Data Visualization Support for Tumor Boards and Clinical Oncology: Scoping Review

Dominik Boehm, Cosima Strantz, Arsenij Ustjanzew, Iryna Manuilova, Alexander Scheiter, Thomas Pauli, Nicole Hechtel, Niklas Reimer, Jan Christoph, Hauke Busch, Thomas Ganslandt, Philipp Unberath

Submitted to: Journal of Medical Internet Research
on: November 22, 2024

Table of Contents

Data Visualization Support for Tumor Boards and Clinical Oncology: Scoping Review

Dominik Boehm[1, 2]; Cosima Strantz[3] MSc; Arsenij Ustjanzew[4] MSc; Iryna Manuilova[5] MSc; Alexander Scheiter[6] Dr med; Thomas Pauli[7] Dr rer nat; Nicole Hechtel[8] Dr med; Niklas Reimer[9, 2] MSc; Jan Christoph[3, 5] Dr rer biol hum; Hauke Busch[9] Dr rer nat; Thomas Ganslandt[3] Dr med; Philipp Unberath[1, 10] Dr rer biol hum

[1]Medical Center for Information and Communication Technology Universitätsklinikum Erlangen Friedrich-Alexander-Universität Erlangen-Nürnberg Erlangen DE
[2]Chair of Medical Informatics Institute for Medical Informatics, Biometrics and Epidemiology Friedrich-Alexander-Universität Erlangen-Nürnberg Erlangen DE
[3]Institute of Medical Biostatistics, Epidemiology and Informatics (IMBEI) University Medical Center of the Johannes Gutenberg-University Mainz Mainz DE
[4]Junior Research Group (Bio-)Medical Data Science Faculty of Medicine Martin-Luther-University Halle-Wittenberg Halle DE
[5]Institute of Pathology University of Regensburg Regensburg DE
[6]Institute of Medical Bioinformatics and Systems Medicine Medical Center, Faculty of Medicine University of Freiburg Freiburg DE
[7]Peter L. Reichertz Institute for Medical Informatics University of Braunschweig - Institute of Technology and Hannover Medical School Hannover DE
[8]Institute for Systems Biology Lübeck Institute of Experimental Dermatology University of Luebeck Luebeck DE
[9]SRH Fürth University of Applied Sciences Fürth DE

Corresponding Author:
Dominik Boehm
Medical Center for Information and Communication Technology
Universitätsklinikum Erlangen
Friedrich-Alexander-Universität Erlangen-Nürnberg
Krankenhausstraße 12
Erlangen
DE

Abstract

Background: Complex and expanding data sets in clinical oncology applications require flexible and interactive visualization of patient data to provide physicians and other medical professionals with a maximum amount of information. In particular, interdisciplinary tumor conferences profit from customized tools to integrate, link, and visualize relevant data from all professions involved.

Objective: Our objective was to identify and present currently available data visualization tools for tumor boards and related areas. We not only want to provide an overview of the digital tools currently used in tumor board settings but also of the data they include, the respective visualization solutions, and their integration into hospital processes.

Methods: The scoping review is based on the Arksey and O'Malley scoping study framework. The following electronic databases were searched for articles: PubMed, Web of Knowledge, and SCOPUS. Articles were deemed eligible if published in English in the last ten years. Eligible articles were first deduplicated, followed by the screening of titles and abstracts. Second, a full-text screening was conducted to decide on article selection. A scoping review protocol was set up and published to prepare for the study, which can be accessed via the IRRID. The manuscript was written following the checklist “Preferred Reporting Items for Systematic Reviews and Meta-Analyses Extension for Scoping Reviews” (PRISMA-ScR).

Results: The review process started with 2049 articles, of which 1014 were included in the title-abstract screening. (112/2049, 5%) Publications were eligible for full-text screening, leading to (60/2049, 3%) Publications eligible for final inclusion. They covered 49 distinct visualization tools and applications. We discovered a variety of innovative visualization solutions, often driven by the complexity of *omics data. However, many projects remain unused and are mostly abandoned once the publications have been written and published.

Conclusions: There is a wide range of projects providing visualization solutions for tumor boards and clinical oncology

applications. Under the few tools that find their way into clinical routine settings, there are both commercial and academic solutions alike. While tables for a variety of data types remain the dominant visualization strategy, the complexity of omics data appears to be the driving force behind many visualization innovations in the area of tumor boards.

(JMIR Preprints 22/11/2024:69104)
DOI: https://doi.org/10.2196/preprints.69104

Preprint Settings

1) Would you like to publish your submitted manuscript as preprint?

✓ **Please make my preprint PDF available to anyone at any time (recommended).**
Please make my preprint PDF available only to logged-in users; I understand that my title and abstract will remain visible to all users.
Only make the preprint title and abstract visible.
No, I do not wish to publish my submitted manuscript as a preprint.

2) If accepted for publication in a JMIR journal, would you like the PDF to be visible to the public?

✓ **Yes, please make my accepted manuscript PDF available to anyone at any time (Recommended).**
Yes, but please make my accepted manuscript PDF available only to logged-in users; I understand that the title and abstract will remain v
Yes, but only make the title and abstract visible (see Important note, above). I understand that if I later pay to participate in <a href="http

Original Manuscript

Dominik Boehm[1, 2], Cosima Strantz[3], Arsenij Ustjanzew[4], Iryna Manuilova[5], Alexander Scheiter[6], Thomas Pauli[7], Nicole Hechtel[8], Niklas Reimer[9], Jan Christoph[3, 5], Hauke Busch[9], Thomas Ganslandt[2], Philipp Unberath[1, 10]

[1] Medical Center for Information and Communication Technology, Universitätsklinikum Erlangen, Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany

[2] Bavarian Cancer Research Center (BZKF)

[3] Chair of Medical Informatics, Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany

[4] Institute of Medical Biostatistics, Epidemiology and Informatics (IMBEI), University Medical Center of the Johannes Gutenberg-University Mainz, Mainz, Germany.

[5] Junior Research Group (Bio-)medical Data Science, Faculty of Medicine, Martin-Luther-University Halle-Wittenberg, Halle, Germany

[6] Institute of Pathology, University of Regensburg, Regensburg, Germany

[7] Institute of Medical Bioinformatics and Systems Medicine, Medical Center, Faculty of Medicine, University of Freiburg, Freiburg, Germany

[8] Hannover Medical School, Peter L. Reichertz Institute for Medical Informatics, Hannover, Germany

[9] Group for Medical Systems Biology, Lübeck Institute of Experimental Dermatology, University of Lübeck, Germany

[10] SRH Fürth University of Applied Sciences, Fürth, Germany

Corresponding Author:
Dominik Boehm
dominik.boehm@uk-erlangen.de

Review

Data Visualization Support for Tumor Boards and Clinical Oncology: Scoping Review

Abstract

Background: Complex and expanding data sets in clinical oncology applications require flexible and interactive visualization of patient data to provide physicians and other medical professionals with a maximum amount of information. In particular, interdisciplinary tumor conferences profit from customized tools to integrate, link, and visualize relevant data from all professions involved.
Objective: Our objective was to identify and present currently available data visualization tools for tumor boards and related areas. We not only want to provide an overview of the digital tools currently used in tumor board settings but also of the data they include, the respective visualization solutions, and their integration into hospital processes.
Methods: The scoping review is based on the Arksey and O'Malley scoping study framework. The following electronic databases were searched for articles: PubMed, Web of Knowledge, and SCOPUS. Articles were deemed eligible if published in English in the last ten years. Eligible articles were first deduplicated, followed by the screening of titles and abstracts. Second, a full-text screening was conducted to decide on article selection. A scoping review protocol was set up and published to prepare for the study, which can be accessed via the IRRID. The manuscript was written following the checklist “Preferred Reporting Items for Systematic Reviews and Meta-Analyses Extension for Scoping Reviews” (PRISMA-ScR).
Results: The review process started with 2049 articles, of which 1014 were included in the title-abstract screening. (112/2049, 5%) Publications were eligible for full-text screening, leading to (60/2049, 3%) Publications eligible for final inclusion. They covered 49 distinct visualization tools and applications. We discovered a variety of innovative visualization solutions, often driven by the complexity of *omics data. However, many projects remain unused and are mostly abandoned once the publications have been written and published.
Conclusions: There is a wide range of projects providing visualization solutions for tumor boards and clinical oncology applications. Under the few tools that find their way into clinical routine settings, there are both commercial and academic solutions alike. While tables for a variety of data types remain the dominant visualization strategy, the complexity of omics data appears to be the driving force behind many visualization innovations in the area of tumor boards.

International Registered Report Identifier (IRRID): DERR2-10.2196/53627

Keywords: clinical oncology; tumor board; cancer conference; multidisciplinary; visualization; software; scoping review; tumor.

