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Original Article

A bibliometric analysis and visualization of spatially resolved transcriptomics

Dezhi Huang[1,2], Yang Gou[1,2], Xiaoqi Wang[1,2], Qiong Li[1,2], Xinlei Li[1,2], Naya Ma[1,2], Yishuo Duan[1,2], Jun Rao[1,2,3,4,*], Xi Zhang[1,2,3,4,*]

[1] *Medical Center of Hematology, Xinqiao Hospital, Army Medical University, Chongqing 400037, China;*
[2] *State Key Laboratory of Trauma, Burns and Combined Injury, Army Medical University, Chongqing 400037, China;*
[3] *Jinfeng Laboratory, Chongqing 400037, China;*
[4] *National Clinical Research Center for Hematologic Diseases, the First Affiliated Hospital of Soochow University, Suzhou, Jiangsu 215006, China.*

ABSTRACT

This research aims to analyze the research status, hotspots, and future development trends of spatially resolved transcriptomics (SRT). We obtained research publications on SRT from the Web of Science Core Collection (WoSCC) database and performed graph analyses with VOSviewer and OriginPro 2018. Included was a total of 2022 papers, involving 13 234 researchers from 2105 institutions in 75 countries. The publication status and characteristics of countries, institutions, authors, and co-occurrence keywords were conducted by bibliometric analysis. The leaders in this field were the United States and Sweden, while China and India were the largest contributors among developing countries. SRT and single-cell sequencing are closely combined. The development of SRT itself, tumor-relevant research, and brain science, are the research hotspots of the present and foreseeable future. The development of bioinformatics facilitates the analytical applications of SRT. SRT and temporal dynamics should be closely combined. Future development in SRT is not only aimed at achieving high throughput and high resolution, but also dedicated to making it cost-effective, simple, rapid, and easy to use. Spatially resolved transcriptomics should be promoted from scientific research to clinical application as soon as possible in order to provide accurate diagnoses and individualized treatment for patients.

Keywords: bibliometric analysis, spatially resolved transcriptomics, single-cell RNA sequencing

INTRODUCTION

In 2020, *Nature Methods* recognized spatially resolved transcriptomics (SRT) as the "Method of the Year". SRT is the next generation technique after single-cell RNA sequencing (scRNA-seq)[1]. Although scRNA-seq technologies have made great progress in discovering novel cell types, revealing genetic heterogeneity among cells, and laying the foundation for the creation of comprehensive cell atlases in different species, samples are inevitably subject to mechanical or enzymatic dissociation into single-cell suspensions, thus losing their native spatial context and information[2–3]. However, the spatial context and information are critical for tissue function, intercellular communication, gene expression, and

*Corresponding to: Jun Rao and Xi Zhang, Medical Center of Hematology, Xinqiao Hospital, Army Medical University, 83 Xinqiaozheng Street, Shapingba District, Chongqing 400037, China. E-mails: raojun1129@126.com and zhangxxi@sina.com.
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regulation[3–4]. Thus, high-resolution, spatially resolved single-cell omics analysis is critically needed for quantifying RNAs in their spatial context, which is crucial to understand gene expression and regulation in complex tissues[4–5].

SRT, which encompasses a diverse set of technologies that encode gene expression measurements with information about the spatial location of each observation in the sample, can quantify the transcriptome while maintaining the original spatial context, thereby allowing molecular features to be associated with cell morphology, physiology, spatial localization, and tissue histology. Additionally, the study of the SRT can unveil subcellular RNA distribution patterns, spatial markers, and spatially regulated biological processes[2,6]. Compared with scRNA-seq, SRT workflows and efforts to integrate spatially resolved transcriptomics and scRNA-seq data have emerged fairly recently and are an area of rapid evolution[7]. Given the recent emergence and rapid evolution of SRT, it is important to catch up on current research hotspots and predict future research trends in SRT.

Bibliometrics is a statistical method that can quantitatively analyze research papers, access quality studies, elucidate key areas of research, and predict the direction of future studies concerning one special topic *via* mathematical and statistical ways[8–9]. To our knowledge, there has been no bibliometric analysis of current research hotspots and future research trends of SRT. Initially, the development of SRT including the number of publications by year was analyzed. After this, we were able to analyze the most influential countries/regions, institutions, journals, authors, co-authors, and most frequent keywords using Vosviewer. Data visualization visually reflected the relationship between different countries/regions, institutions, and authors as well as the degree of existing academic collaboration between countries/regions, institutions, and authors. Furthermore, keyword visualization could rapidly facilitate us to know SRT at both the macro and the general levels, including closely related techniques and the most widely utilized areas of SRT, and to understand current research hotspots and grasp future research trends. Finally, we analyzed its future outlook and forecast the development trends of SRT.

