interactive visualization tool BiblioMaps. The information comes from 5,835 publications from the Web of Science database, with a consistent and significant increase in outputs over time, especially since 2020, peaking in 2024 (31.57%), indicating more engaging interest and increasing importance of multiomics approaches in the contemporary biomedical and life sciences fields. Geographically, China is the leading contributor to publications (50.78%), followed by the United States (23.67%), and the UK (5.98%), with the disciplinary lead being dominated by East Asian and Western publications. The statistics on international collaboration (26.21% collaboration rate) highlight the international and interdisciplinary nature of multiomics science, including familiarity with US collaborations, European collaborations, and up-and-coming scientist hubs such as Turkey. We see the greatest number of publications from researchers like Wang Y (122 publications), Zhang Y (112 publications), Li Y (103 publications), and other authors featured in the 2nd or 3rd tier of publication counts. Thus, we suggest that these are established groups and potential collaborative networks. When considering labels or keyword usage, the representation of keywords like "expression" (18.63%), "identification" (7.25%), or "gene expression" (6.96%) suggests a preference for molecular mechanisms and biological process activity, as well as for studies related to disease and disease biology, especially cancer. In summary, we observed genomic, transcriptomic, proteomic, and metabolomic combinations for understanding complex diseases or biological systems.

Key journals in the field are Scientific Reports (Sci Rep-UK), Nature Communications (Nat Commun), and the International Journal of Molecular Sciences (Int J Mol Sci), all of which are well-regarded platforms for disseminating multiomics research. Subject category analyses further show that the field is mainly rooted in biochemistry and molecular biology, genetics and heredity, and oncology, while a number of other disciplines such as computational biology, plant sciences, and immunology are also being incorporated, thus emphasizing the interdisciplinary nature of the field. With BiblioMaps, thematic clusters and subtopics could be revealed through bibliographic coupling, yielding five major topics and 22 subtopics. Among the notable thematic areas are breast cancer, proteomics, Arabidopsis, and Mendelian randomization, showing how multiomics integrates various biological levels to discern interactions in complex systems. Furthermore, the network visualization of authors and journal sources illustrates the collaborative structure of the field, with journals such as Frontiers in Immunology, Scientific Reports, and Nature Communications serving as central nodes connecting researchers across disciplines.

In conclusion, this study charts the structural and thematic changes in multiomics and illustrates the efficacy of interactive bibliometric tools, such as BiblioMaps, to assist in knowledge discovery, track research trends, and promote the interdisciplinary nature of multiomics research. Future work will be devoted to tool improvements to facilitate the tracking of emerging topics in real time and to extend the use of similar tools to other complex scientific fields.



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