Introduction

Background

Interventions by multidisciplinary teams, particularly through tumor boards or multidisciplinary cancer conferences (MCCs), have demonstrated substantial improvements in cancer care quality [1–3]. The challenge of visualizing complex, multimodal data that is continually expanding is especially notable in these multidisciplinary environments [4]. These data encompass a wide range from demographic details and laboratory findings to tumor imaging, therapeutic timelines, and genomic information, offering extensive possibilities for combined visualization and data aggregation. The critical need for digital tools and tailored visualization solutions becomes clear, given the stringent time limitations that are common in clinical oncology. Treatment decision periods are often constrained to 10 to 20 minutes per patient [5], underscoring the necessity for well-aggregated and annotated data that allows healthcare professionals to incorporate all pertinent details into their decision-making processes. Beyond the time constraints, the increasing complexity of patient data makes it difficult to fully understand a patient's health status without effective visualization support,

particularly when dealing with multiple data points along the patient's journey [6,7]. Although tools for visualizing such multimodal data do exist in these contexts [8–10], there is currently no comprehensive overview of the actively utilized and established visualization tools, as well as their distinct features on a global level.

The emergence and evolution of molecular tumor boards (MTBs) further highlight the need for advanced visualization tools. They require the integration of large amounts of genomic data with conventional clinical information and demand robust visualization tools to assist participating medical professionals in making informed treatment decisions efficiently [11,12]. With the shift toward virtual MTBs and an increase in outpatient referrals, the demographic of tumor board participants has broadened to include a more diverse group, encompassing various specialties and sometimes spanning different languages. This shift necessitates visualizations that are both intuitive and comprehensive, accommodating participants' varied levels of familiarity with each patient's history [13]. To address these needs, specialized software platforms such as cBioPortal [14–16], The Cancer Core Europe Molecular Tumor Board Portal [17], and Alteration annotations for Molecular tumor BoARds (AMBAR) [18] have been developed, providing detailed visual representations of genomic data in cancer samples.

In addition to these platforms, resources like OncoKB [19] and CIViC [20] have been established. These knowledge bases deliver structured and aggregated information concerning targeted therapies, which is crucial for maintaining consistency in therapeutic recommendations across tumor boards, especially for patients with rare cancers or unique mutation patterns [21]. Additionally, research indicates that variability in the tools and methodologies utilized can lead to inconsistencies in therapy recommendations [22], further underlining the need for standardization.

Due to the heterogeneous nature of data formats and application interfaces, integrating data from various sources to enable comprehensive visualization is a challenging task, often requiring custom extract, transform, and load (ETL) workflows to homogenize the data and convert them into a shared format [23]. Depending on the data concerned, this gets further complicated by data privacy regulations [24]. Initiatives like the Medical Informatics Initiative [25], the Bavarian Center for Cancer Research [26], and the German Network for Personalized Medicine [27] spearhead efforts in Germany to standardize data sets and processes to facilitate decision-making within the healthcare sector better. These initiatives are also investing resources to improve existing tools like cBioPortal, enhancing their capabilities to document and visualize therapeutic decisions during MTBs. These initiatives are also investing resources to improve existing tools like cBioPortal, enhancing their capabilities to document and visualize therapeutic decisions during MTBs [28,29].

Objectives

Given the described circumstances and the increasing complexity and volume of data in clinical oncology, there is a rising need for advanced visualization tools that effectively leverage these data for decision-making in tumor board settings. Integrating such software solutions into existing clinical workflows is challenging yet essential, as it ensures that data from various sources are readily accessible for effective use in tumor boards. This scoping review aims to explore and describe the available visualization support for MCCs, outline the key visualization strategies employed, and examine their accessibility as well as their integration into clinical processes. The goal is to provide a comprehensive overview of the current landscape and future directions of digital support tools in tumor board settings.

Methods

Design

This scoping review was conducted using the scoping study framework of Arksey and O'Malley as a methodological blueprint. Arksey and O'Malley describe a five-step model for the design of scoping studies: (1) identification of the research questions; (2) identification of relevant studies; (3) study selection; (4) data extraction and charting; and (5) collating, summarizing, and reporting the results. A scoping review protocol was created in preparation for the review, describing the study using these steps [30]. The following chapters will highlight any deviations from the described templates and processes.

Search Strategy

Our search strategy included the established electronic databases PubMed, Scopus, and Web of Knowledge. Individualized queries were designed, tested, and finally validated by a research librarian. The detailed query development is described in the corresponding scoping review protocol [31]. Additionally, the individual queries can be found in the appendix (Multimedia Appendix 1).

Eligibility and Screening

Before data extraction and analysis, all initially included articles were subjected to two rounds of screening. First, a title-abstract screening was performed by at least two blinded reviewers. In case of conflicting decisions, an additional reviewer was included for a majority decision [32]. Secondly, all articles were subjected to a full-text screening, examining the entire publication's contents for relevance to the review. Only articles published in English in the last 10 years were included. Since an initial search showed a large variety of target literature types, we decided not to use any further meta-inclusion or exclusion criteria to include all potentially relevant articles. The objective was to include articles in the review that provided information on the visualization solutions used in molecular and organ tumor boards. More specifically, they should be able to (partially) answer the overarching research question:

What are the key features of data visualization solutions used in molecular and organ tumor boards, and how are these elements integrated and used within the clinical setting?

The inclusion and exclusion criteria, summarized in Textbox 1, were defined in extensive discussions among all reviewers and pretested before each screening phase. All screening phases were conducted using Rayyan.ai [33] to structure and document inclusion decisions. Data extraction was then performed by a single reviewer per article.

Textbox 1. Inclusion and exclusion criteria for the scoping review.

- Inclusion criteria
  - Study types: any type of published peer-reviewed original research using qualitative, quantitative, or mixed methods
  - Time period: any article published between 2013 and 2023 (inclusive)
  - Language: English
  - Concept: any study that includes applications with visualization features in the area of molecular and organ tumor boards or in general
- Exclusion criteria
  - Time period: thematic article published before 2013
  - Language: studies published in other languages

Data Extraction and Analysis

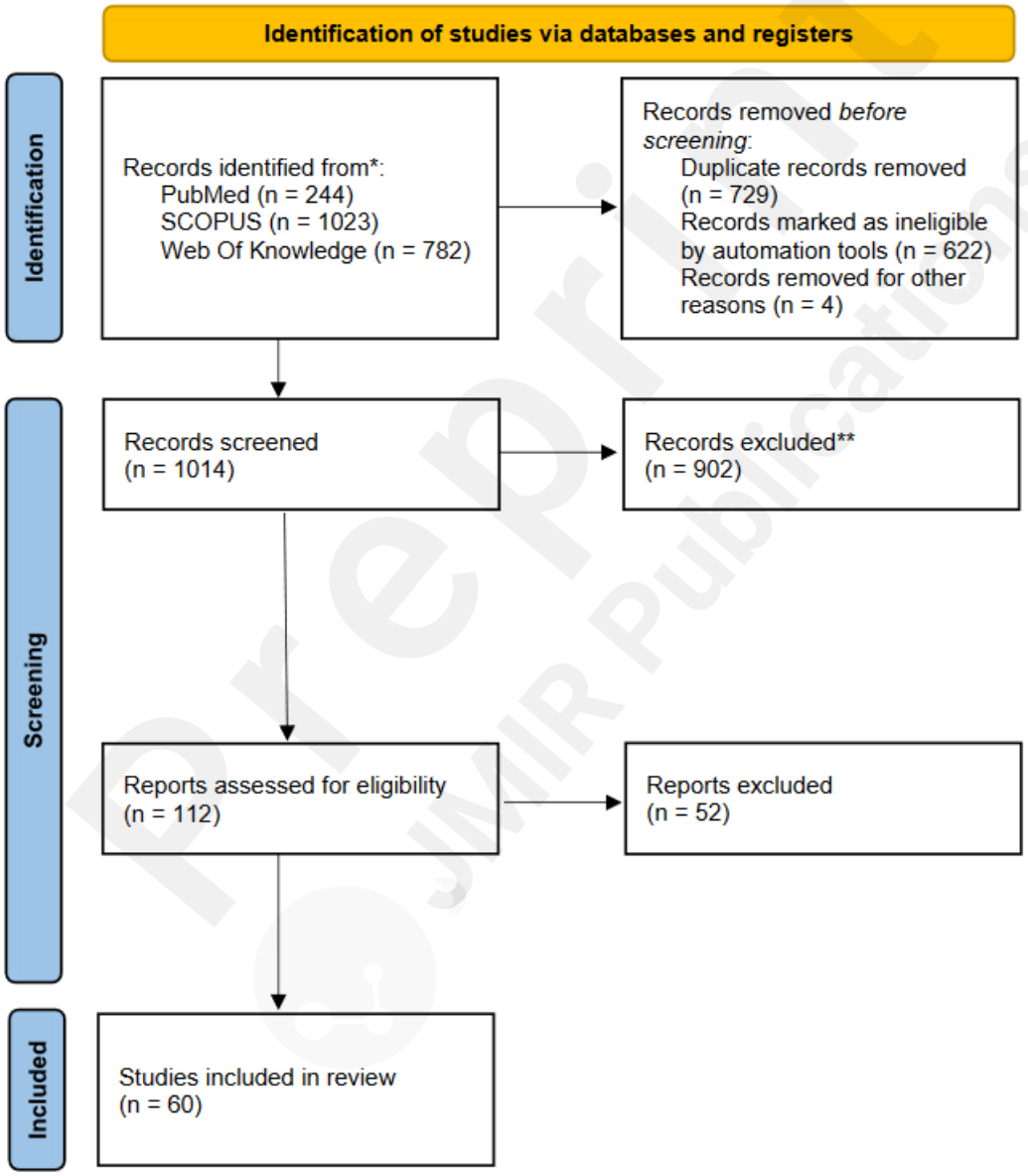
The data extraction template included meta information as well as data on the found data types and their respective visualization solutions. Identified tools were subjected to an additional manual literature search to close potential data gaps.