METHODS

Data source and search strategy

In this study, data from the Web of Science Core Collection (WoSCC) database (https://www.webofscience.com/wos/woscc/basic-search) was extracted from the initial publication year to 30 November 2022. The search strategy was as follows: TS (topics) = spatial transcriptome* OR spatial transcriptomic* OR spatially resolved transcriptomic*; LANGUAGE: English; DOCUMENT TYPES: article AND review. Due to the inherent drawbacks of retrieval techniques, we deleted the papers with a large deviation based on paper title, keywords, and abstract. A total of 2022 papers were obtained from the initial 2249 papers.

Data analysis and visualization

Science mapping is an essential bibliometrics procedure that can represent the situation of the discipline and the state of development. There are many software for bibliometric analysis from various companies[10]. The most widely-used free bibliometric analysis software is VOSviewer (version 1.6.18; Centre for Science and Technology Studies, Leiden University, Leiden, the Netherlands). This was used to visualize the relationships among the authors, countries, journals, co-citations, and terms[11–12]. OriginPro 2018 (OriginLab, Northampton, Massachusetts, USA) was used to make histograms and line charts. If two research objects had the same numerical value, the rank would be higher with a bigger total link strength.

RESULTS

Global publications by year

In total, 2022 publications on the topic of SRT were identified in the WoSCC database from 2003 to 2022, including 1684 articles and 338 reviews (***Fig. 1***).

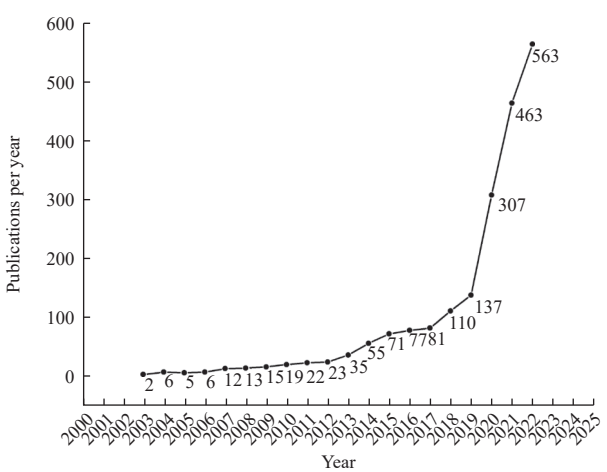

Fig. 1 **Global trends in the number of annual publications on spatially resolved transcriptomics from 2003 to 2022.**

In 2022, 563 publications were already published as of November 30. From 2003 to 2012, there were few publications about SRT. From 2013 onward, the number of publications gradually increased, reaching 307 in 2020, which represented a big jump compared with 2019.

Global publications and citations by country/region

In general, 75 countries/regions engaged in relevant research on SRT. Among them, 41 countries/regions published at least 5 papers. The top 10 ranked countries/regions are presented in ***Table 1***. In terms of the number of publications, the USA ranked first with 894 publications, followed by China (497 publications), England (221 publications), Germany (214 publications), and Sweden (131 publications). From the aspect of citation numbers, the USA ranked first with 37 856 citations, followed by Sweden (17 567 citations), Germany (15 647 citations), England (11 993 citations), and India (9078 citations).

Fig. 2 shows three clusters with 41 nodes with a threshold of five. Each node represented a country, and the size of the node was positively correlated with the number of publications. The thickness of the link between the two countries represented the degree of

Table 1 **Top 10 countries/regions of publications and citations on spatially resolved transcriptomics**

Rank	Country/Region	Publications	Rank	Country/Region	Citations
1	USA	894	1	USA	37 856
2	China	497	2	Sweden	17 567
3	England	221	3	Germany	15 647
4	Germany	214	4	England	11 993
5	Sweden	131	5	India	9078
6	Australia	111	6	Denmark	8974
7	Canada	99	7	China	7481
8	Japan	93	8	Netherlands	7470
9	Netherlands	93	9	Switzerland	5488
10	France	91	10	Scotland	5051

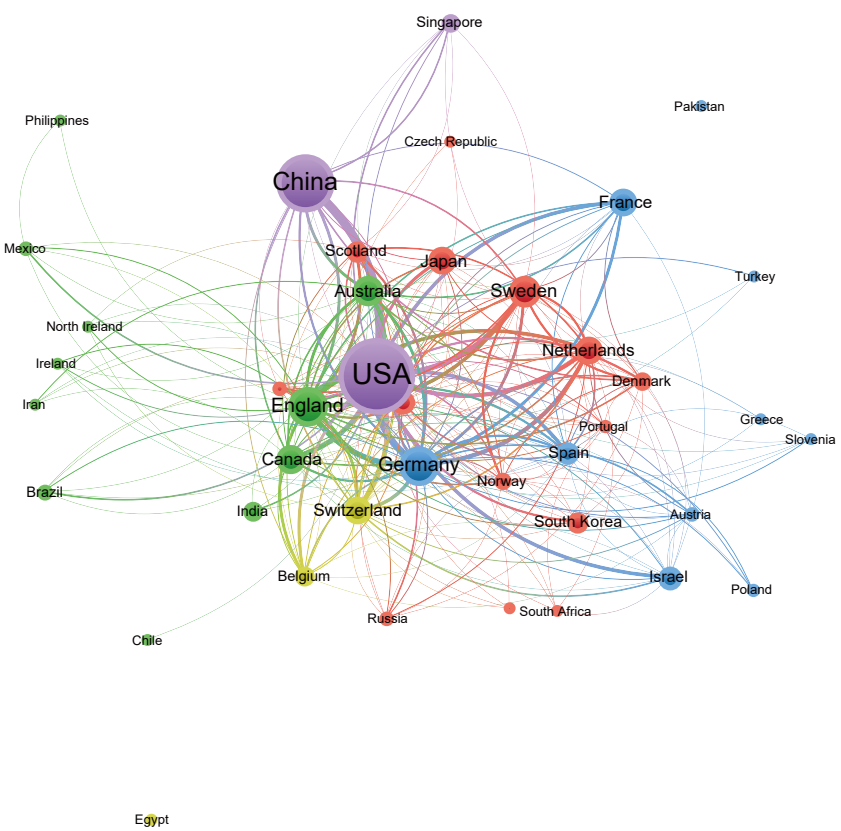

Fig. 2 **Co-authorship networks of countries on spatially resolved transcriptomics.**

cooperation. The largest cluster (red) contained 17 countries, with the USA representing the most prominent country. The second largest cluster (green) contained 14 countries, mainly consisting of island countries or peninsular countries. The last cluster (blue) contained 10 countries, mainly composed of the continental countries of Europe. The USA was observed as the number one cooperation partner for most countries.

Global publications and citations by institution

A total number of 2476 institutions contributed to publications on SRT. The top 10 institutions of publications and citations are listed in ***Table 2***. From the perspective of publications, five were from the USA, while China and Sweden both had two, with the remaining one from England. The Chinese Academy of Sciences (80 publications) ranked first, followed by Karolinska Institute (67 publications), Harvard Medical School and University of Cambridge (66 publications), and the University of Cambridge (57 publications). In terms of citations, five were from the USA, four were from Sweden, and the remaining one was from England. The top four institutions of citations were all from Sweden, which were the Karolinska Institute (14 002 citations), KTH Royal Institute of Technology (13 612 citations), Uppsala University (12 532 citations), and Stockholm University (8683 citations). They were followed by five US institutions and one England institution.

Table 2 **Top 10 institutions of publications and citations on spatially resolved transcriptomics**

Rank	Institution	Publications	Country	Rank	Institution	Citations	Country
1	Chinese Academy of Sciences	80	China	1	Karolinska Institute	14 002	Sweden
2	Karolinska Institute	67	Sweden	2	KTH Royal Institute of Technology	13 612	Sweden
3	Harvard Medical School	66	USA	3	Uppsala University	12 532	Sweden
4	University of Cambridge	57	England	4	Stockholm University	8683	Sweden
5	KTH Royal Institute of Technology	53	Sweden	5	Harvard University	6348	USA
6	Harvard University	52	USA	6	New York University	5298	USA
7	Broad Institute MIT and Harvard	49	USA	7	Broad Institute MIT and Harvard	5040	USA
8	Stanford University	47	USA	8	New York Genome Center	4837	USA
9	University of California Los Angeles	46	USA	9	MIT	4511	USA
10	Univ Chinese Acad Sci	46	China	10	University of Cambridge	3872	England

To evaluate the characteristics of collaborative institutions in the field of SRT, institution co-authorship analysis was conducted by using VOSviewer with a threshold of 20. There were 49 nodes with 5 clusters in this network map (***Fig. 3***). The largest cluster (red) was composed of 15 institutions mainly from China and the British commonwealth of nations. The next three clusters (green, blue, and yellow) were composed of 11, 10, and 7 institutions, mainly from the USA. The remaining one was composed of 6 institutions mainly from Sweden. An institution generally cooperates most with institutions from the same country or region, such as Harvard University and Harvard Medical School, the Chinese Academy of Sciences and University of Chinese Academy of Sciences, and Karolinska Institute and KTH Royal Institute of Technology.

Citations and journals

A wide range of 648 journals published the 2022 retrieved papers. ***Table 3*** lists the 20 most productive journals for SRT paper publications, and the journals were sorted by citation numbers. *Science* had the largest number of citations (11 064), although it only published 17 papers on SRT research. The second to fifth places were *Cell* (8300 citations), *Nature* (5117 citations), *PNAS* (4972 citations), and *Nature Biotechnology* (3604 citations).

Based on the retrieved data, 13 234 authors contributed to the 2022 retrieved papers on SRT. The top 10 productive authors involved in SRT are listed in ***Table 4***. Among them, six authors are from Sweden, three authors are from the USA, and the last one is from Israel. Lundeberg J (35 publications) was identified as the most active author in the field of SRT research, followed by Chen F, Larsson L, Regev A, and Ståhl PL (14 publications).