Ethical Considerations

Since our review did not involve human participants, no ethical approval was required for this study.

Results

Figure 1. PRISMA flowchart

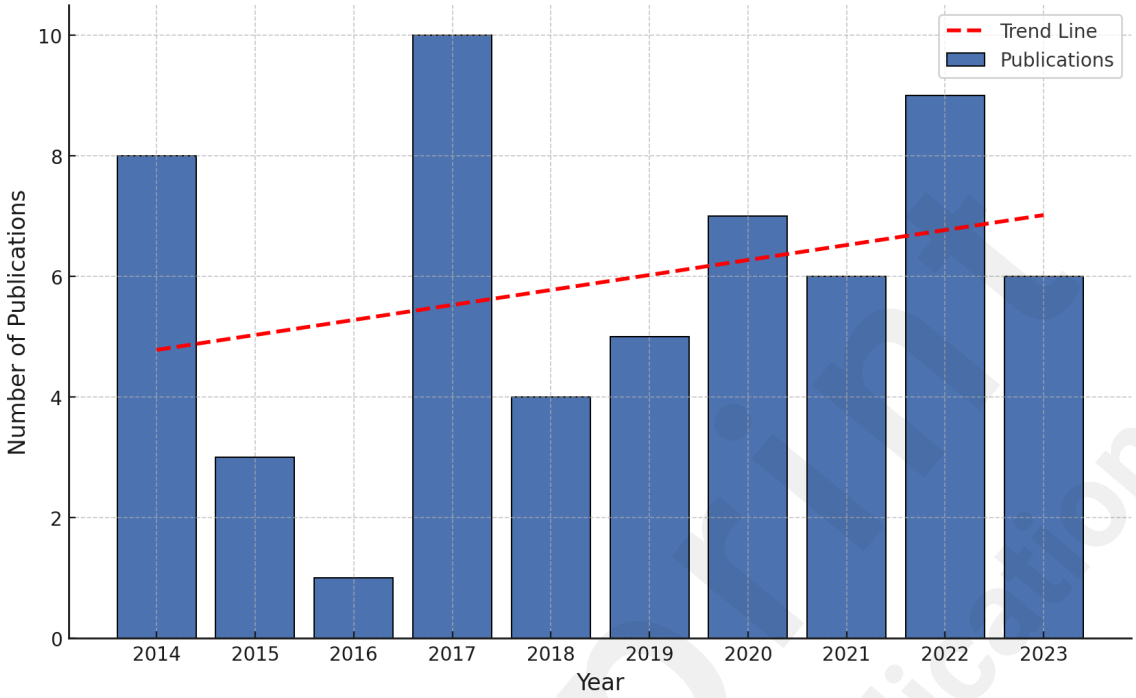


General Results

The review process started with 2049 articles, of which (1014/2049, 49%) were included in the title-abstract screening. (112/2049, 5%) Publications were deemed eligible for full-text screening, resulting in (60/2049, 3%) Publications suitable for final inclusion. The process has been

documented in a PRISMA flowchart (Figure 1). The included articles covered 49 distinct visualization tools and applications. The distribution of relevant publications over the last 10 years was relatively consistent, with a slight decline before 2016 and an overall upward trend (Figure 2).

Figure 2. Publication distribution by year.

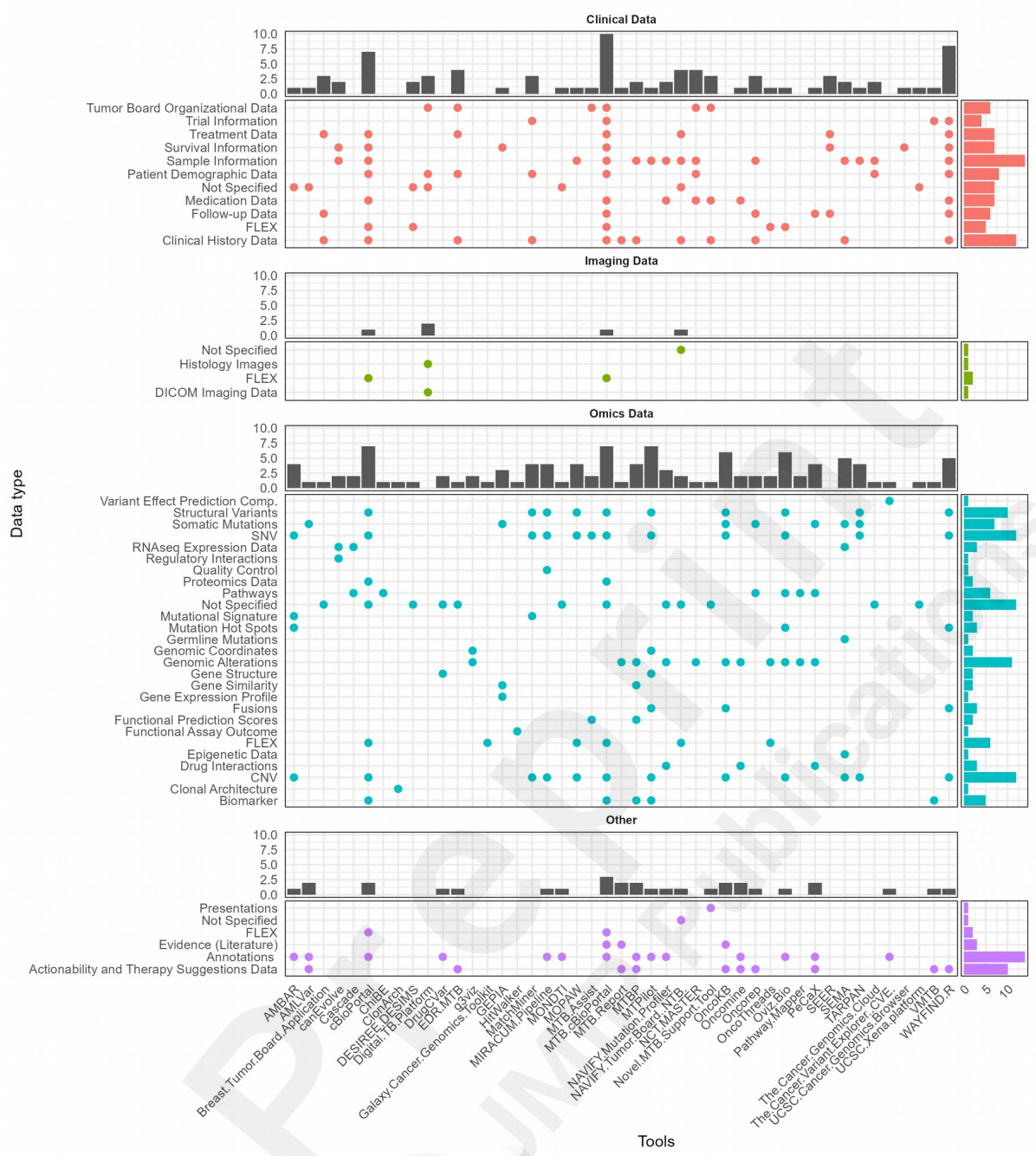


Overview: Data Types and Visualization Strategies

The majority of the identified visualization tools are capable of processing omics data (47/49, 96%), including primarily a variety of genomics data but also proteomics and transcriptomics data. The second most prevalent type of data is clinical data (31/49, 39%), followed by annotations with external data sources (19/49, 39%).

Of particular interest is the mapping between data types and visualization strategies (Figures 4,5,6), as it reveals the driving forces behind new developments, as well as implicit user requirements. While (interactive) tables remain the most frequently used form of visualization for MTB data, omics data, and multidisciplinary applications provide incentives for new visualization solutions as well as for the joint visualization of multiple data types. The following chapter presents the most common and/or noteworthy data types and visualization techniques. For a complete overview of all data types and visualization techniques, refer to the appendix (Appendix 1).