Researchers should be aware of existing collaborations in their research field to prevent isolation and improve productivity[13]. ***Fig. 4*** illustrates the collaboration network of the key authors. The minimum number of authors' documents was set by six, and authors without connections were not presented to facilitate the interpretation of the network map. The most influential authors from the top 6 clusters could be identified in the groups: cluster 1, in red, was led by Chen F; cluster 2, in green, was led by Itzkovitz S; cluster 3, in dark blue, was led by Ståhl PL; cluster 4, in yellow, was led by Lundeberg J; cluster 5 in purple, was led by Nilsson M; and cluster 6, in light blue, was led by Wang W.

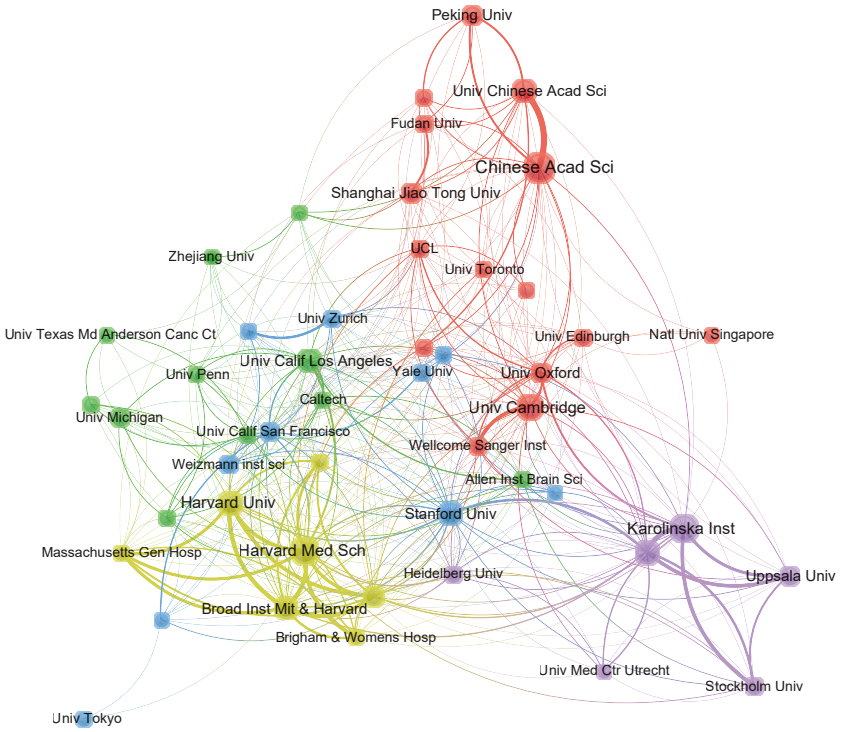

Fig. 3 **Co-authorship networks of institutions on spatially resolved transcriptomics.**

Table 3 **Top 20 cited journals on spatially resolved transcriptomics**

Rank	Journal	Citations	Publications	IF
1	*Science*	11 064	17	63.7124
2	*Cell*	8300	31	66.8493
3	*Nature*	5117	38	69.5026
4	*PNAS*	4972	33	12.7784
5	*Nature Biotechnology*	3604	28	68.1623
6	*Nature Communications*	2579	85	17.6939
7	*Nature Methods*	1978	24	47.9904
8	*Nature Reviews Genetics*	1496	7	59.5795
9	*Plant Cell*	1408	9	12.0847
10	*Plant Journal*	1339	19	7.0912
11	*BMC Genomics*	996	36	4.5471
12	*Scientific Reports*	886	50	4.9958
13	*Development*	803	16	6.8622
14	*Nature Neuroscience*	793	15	28.7708
15	*Genome Biology*	611	18	17.9066
16	*Molecular Cell*	609	6	19.3287
17	*Nature Genetics*	582	10	41.3069
18	*Genome Research*	579	15	9.4381
19	*Nature Cell Biology*	531	7	28.2138
20	*Developmental Cell*	530	12	13.4168

IF: impact factor.

The co-cited author is also a key criterion for assessing the contribution of researchers. The top 10 most co-cited authors involved in SRT are listed in ***Table 5***. Among them, eight authors are from the USA and the remaining two authors are from Sweden and Singapore, respectively. The top 3 co-cited authors were Ståhl PL (349), Stuart T (286), and Trapnell C (263). These publications laid the foundation for research in the SRT field.

Keywords

Keywords represent nouns or phrases that can

Table 4 **Top 10 prolific authors on spatially resolved transcriptomics**

Rank	Author	Publications	Total link strength	Affiliation	Country
1	Lundeberg J	35	2934	KTH Royal Institute of Technology	Sweden
2	Chen F	14	354	Broad Institute of MIT and Harvard	USA
3	Larsson L	14	669	Karolinska Institutet	Sweden
4	Regev A	14	2788	Broad Institute of MIT and Harvard	USA
5	Ståhl PL	14	1696	KTH Royal Institute of Technology	Sweden
6	Itzkovitz S	13	1618	Weizmann Institute of Science	Israel
7	Navarro JF	13	1728	KTH Royal Institute of Technology	Sweden
8	Nilsson M	13	388	Stockholm University	Sweden
9	Salmén F	12	1873	KTH Royal Institute of Technology	Sweden
10	Macosko EZ	11	391	Broad Institute of MIT and Harvard	USA

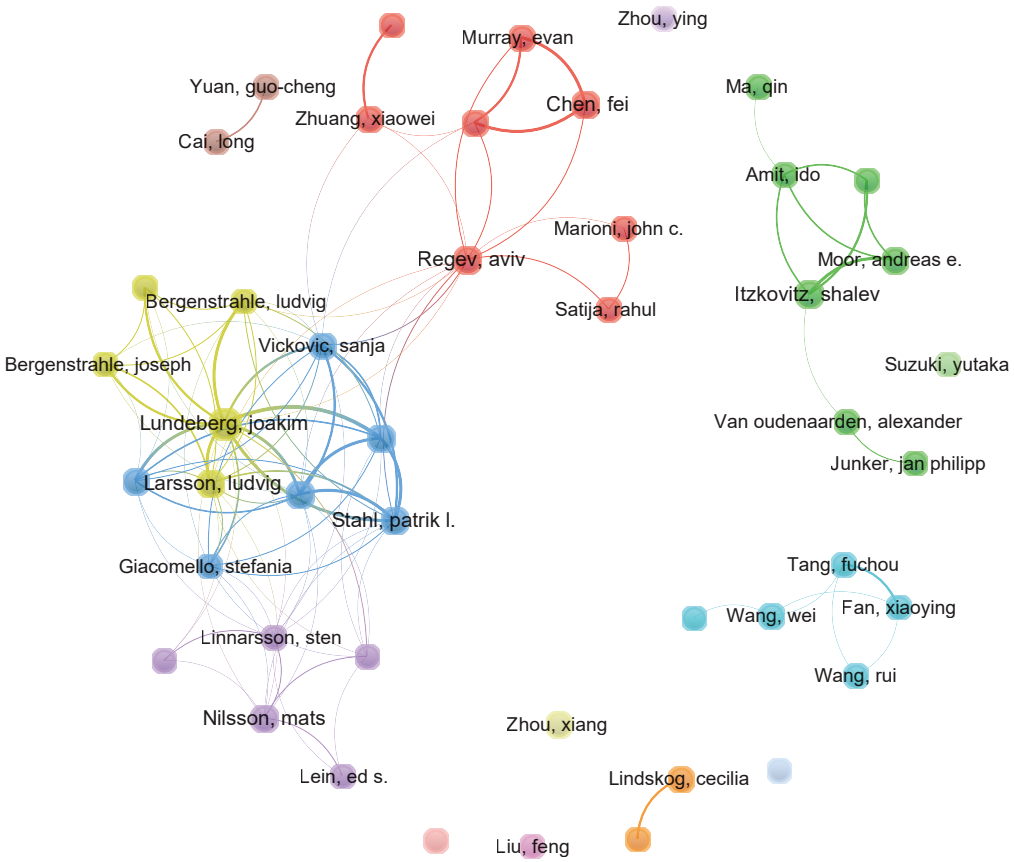

Fig. 4 **Co-authorship networks of authors on spatially resolved transcriptomics.**

Table 5 **Top 10 co-citation authors on spatially resolved transcriptomics**

Rank	Author	Co-citations	Total link strength	Affiliation	Country
1	Ståhl PL	349	10 081	KTH Royal Institute of Technology	Sweden
2	Stuart T	286	7913	New York Genome Center	USA
3	Trapnell C	263	5795	University of Washington School of Medicine	USA
4	Rodriques SG	246	8333	Massachusetts Institute of Technology	USA
5	Rodriques SG	240	8238	Massachusetts Institute of Technology	USA
6	Chen KH	221	7835	Genome Institute of Singapore	Singapore
7	Moffitt JR	213	7316	Harvard University	USA
8	C-H L Eng	205	7341	California Institute of Technology	USA
9	Love MI	203	2869	University of North Carolina-Chapel Hill	USA
10	Wang X	193	6272	Broad Institute of MIT and Harvard	USA

reflect the full meaning or core content of literature, which can shed light on which research topics in a field are popular (or less so)[14–15]. Before performing visualization, we used a thesaurus file to merge the keywords with words of the same meaning to improve the quality of keyword co-occurrence analysis. For instance, "rnaseq", "rna-seq" and "rna sequencing" could be merged into the same keyword. Thus, a total of 4188 author keywords were exported from the included studies. The top 20 most frequently appeared keywords are presented in ***Table 6***. The keyword "Transcriptomics" had the highest frequency of 225 times, followed by "Spatially Resolved Transcriptomics" (153 times), "Gene Expression" (90 times), "Single-Cell RNA Sequencing" (85 times), and "RNA Sequencing" (78 times).