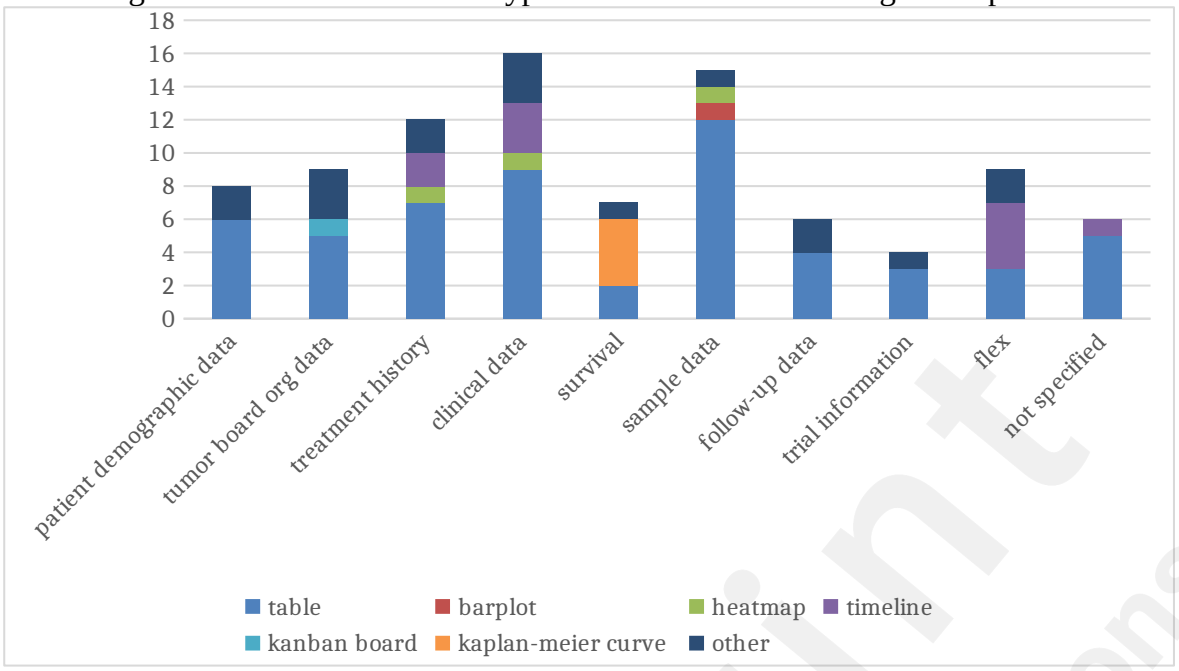
Figure 3. Data Type Overview. Filled fields represent the existence of visualization for the data type. FLEX rows represent generalized visualization solutions for the category that can be primarily used through user-defined data.



Patient-Related Data

The most commonly available and visualized patient-related data were clinical (16/49, 32%) and sample data (15/49, 31%) (Figure 4), with the diagnosis being the most prevalent. These were mostly presented in the form of tables summarizing existing clinical information. Treatment history was also readily available as well (12/49, 24%) and included information on medications and treatment metadata. Another notable visualization technique was timelines, often representing the treatment history. The remaining visualization types - e.g., heatmaps -primarily visualized the co-occurrence of clinical data with other data types, especially omics data (Figure 5). A small but significant number of tools also included organizational data of tumor boards, covering session information, participants, and resulting decisions. These tools were mostly designed with a focus on software support for tumor board meetings. A significant number of tools also enabled users to supply flexible custom data (9/49, 18%) for visualization. This is primarily available in applications that offer timeline visualization, like Oncothreads.

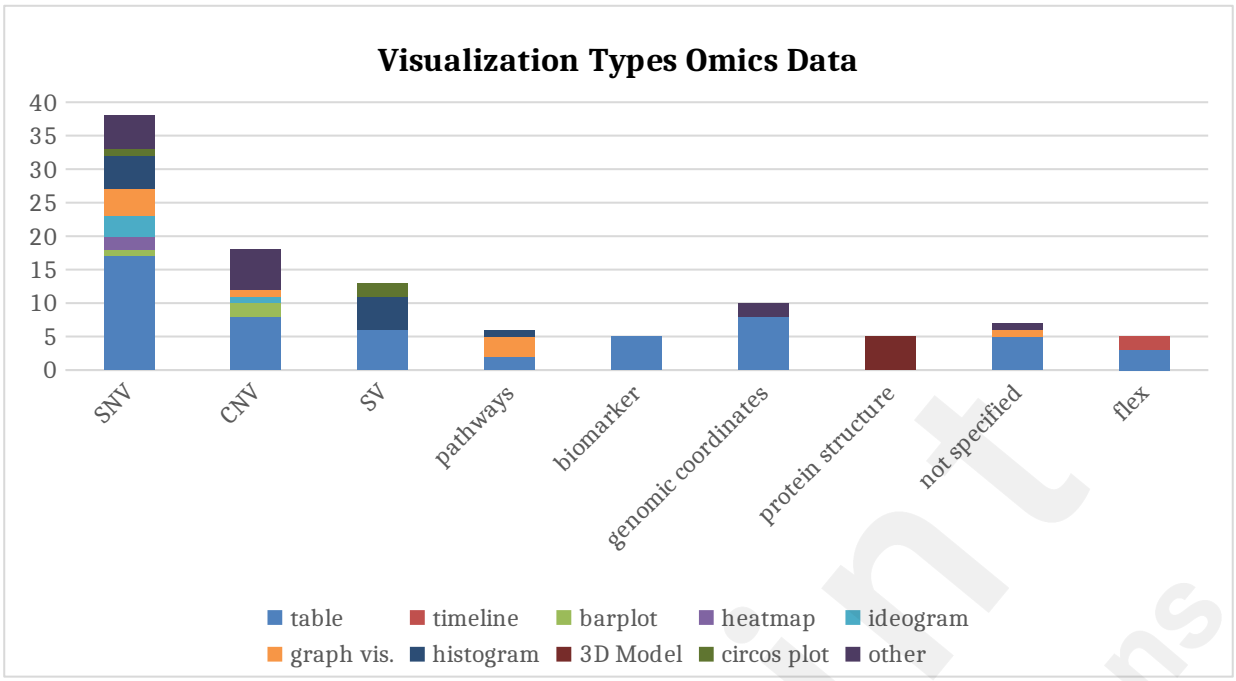
Figure 4. Distribution of data types and visualization strategies for patient-related data.



Omics data

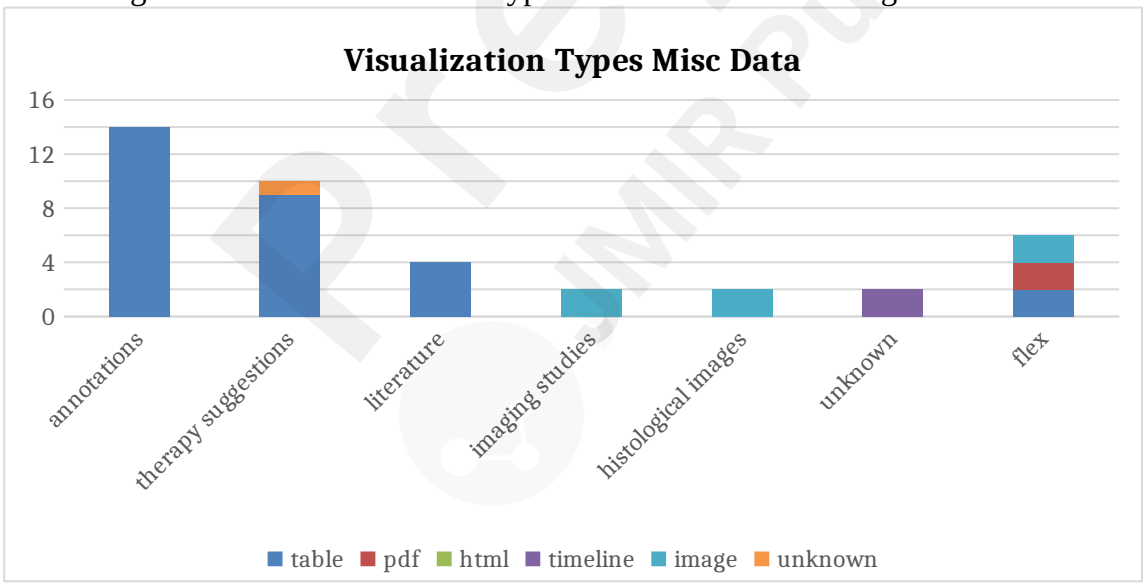
Omics data, but especially genomic data, is the most commonly available data type, with SNVs being visualized in about two-thirds of the applications discussed (38/49, 78%), followed by Copy Number Variations (CNVs) (18/49, 37%) and structural variants (13/49, 27%). Additionally, there was a considerable number of tools, like Pathway Mapper [36], that offered innovative visualization solutions for one specific data type.

Figure 5. Distribution of data types and visualization strategies for omics data.



The data is visualized using a variety of techniques (see Figure 5), with tables still being the most prevalent technique. In comparison to clinical data, however, signaling pathways are consistently presented using graphical visualization techniques. Protein structures are usually represented by 3D models. Some applications integrate omics data into their timeline features, depending on how much chronological data is available. In addition to patient-related clinical data and omics data, a range of other data types have been visualized (Figure 6).

Figure 6. Distribution of data types and visualization strategies for miscellaneous data.



These ranged from imaging studies to annotations from external data sources, with annotations (14/49, 29%) and therapy suggestions (10/49, 20%) being the most common. As expected, imaging studies and histological images are generally simply displayed without additional visualization functions.

Integration of Visualization Solutions into the Clinical Setting

In general, there is a lack of integration of standalone applications into digital hospital systems. However, some tools use semi-standardized data formats; only standards such as HL7-FHIR are

used.

Nevertheless, a lot of emphasis is placed on integration into clinical and research processes. Even though many tools primarily focus on research applications, those that aim to play an active role in the presentation or documentation of tumor board content, such as MTPpilot [9], MTB-cBioPortal [28], or the Digital TB Platform [34], propose solutions to some of the challenges faced by multidisciplinary conferences. These applications also tended to use structured evaluations to ensure the quality and process enhancements of the developed tools.

Accessibility

Most applications were available with open-source access (21/49, 43%). Often overlapping with this group, several tools were also accessible in a container format (9/49, 18%). This almost exclusively refers to the availability of Docker containers. Web applications (12/49, 24%) were also quite common. For a similar number of tools, there was no information available, or it was not accessible (12/49, 24%). There were also a small number of commercial tools (3/49, 6%), namely Navify Tumor Board [35], Navify Mutation Profiler [36] , and Wayfind-R [37], that were part of academic publications.

Existing Usage in Hospitals

A smaller proportion of the described visualization tools (8/49, 16%) are already established in clinical routine. For example, the MTB-cBioPortal and MTBP [38]. Although there are additional solutions, including canEvolve [39] and TARPAN [40] (4/49, 8%), that are used exclusively in hospital research, there is no documentation of actual clinical implementation for the majority (37/49, 75%).

Systematic Evaluation

About one-third of the identified tools were systematically evaluated in some form (16/49, 33%). However, the quality and quantity of the evaluations were very heterogeneous. While the systematic evaluation was the focus of some articles covering several different tumor boards and types of cancer, other publications focused on different topics. However, all articles included in the group of systematic evaluations at least conducted structured interviews with users.

Discussion

Principal Results

The results of this scoping review show the key aspects of data visualization solutions in the realm of tumor boards and clinical oncology. We were able to extract 60 relevant publications from the body of literature, in which 49 distinct tools and applications were discussed. Over the past 10 years, there has been substantial and consistent work on visualization issues, especially driven by growing datasets and novel data types in omics applications.

This is also reflected in the distribution of visualization types by data type (Figures 3, 5, 7) as well. There is a significant gap between the complexity of visualization for omics data and all other data types. In this article, we can only speculate as to why this is the case since there are numerous and diverse drivers for innovation in the field of visualization [41]. We assume that highly complex biomedical information – such as omics data - is understandable to medical professionals in their field even without visualization aids. In contrast, however, there is a need for additional visualization solutions to increase the ability to transfer information quickly so that a multidisciplinary team can

draw reliable conclusions based on this data, especially in a limited time frame.

Another interesting observation is the lack of innovation when it comes to clinical data. While visualization techniques for other data are rather widely used, clinical data is almost exclusively communicated in the form of tables. This may be for several reasons. Firstly, this is perhaps the optimal form of visualization for most applications. However, it could also reflect a resistance to change or a lack of awareness of alternative, more dynamic visualization methods that could enhance data interpretation and decision-making or interactivity of table components, for example, AMLVaran [42]. However, interactivity is not limited to table components offering additional information on hovering or using basic search functions. Even complex visualization techniques such as phylogenetic trees used by clonarchs [43] to visualize the phylogenetic similarity between clones deploy interactivity to enable the user to select which data to visualize and to focus on specific relationships or data features.

One of the key accessibility issues faced by many tools is the transformation from research projects into routine applications. This requires constant maintenance and, therefore, continuous funding. Promising projects like MAGI[44] are published and, at some point, no longer receive updates. This unfortunate circumstance presents a resource problem, as often applications are developed as prototypes without the extensive design and planning that is required to create maintainable software. While this is unavoidable to some extent, these issues can be mitigated by creating reusable software and making it accessible via an API or as a module that may be integrated into or with other projects. The feasibility of this approach is evident when looking at applications such as cBioPortal that incorporate and employ several tools that supply visualization features for specific tasks.

Of special interest to us were potential visualization solutions for patient-reported outcome measures (PROMs) and questionnaires in general. However, unfortunately, no such visualization strategies were described. We assume this is primarily due to a general lack of data, as follow-up information is generally difficult to obtain, and digital representation of PROMs outside of research settings is currently rare.

Limitations

The described review process and its findings have a few key limitations. Firstly, there is a dependency on academic publications covering the visualization solutions we aimed to include. This means that commercial solutions that might offer important insights and exist may be overlooked if they haven’t been mentioned in a research article. In general, commercial solutions are a lot more restrictive regarding the amount of publicly available information. Secondly, the quality of information contained in source publications varied wildly. Visualization features are often described only briefly or as a side note. While it is not feasible to describe every reaction to a mouse click, the discussion of visualization and UI capabilities is often replaced by a single screenshot. This is unfortunate as these components play a key role in the usability of innovative applications and are a necessity when it comes to user acceptance. Thirdly, due to the often-experimental nature of (molecular) tumor boards, some tools are included in this review that reside on the boundary between biomedical research and clinical application. Nevertheless, their potential ability to communicate complex information efficiently, especially in the field of omics, was deemed important by the research team. Given that tumor boards are multidisciplinary conferences that require all participants to comprehend the information provided, strong visualization supporting the explanation of – for example – relevant pathways and other disease mechanics is essential. Lastly, visualization and UI components are, in turn, highly flexible and, therefore, heterogeneous. Due to this, comparing different tools requires a certain degree of generalization, which may affect the grade of detail on the individual tool level. That said, we consider this a necessary step to offer a relevant overview of the

current state of visualization solutions for tumor boards and clinical oncology.

Comparison with Prior Work

A Narrative Review by Abudiyab and Alanazi explores the role of data visualization techniques in healthcare, focusing on their application, benefits, and future directions. Data visualization encompasses various forms like graphs, charts, and diagrams, aiding healthcare providers in understanding trends and making informed decisions. The review employs a descriptive analysis methodology, sourcing articles from databases like PubMed and Google Scholar. Visualization techniques are crucial in modern healthcare due to the increasing volume and complexity of data. As defined by Gartner (2021), interactive visualization can be understood as the manipulation of graphical information through color, brightness, movement, and geometry to elevate the meaning of the data presented. Historical context highlights Florence Nightingale's pioneering use of visualization for healthcare data in the 19th century. The review underscores several benefits, including improved patient care, disease trend recognition, simplified data presentation, accelerated performance, and error detection.

Scheer et al. conducted a scoping review of visualization solutions with a focus on time-oriented data. Information visualization and visual analytics simplify complex time-oriented patient data, enabling focus on underlying patterns. This review aims to identify visualization techniques for time-oriented healthcare data, facilitating patient comparison. Employing the PRISMA-ScR checklist, 22 articles were selected from 249 screened, focusing on medical context, objectives, data types, and visualization techniques. Published between 2003 and 2019, these articles primarily focused on clinical research, utilizing various visualization methods such as timelines, temporal line charts, histograms, and scatterplots. These systems effectively simplify complexity through visualization and support diverse medical objectives, delineating single patients, multiple patients, and cohorts. Cohorts are typically visualized in condensed form, while individual patient visualization tends to provide finer details. All systems enable viewing and comparing patient data, although explicit comparison between single patients and cohorts is limited. Despite primarily using basic visualization techniques, some systems employ new visualizations customized to specific tasks. Overall, the comparison of measurements between single patients and cohorts requires further systematic research and exploration in a design space [45].

O’Donoghue et al. focus on Visualization of Biomedical Data. The visualized data spans multiple biomedical areas, such as genomics, epigenetics, protein structures, cellular processes, and molecular interactions. This includes three-dimensional genomics, single-cell RNA sequencing, protein structure, phosphoproteomics, and metagenomics. Data is visualized through tailored visualizations integrating various data sets with supporting context to make the visualizations comprehensible to peers in the field. Techniques include the use of high data density displays, color maps designed to reflect true data patterns, and the avoidance of poor practices like rainbow color maps. Tools and methods like parallel coordinate plots, heat maps, and three-dimensional visualization techniques are used based on the type of data. Visualization methods are used to help address diagnostic errors, which often arise from improper cognitive processing of visual data, especially in visually intensive fields like radiology. The document suggests that better visualization practices could significantly reduce misdiagnoses, indicating the importance of these tools in clinical settings. While there are many powerful visualization tools available, they are underutilized in biomedical research. This underutilization could be due to a lack of awareness or training on how to effectively use these advanced tools. It points out the need for improved education and resources to make these tools more accessible and effectively used by more researchers and clinicians. It's suggested that visualization methods are currently not as widely used as they could be in hospitals, especially given their potential to reduce diagnostic errors [11].