Table 6 **Top 20 keywords of publications on spatially resolved transcriptomics**

Rank	Keyword	Frequency	Total link strength
1	Transcriptomics	225	246
2	Spatially resolved transcriptomics	153	160
3	Gene expression	90	113
4	Single-cell RNA sequencing	85	88
5	RNA sequencing	78	85
6	Tumor microenvironment	42	54
7	Single-cell	35	60
8	Proteomics	28	39
9	Microarray	26	43
10	Tumor heterogeneity	23	38
11	Development	22	38
12	Alzheimer's disease	21	30
13	Immunotherapy	21	35
14	Genomics	17	25
15	Hippocampus	17	24
16	Bioinformatics	16	22
17	Evolution	16	9
18	Laser capture microdissection	16	27
18	Breast cancer	15	20
20	Deep learning	15	16

VOSviewer was utilized to generate the overlay visualization map of author keywords (***Fig. 5***). Totally, 71 author keywords were collected, with a calculated threshold of seven. The size of the nodes and the words represented the weights of the nodes. The bigger the node and word, the larger the weight. The line between two keywords representing the co-occurrence frequency of the keyword and the thickness of the line was positively correlated with the co-occurrence frequency of the keyword. The color displayed the occurrence time of keywords: the closer the color was to yellow, the closer the topic was to the present. Most articles published before 2018 focused on "animal experiments" and "botany research", whereas "human research" and "clinical application" have become more common in recent years, and are likely to remain major areas of research in the future.

DISCUSSION

SRT is a rapidly growing field that can link single-cell transcriptomic profiles with connectional, morphological, physiological, and functional properties while providing cellular locations at the single-cell or subcellular resolution[3,16]. In this study, we analyzed the date of publication, countries, institutions, journals, authors, and keywords of published papers on SRT based on bibliometric and visualization analysis by VOSviewer, in order to reveal the current research hotspots and predict future research trends of SRT study worldwide.

Research status quo

From 2003 to November 30, 2022, a total of 2022 effective documents on spatial transcription technology were obtained from the WoSCC database. Judging from the number of publications each year, the growth was relatively stable before 2020. In 2020, 307 papers were published, an increase of 123% compared to 137 articles in 2019. This can reflect why Nature Methods crowned SRT Method of Year 2020 to a certain degree. In 2022, 563 articles had already been published as of November 30. It is foreseeable that the publication of literature on SRT research will continue to grow rapidly.

From the perspective of countries and regions, the USA was far ahead of the second in terms of the

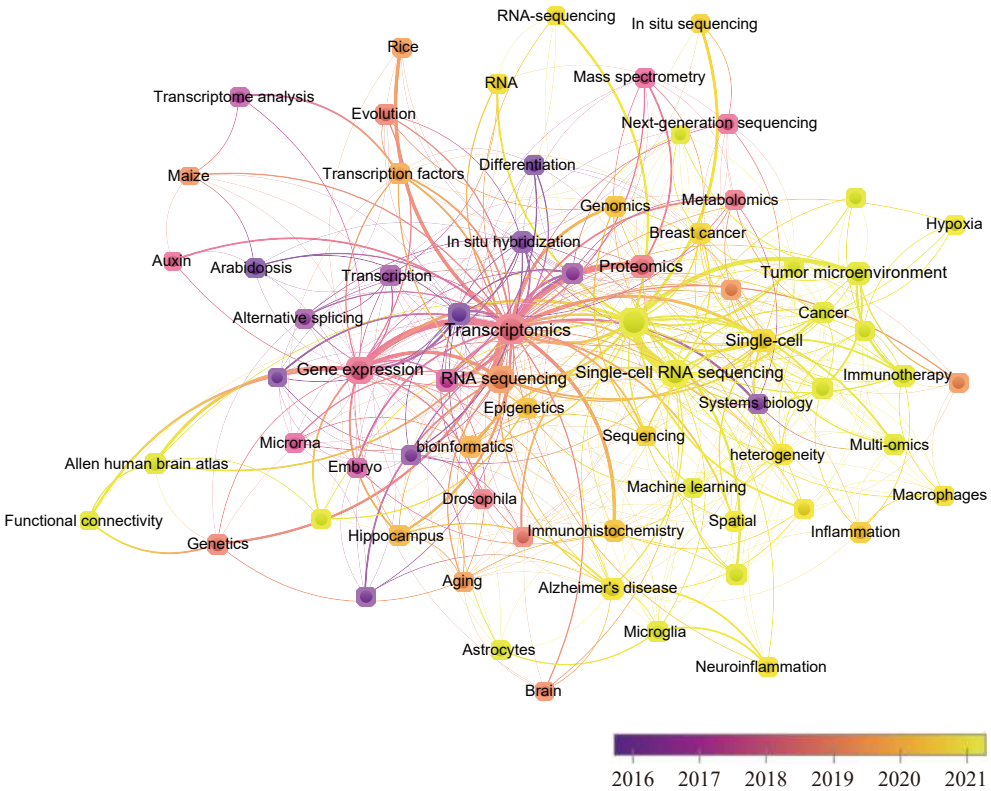

Fig. 5 **Overlay visualization map of co-occurrence keywords on spatially resolved transcriptomics by the year.**