Conclusions

The scoping review reveals that while numerous data visualization tools have been developed for tumor boards, many of them are either not adopted into routine practice or remain in the research phase. Omics data, particularly genomic information, is a major driver behind visualization innovation, yet the integration of these solutions into clinical workflows is often hindered by technical and organizational barriers. Tables remain a primary tool for visualizing clinical data, but there is potential for greater use of interactive and integrative visualization techniques. Moving forward, improving the accessibility and clinical integration of these tools, particularly through standardization and user-centered design, is crucial to ensuring their widespread adoption and enhancing multidisciplinary decision-making in oncology settings.

Acknowledgments

This work was funded by the German Federal Ministry for Education and Research through the PM4Onco project (01ZZ2322S, 01ZZ2322N, 01ZZ2322R, 01ZZ2322Q, 01ZZ2322A), and by the Bavarian Cancer Research Center (BZKF). This work was performed in (partial) fulfillment of the requirements for obtaining the degree “Dr. rer. biol. hum.” at the Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU).

Conflicts of Interest

None declared.

Abbreviations

MTB: molecular tumor board
MCC: multidisciplinary cancer conference
PRISMA-ScR: preferred reporting items for systematic reviews and meta-analyses extension for scoping reviews
ETL: extract-transform-load
API: application programming interface
UI: user interface

References

1. Di Pilla A, Cozzolino MR, Mannocci A, Carini E, Spina F, Castrini F, Grieco A, Messina R, Damiani G, Specchia ML. The Impact of Tumor Boards on Breast Cancer Care: Evidence from a Systematic Literature Review and Meta-Analysis. Int J Environ Res Public Health Switzerland; 2022 Nov 14;19(22). PMID:36429708

2. Lamb BW, Green JSA, Benn J, Brown KF, Vincent CA, Sevdalis N. Improving Decision Making in Multidisciplinary Tumor Boards: Prospective Longitudinal Evaluation of a Multicomponent Intervention for 1,421 Patients. J Am Coll Surg 2013 Sep;217(3):412. doi: 10.1016/j.jamcollsurg.2013.04.035

3. Specchia ML, Frisicale EM, Carini E, Di Pilla A, Cappa D, Barbara A, Ricciardi W, Damiani G. The impact of tumor board on cancer care: evidence from an umbrella review. BMC Health

Serv Res 2020 Jan 31;20(1):73. doi: 10.1186/s12913-020-4930-3

4. Luchini C, Lawlor RT, Milella M, Scarpa A. Molecular Tumor Boards in Clinical Practice. Trends Cancer Elsevier; 2020 Sep 1;6(9):738–744. PMID:32517959

5. Larburu N, Muro N, Arrue M, Álvarez R, Kerexeta J. DESIREE - a web-based software ecosystem for the personalized, collaborative and multidisciplinary management of primary breast cancer. 2018 IEEE 20th Int Conf E-Health Netw Appl Serv Heal 2018. p. 1–2. doi: 10.1109/HealthCom.2018.8531099

6. Wanderer JP, Nelson SE, Ehrenfeld JM, Monahan S, Park S. Clinical Data Visualization: The Current State and Future Needs. J Med Syst 2016 Oct 27;40(12):275. doi: 10.1007/s10916-016-0643-x

7. Ledesma A, Bidargaddi N, Strobel J, Schrader G, Nieminen H, Korhonen I, Ermes M. Health timeline: an insight-based study of a timeline visualization of clinical data. BMC Med Inform Decis Mak 2019 Aug 22;19(1):170. doi: 10.1186/s12911-019-0885-x

8. Lawonn K, Smit N n., Bühler K, Preim B. A Survey on Multimodal Medical Data Visualization. Comput Graph Forum 2018;37(1):413–438. doi: 10.1111/cgf.13306

9. Kahraman A, Arnold FM, Hanimann J, Nowak M, Pauli C, Britschgi C, Moch H, Zoche M. MTPpilot: An Interactive Software for Visualization of Next-Generation Sequencing Results in Molecular Tumor Boards. JCO Clin Cancer Inform Wolters Kluwer; 2022 Dec; (6):e2200032. doi: 10.1200/CCI.22.00032

10. Canuel V, Rance B, Avillach P, Degoulet P, Burgun A. Translational research platforms integrating clinical and omics data: a review of publicly available solutions. Brief Bioinform 2015 Mar 1;16(2):280–290. doi: 10.1093/bib/bbu006

11. O'Donoghue SI, Baldi BF, Clark SJ, Darling AE, Hogan JM, Kaur S, Maier-Hein L, McCarthy DJ, Moore WJ, Stenau E, Swedlow JR, Vuong J, Procter JB. Visualization of Biomedical Data. Annu Rev Biomed Data Sci 2018;1(1):275–304. doi: 10.1146/annurev-biodatasci-080917-013424

12. Schapranow M-P, Borchert F, Bougatf N, Hund H, Eils R. Software-Tool Support for Collaborative, Virtual, Multi-Site Molecular Tumor Boards. Sn Comput Sci 2023;4(4):358. PMID:37131499

13. Pishvaian MJ, Blais EM, Bender RJ, Rao S, Boca SM, Chung V, Hendifar AE, Mikhail S, Sohal DPS, Pohlmann PR, Moore KN, He K, Monk BJ, Coleman RL, Herzog TJ, Halverson DD, DeArbeloa P, Petricoin EF, Madhavan S. A virtual molecular tumor board to improve efficiency and scalability of delivering precision oncology to physicians and their patients. JAMIA Open 2019 Dec;2(4):505–515. PMID:32025647

14. Gao J, Aksoy BA, Dogrusoz U, Dresdner G, Gross B, Sumer SO, Sun Y, Jacobsen A, Sinha R, Larsson E, Cerami E, Sander C, Schultz N. Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. Sci Signal 2013 Apr 2;6(269):pl1. PMID:23550210

15. de Bruijn I, Kundra R, Mastrogiacomo B, Tran TN, Sikina L, Mazor T, Li X, Ochoa A, Zhao G, Lai B, Abeshouse A, Baiceanu D, Ciftci E, Dogrusoz U, Dufilie A, Erkoc Z, Garcia Lara E, Fu Z,

Gross BE, Haynes CD, Heath A, Higgins DM, Jagannathan P, Kalletla K, Kumari P, Lindsay JR, Lisman A, Leenknegt B, Lukasse P, Madala D, Madupuri R, van Nierop P, Plantalech O, Quach J, Resnick A, Rodenburg SYA, Satravada BA, Schaeffer F, Sheridan R, Singh J, Sirohi R, Sumer SO, van Hagen S, Wang A, Wilson M, Zhang H, Zhu K, Rusk N, Brown S, Lavery JA, Panageas KS, Rudolph JE, LeNoue-Newton ML, Warner JL, Guo X, Hunter-Zinck H, Yu TV, Pillai S, Nichols C, Gardos SM, Philip J, Bpc Core Team G, Project Genie Consortium A, Kehl KL, Riely GJ, Schrag D, Lee J, Fiandalo MV, Sweeney SM, Pugh TJ, Sander C, Cerami E, Gao J, Schultz N. Analysis and Visualization of Longitudinal Genomic and Clinical Data from the AACR Project GENIE Biopharma Collaborative in cBioPortal. Cancer Res 2023 Sep 5; PMID:37668528

16. Cerami E, Gao J, Dogrusoz U, Gross BE, Sumer SO, Aksoy BA, Jacobsen A, Byrne CJ, Heuer ML, Larsson E, Antipin Y, Reva B, Goldberg AP, Sander C, Schultz N. The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. Cancer Discov 2012 May;2(5):401–404. PMID:22588877

17. Tamborero D, Dienstmann R, Rachid MH, Boekel J, Baird R, Braña I, De Petris L, Yachnin J, Massard C, Opdam FL, Schlenk R, Vernieri C, Garralda E, Masucci M, Villalobos X, Chavarria E, Calvo F, Fröhling S, Eggermont A, Apolone G, Voest EE, Caldas C, Tabernero J, Ernberg I, Rodon J, Lehtiö J. Support systems to guide clinical decision-making in precision oncology: The Cancer Core Europe Molecular Tumor Board Portal. Nat Med Nature Publishing Group; 2020 Jul;26(7):992–994. doi: 10.1038/s41591-020-0969-2

18. Fürstberger A, Ikonomi N, Kestler AMR, Marienfeld R, Schwab JD, Kuhn P, Seufferlein T, Kestler HA. AMBAR - Interactive Alteration annotations for molecular tumor boards. Comput Methods Programs Biomed 2023 Oct;240:107697. PMID:37441893