number of publications and the number of citations. The USA had a leading position in the research of SRT. In addition, developed countries made greater contributions to the research of SRT. Fortunately, as developing countries, China and India also performed well. China ranked second and seventh in the number of publications and citations, respectively, and India ranked fifth in the number of citations.

Among the top 10 institutions for publications, the Chinese Academy of Sciences ranked first with 80 papers. The institution number of the USA, China, Sweden, and England accounted for 5, 2, 2, and 1. Among the top 10 institutions cited in the literature, the top 4 were from Sweden, followed by five institutions from the USA, and one from England. From this, we can see that academic institutions in the USA and Sweden have contributed the most to the research on SRT.

We ranked journals by the number of citations in SRT, which objectively reflects the importance of the literature published in the journal. *Science* ranked first with 11 064 citations, followed by *Cell*, *Nature*, *PNAS*, and *Nature Biotechnology*.

Among the top 10 authors in the number of publications, Lundeberg J from KTH Royal Institute of Technology in Sweden ranked first with 35 papers. Except for the sixth author Itzkovitz S from Israel, the remaining eight authors were all from Sweden and the USA. In terms of author collaboration, American researchers and Swedish researchers worked most closely. Among the top 10 authors in the co-cited analysis, except for the first from Sweden, and the sixth from Singapore, the remaining 8 are all from the USA. This further demonstrates the absolute leading position of the USA in the field of SRT research.

Research hotspots and frontiers

Through keyword co-occurrence analysis, we were able to discover current research hotspots and predict future development trends. Overall, there are mainly three aspects: the development of SRT itself, tumor-relevant research, and brain science.

Transcriptomics ranked first with 225 times. Spatially resolved transcriptomics, as the research object in this study, ranked second with 153 times. Single-cell RNA sequencing and RNA sequencing ranked fourth and fifth, respectively, with 85 and 78 times. It could be proved that SRT and single-cell RNA sequencing (scRNA-seq) are most tightly combined by quantitative methods. Moreover, this can be explained from a technical perspective. On one hand, cells' spatial information as well as their gene expression are inherently lost in single-cell transcriptomics which could be provided by SRT,

leading to new directions for leveraging spatial information to develop computational approaches for cell-cell communication inference and analysis[17–18]. On the other hand, current SRT approaches themselves cannot yet provide deep transcriptomic information on precisely localized single cells in tissue due to their low resolution and coverage[7,18]. Therefore, lots of research are based on the combination of SRT and scRNA-seq[19–20].

Keywords such as "laser capture microdissection" and "*in situ* hybridization (ISH)" occurred 16 and 14 times, both representing key technologies commonly used in SRT. ISH is the method of imaging-based single-cell genomics and transcriptomics[21]. This can provide high spatial resolution even to a subcellular scale, but often requires a priori selection of targets and high-sensitive single-molecule imaging systems, which can only be performed on fixed sections, making these methods less suited for high-throughput exploratory analyses[22–24]. Laser capture micro-dissection (LCM) is a technique in which a laser beam is used to cut out tissue regions identified under a microscope[21]. Microdissected samples are amenable to many low-input sequencing methods. Equipment for LCM is commercially available and accessible in many core facilities[6]. However, there are some limitations. Firstly, the tissue is removed from the surrounding spatial context and processed separately, hindering the ability to analyze gradients of gene expression and examine spatial relationships within intact sections[25]. Secondly, the sensitivity of LCM-based assays is limited by laser-induced degradation of nucleic acids, and the technical complexity of handling and preparing libraries for multiple microscopic samples is considerable[26]. Thus, researchers devote themselves to improving resolution and throughput. At the same time, a reduction in price and ease of operation are extremely desirable. Many novel methods have been developed for SRT, such as single-molecule fluorescence *in situ* hybridization (smFISH)[27], MERFISH[28–29], seqFISH[30–33], LCM-seq[34], slide-seq[35], and the 10x Genomics Visium platform[36].

In terms of the application of SRT, we could find its main applications through keywords such as tumor microenvironment (TME), tumor heterogeneity, Alzheimer's disease, immunotherapy, hippocampus, and breast cancer. In general, the main research targets are tumors and brain. Specifically, in terms of application to tumors, a limited amount of studies have been published on human intestinal development[37], breast cancer[22,38–40], gastric cancer[41], prostate cancer[42–43], lung adenocarcinoma[44], pancreatic ductal adenocarcinomas[45], hepatocellular carcinoma (HCC)[46], glioma[47], and ovarian carcinoma[48]. The occurrence and development of tumors depend on the TME, and heterogeneity is the main obstacle to effective and individualized tumor treatment[49–50]. Although heterogeneity was not among the top 20 keywords, it was also the keyword that appeared in these articles frequently[17,51]. As little was known about spatial-temporal molecular features of hypothalamic glial and neuronal development in humans, many researchers used SRT to explore brain, such as human hypothalamus development[52], human cortical sections analysis[53], Alzheimer's disease[54], mouse primary motor cortex[55–56], and postnatal mouse brain[57]. ***Fig. 5*** shows that tumor and brain research were both recent research hotspots.

Last but not least, considering the complexity and huge amount of information contained in this spatially resolved data format, technological advances have made it possible to measure spatially resolved gene expression at high throughput[58]. In keywords analysis, the keyword 'Bioinformatics' ranked sixteenth, further highlighting its importance in SRT. Navarro *et al*. developed ST Viewer, which allows real-time interaction, analysis, and visualization of Spatial Resolved Transcriptomics datasets through a seamless and smooth user interface[59]. A new analysis approach known as FISH Iterative Cell-Type assignment (FICT) can accurately identify cell types and sub-types, improving on expression-only methods and other methods proposed for clustering spatially resolved transcriptomics data[60]. A theoretical model *Sepal* seemed to be less informed by genes' expression levels and showed better time performance when run with multiple cores[61]. While these tools improve cell typing, they all share the problem of being specialized tools that require access to Linux command line terminals, programming expertise, and high-performance hardware[62]. Recently, Tiesmeyer *et al*. developed SSAM-lite, a tool that provides an easy-to-use graphical interface to perform rapid and segmentation-free cell-typing of SRT data in a web browser, so can be run locally and does not require computational experts or specialized hardware[62].

Future outlook and development trend

In the past, many researchers carried out a spatial transcriptional analysis of tissues without temporal dynamics. Recently, many studies have combined spatially resolved transcriptomics and temporal dynamics as spatiotemporal dynamics to conduct a more three-dimensional and comprehensive analysis of cells, tissues, and individuals[37,52,63–65]. This is not

only from the perspective of spatial structure but also from the perspective of temporal dynamics. It also helps for a more in-depth and accurate understanding of its development or the occurrence and progression of diseases. In addition to focusing on improving resolution and throughput, future development of SRT should also make it simpler, less time-consuming, more cost-effective, and easier to operate. On this basis, SRT should be promoted from the scientific research field to clinical application as soon as possible to make more accurate diagnoses and develop individualized treatments for patients.

Strengths and limitations

The present study comprehensively analyzed the global status and trends of SRT research using the scientific method of bibliometric analysis. We systematically searched the WoSCC and downloaded all relevant data as of 30 November 2022. Compared with traditional narrative reviews, bibliometric analysis provides a visualized, quantitative, and macrographic insight into current research hotspots and future research trends.

However, there were some limitations in our sutdy like other scientometric studies. Firstly, all publications were retrieved from WoSCC, while other large databases such as PubMed, Embase, and Scopus were excluded, which may lead to some bias in the present dataset. Despite this, we need to note that WoSCC is the most commonly applied tool for scientometric analyses[66]. Secondly, the study was completely composed of original articles and reviews, as books, data papers, conference abstracts, and other types of publications were not included in the collected dataset. For this reason, the data collected here may not represent the available literature thoroughly. Thirdly, recent publications, even when published in high-profile journals, typically had fewer citations than studies published several years ago. As such, recent publications were likely to have been underweighted in our study due to this time effect[67].

Conclusions

This study is the first bibliometric analysis of spatially resolved transcriptomics. We drew scientific maps of countries, institutions, authors, and co-occurrence keywords to determine the SRT research status quo, research trends, and research hotspots. In the research of SRT, the United States and Sweden are the two leading countries, and China and India are the largest contributors among developing countries. The largest contributions from research institutions also come from the United States and Sweden. The most influential magazine is *Science*. Lundeberg J is the most prolific author and Ståhl PL is the most co-cited author. From the perspective of keyword co-occurrence analysis, the development of SRT itself, tumor-relevant research, and brain science are the current research hotspots. The development of bioinformatics facilitates the analytical applications of SRT. The number of publications in this field continues to grow. However, there are still limited quantities of studies on diseases using SRT, so there is still a huge room for SRT to be developed and applied to disease research. SRT and temporal dynamics should be closely combined. The future development of SRT is not only aimed at achieving high throughput and high resolution, but also dedicated to making it cost-effective, simple, rapid, and easy to use. It is our hope that SRT can move from the realm of scientific research to clinical application as soon as possible, to provide accurate diagnoses and individualized treatment for patients.

Acknowledgments

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