19. Chakravarty D, Gao J, Phillips S, Kundra R, Zhang H, Wang J, Rudolph JE, Yaeger R, Soumerai T, Nissan MH, Chang MT, Chandarlapaty S, Traina TA, Paik PK, Ho AL, Hantash FM, Grupe A, Baxi SS, Callahan MK, Snyder A, Chi P, Danila DC, Gounder M, Harding JJ, Hellmann MD, Iyer G, Janjigian YY, Kaley T, Levine DA, Lowery M, Omuro A, Postow MA, Rathkopf D, Shoushtari AN, Shukla N, Voss MH, Paraiso E, Zehir A, Berger MF, Taylor BS, Saltz LB, Riely GJ, Ladanyi M, Hyman DM, Baselga J, Sabbatini P, Solit DB, Schultz N. OncoKB: A Precision Oncology Knowledge Base. JCO Precis Oncol Wolters Kluwer; 2017 Nov;(1):1–16. doi: 10.1200/PO.17.00011

20. Griffith M, Spies NC, Krysiak K, McMichael JF, Coffman AC, Danos AM, Ainscough BJ, Ramirez CA, Rieke DT, Kujan L, Barnell EK, Wagner AH, Skidmore ZL, Wollam A, Liu CJ, Jones MR, Bilski RL, Lesurf R, Feng Y-Y, Shah NM, Bonakdar M, Trani L, Matlock M, Ramu A, Campbell KM, Spies GC, Graubert AP, Gangavarapu K, Eldred JM, Larson DE, Walker JR, Good BM, Wu C, Su AI, Dienstmann R, Margolin AA, Tamborero D, Lopez-Bigas N, Jones SJM, Bose R, Spencer DH, Wartman LD, Wilson RK, Mardis ER, Griffith OL. CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nat Genet 2017 Jan 31;49(2):170–174. PMID:28138153

21. Koopman B, Groen HJM, Ligtenberg MJL, Grünberg K, Monkhorst K, de Langen AJ, Boelens MC, Paats MS, von der Thüsen JH, Dinjens WNM, Solleveld N, van Wezel T, Gelderblom H, Hendriks LE, Speel EM, Theunissen TE, Kroeze LI, Mehra N, Piet B, van der Wekken AJ, ter Elst A, Timens W, Willems SM, Meijers RWJ, de Leng WWJ, van Lindert ASR, Radonic T, Hashemi SMS, Heideman DAM, Schuuring E, van Kempen LC. Multicenter Comparison of Molecular Tumor Boards in The Netherlands: Definition, Composition, Methods, and

Targeted Therapy Recommendations. The Oncologist 2021 Aug;26(8):e1347–e1358. PMID:33111480

22. Rieke DT, Lamping M, Schuh M, Le Tourneau C, Basté N, Burkard ME, Metzeler KH, Leyvraz S, Keilholz U. Comparison of Treatment Recommendations by Molecular Tumor Boards Worldwide. JCO Precis Oncol Wolters Kluwer; 2018 Dec;(2):1–14. doi: 10.1200/PO.18.00098

23. Cheng KY, Pazmino S, Schreiweis B. ETL Processes for Integrating Healthcare Data - Tools and Architecture Patterns. Stud Health Technol Inform 2022 Nov 3;299:151–156. PMID:36325856

24. Molnár-Gábor F, Sellner J, Pagil S, Slokenberga S, Tzortzatou-Nanopoulou O, Nyström K. Harmonization after the GDPR? Divergences in the rules for genetic and health data sharing in four member states and ways to overcome them by EU measures: Insights from Germany, Greece, Latvia and Sweden. Semin Cancer Biol 2022 Sep 1;84:271–283. doi: 10.1016/j.semcancer.2021.12.001

25. Semler S, Wissing F, Heyder R. German Medical Informatics Initiative: A National Approach to Integrating Health Data from Patient Care and Medical Research. Methods Inf Med 2018 Jul;57(S 01):e50–e56. doi: 10.3414/ME18-03-0003

26. Arbeitsgruppe Molekulares Tumorboard / Molekulare Medizin (MOLTB) | BZKF. Available from: https://bzkf.de/arbeitsgruppe-molekulares-tumorboard-molekulare-medizin-moltb/ [accessed Mar 27, 2023]

27. Medizin dnpm | DN für P. Über das DNPM. dnpm. Available from: https://dnpm.de/de/ueber-uns/ [accessed Mar 27, 2023]

28. Reimer N, Unberath P, Busch H, Börries M, Metzger P, Ustjanzew A, Renner C, Prokosch H-U, Christoph J. Challenges and Experiences Extending the cBioPortal for Cancer Genomics to a Molecular Tumor Board Platform. Stud Health Technol Inform 2021 Nov 18;287:139–143. PMID:34795098

29. Reimer N, Unberath P, Busch H, Ingenerf J. FhirSpark - Implementing a Mediation Layer to Bring FHIR to the cBioPortal for Cancer Genomics. Stud Health Technol Inform 2021 May 27;281:303–307. PMID:34042754

30. Arksey H, O'Malley L. Scoping studies: towards a methodological framework. Int J Soc Res Methodol Routledge; 2005 Feb 1;8(1):19–32. doi: 10.1080/1364557032000119616

31. Boehm D, Strantz C, Christoph J, Busch H, Ganslandt T, Unberath P. Data Visualization Support for Tumor Boards and Clinical Oncology: Protocol for a Scoping Review. JMIR Res Protoc 2024 Mar 5;13:e53627. PMID:38441925

32. von Elm E, Schreiber G, Haupt CC. Methodische Anleitung für Scoping Reviews (JBI-Methodologie). Z Für Evidenz Fortbild Qual Im Gesundheitswesen 2019 Jun 1;143:1–7. doi: 10.1016/j.zefq.2019.05.004

33. Ouzzani M, Hammady H, Fedorowicz Z, Elmagarmid A. Rayyan—a web and mobile app for systematic reviews. Syst Rev 2016;5(1):210. doi: 10.1186/s13643-016-0384-4

34. Nobori A, Jumniensuk C, Chen X, Enzmann D, Dry S, Nelson S, Arnold CW. Electronic Health Record-Integrated Tumor Board Application to Save Preparation Time and Reduce Errors. JCO Clin Cancer Inform 2022 Jan;6:e2100142. PMID:35025671

35. Hammer RD, Fowler D, Sheets LR, Siadimas A, Guo C, Prime MS. A digital tumor board solution impacts case discussion time and postponement of cases in tumor boards. Health Technol 2021 May 1;11(3):525–533. doi: 10.1007/s12553-021-00533-x

36. Yaung SJ, Krishna S, Xi L, Ju C, Palma JF, Schmid M. Assessment of a Highly Curated Somatic Oncology Database to Aid in the Interpretation of Clinically Important Variants in Next-Generation Sequencing Results. J Mol Diagn JMD 2020 Nov;22(11):1356–1366. PMID:32961319

37. Le Tourneau C, Perret C, Hackshaw A, Blay J-Y, Nabholz C, Geissler J, Do T, von Meyenn M, Dienstmann R. An Approach to Solving the Complex Clinicogenomic Data Landscape in Precision Oncology: Learnings From the Design of WAYFIND-R, a Global Precision Oncology Registry. JCO Precis Oncol 2022 Jul;6:e2200019. PMID:35939770

38. Tamborero D, Dienstmann R, Rachid MH, Boekel J, Lopez-Fernandez A, Jonsson M, Razzak A, Braña I, De Petris L, Yachnin J, Baird RD, Loriot Y, Massard C, Martin-Romano P, Opdam F, Schlenk RF, Vernieri C, Masucci M, Villalobos X, Chavarria E, Cancer Core Europe consortium, Balmaña J, Apolone G, Caldas C, Bergh J, Ernberg I, Fröhling S, Garralda E, Karlsson C, Tabernero J, Voest E, Rodon J, Lehtiö J. The Molecular Tumor Board Portal supports clinical decisions and automated reporting for precision oncology. Nat Cancer 2022 Feb;3(2):251–261. PMID:35221333

39. Samur MK, Yan Z, Wang X, Cao Q, Munshi NC, Li C, Shah PK. canEvolve: A Web Portal for Integrative Oncogenomics. PLOS ONE Public Library of Science; 2013 Feb 13;8(2):e56228. doi: 10.1371/journal.pone.0056228

40. Ashby C, Rutherford M, Bauer MA, Peterson EA, Wang Y, Boyle EM, Wardell CP, Walker BA. TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. BMC Bioinformatics 2020 Apr 15;21(1):144. PMID:32293247

41. Streeb D, El-Assady M, Keim DA, Chen M. Why Visualize? Untangling a Large Network of Arguments. IEEE Trans Vis Comput Graph 2021 Mar;27(3):2220–2236. doi: 10.1109/TVCG.2019.2940026

42. Wünsch C, Banck H, Müller-Tidow C, Dugas M. AMLVaran: a software approach to implement variant analysis of targeted NGS sequencing data in an oncological care setting. BMC Med Genomics 2020 Feb 4;13(1):17. doi: 10.1186/s12920-020-0668-3

43. Wu J, El-Kebir M. ClonArch: visualizing the spatial clonal architecture of tumors. Bioinformatics 2020 Jul 1;36(Supplement_1):i161–i168. doi: 10.1093/bioinformatics/btaa471

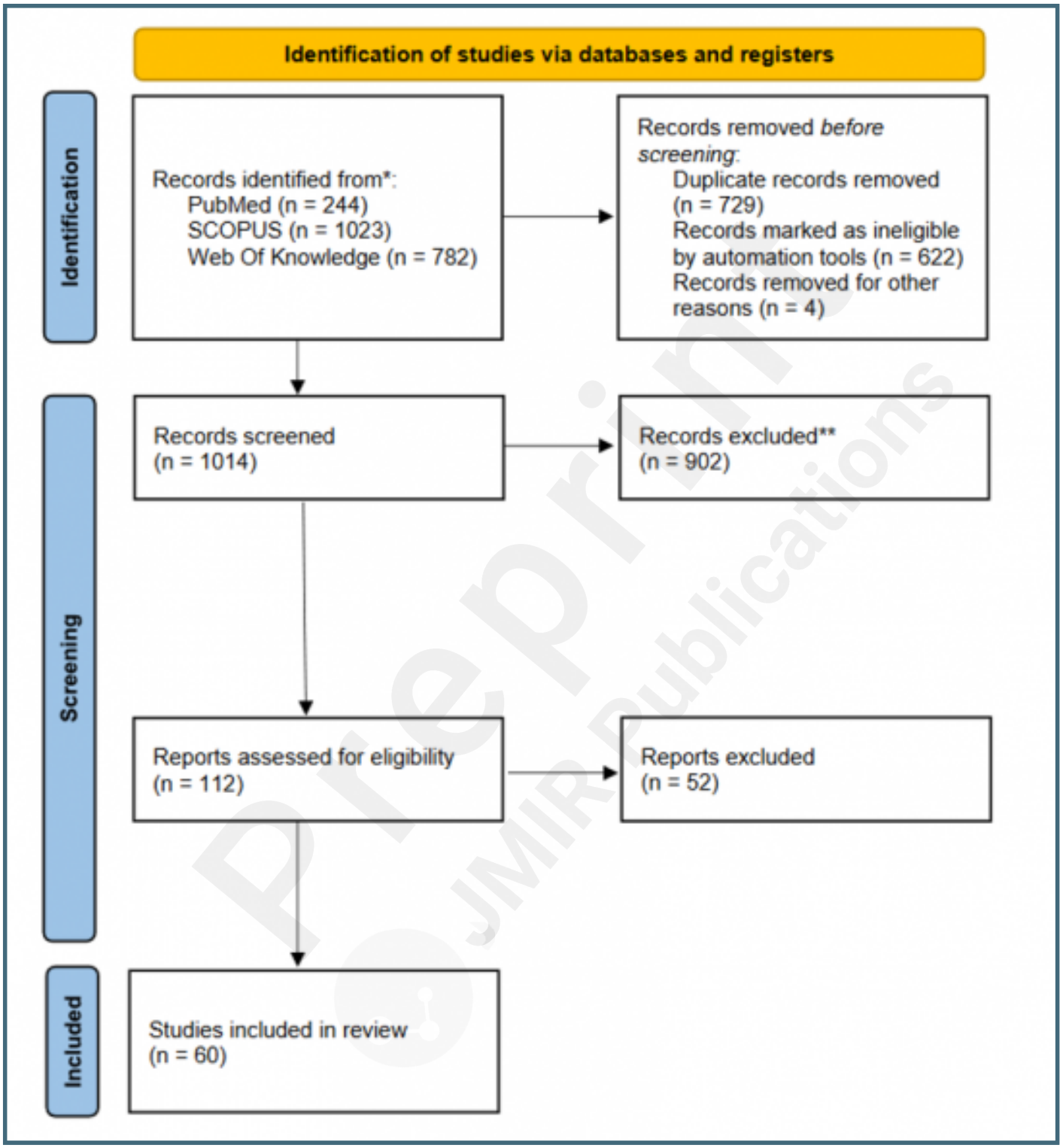
44. Leiserson MDM, Gramazio CC, Hu J, Wu H-T, Laidlaw DH, Raphael BJ. MAGI: visualization and collaborative annotation of genomic aberrations. Nat Methods Nature Publishing Group; 2015 Jun;12(6):483–484. doi: 10.1038/nmeth.3412

45. Scheer J, Volkert A, Brich N, Weinert L, Santhanam N, Krone M, Ganslandt T, Boeker M, Nagel T. Visualization Techniques of Time-Oriented Data for the Comparison of Single Patients With Multiple Patients or Cohorts: Scoping Review. J Med Internet Res Canada; 2022 Oct 24;24(10):e38041. PMID:36279164

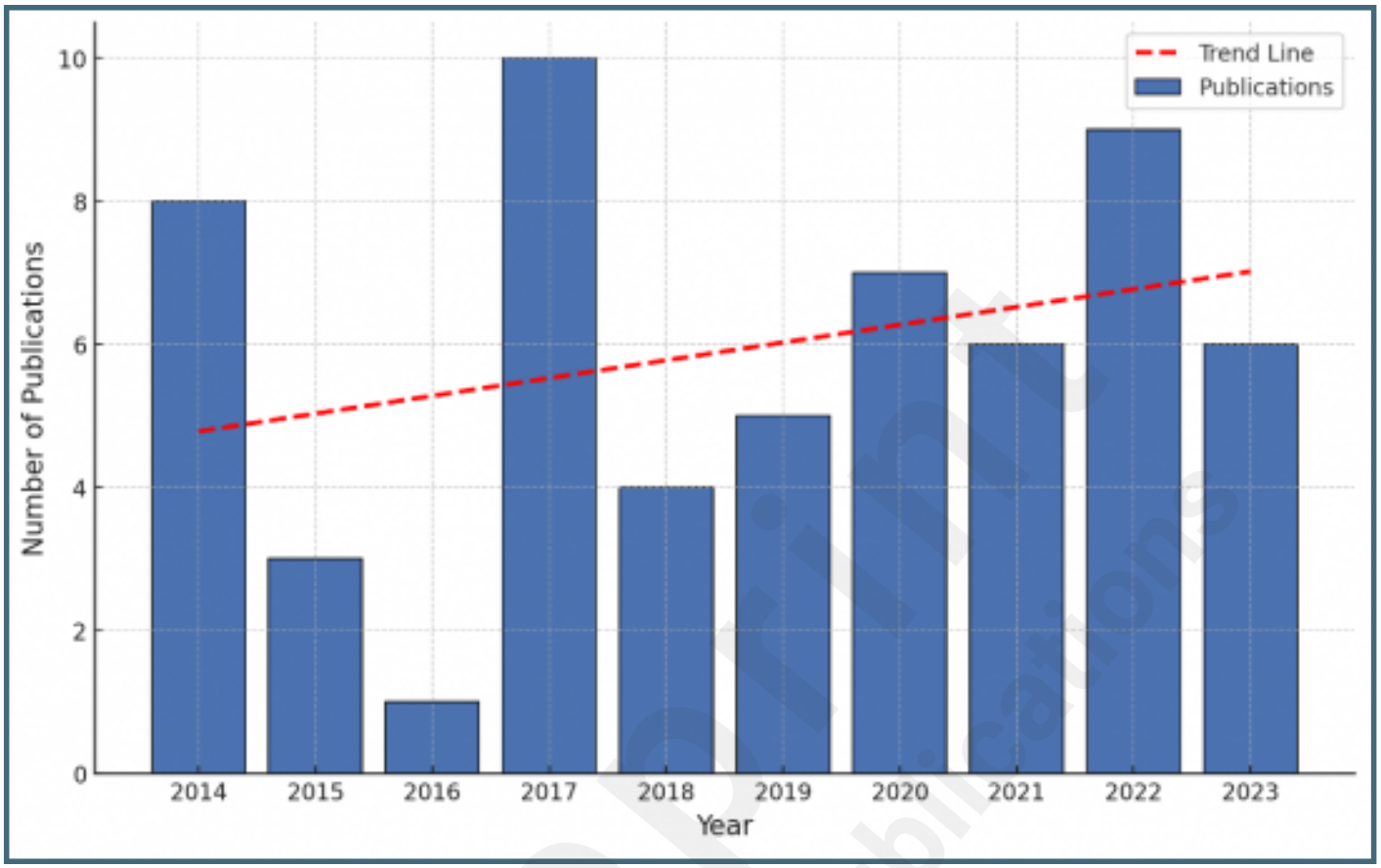
Supplementary Files

Figures

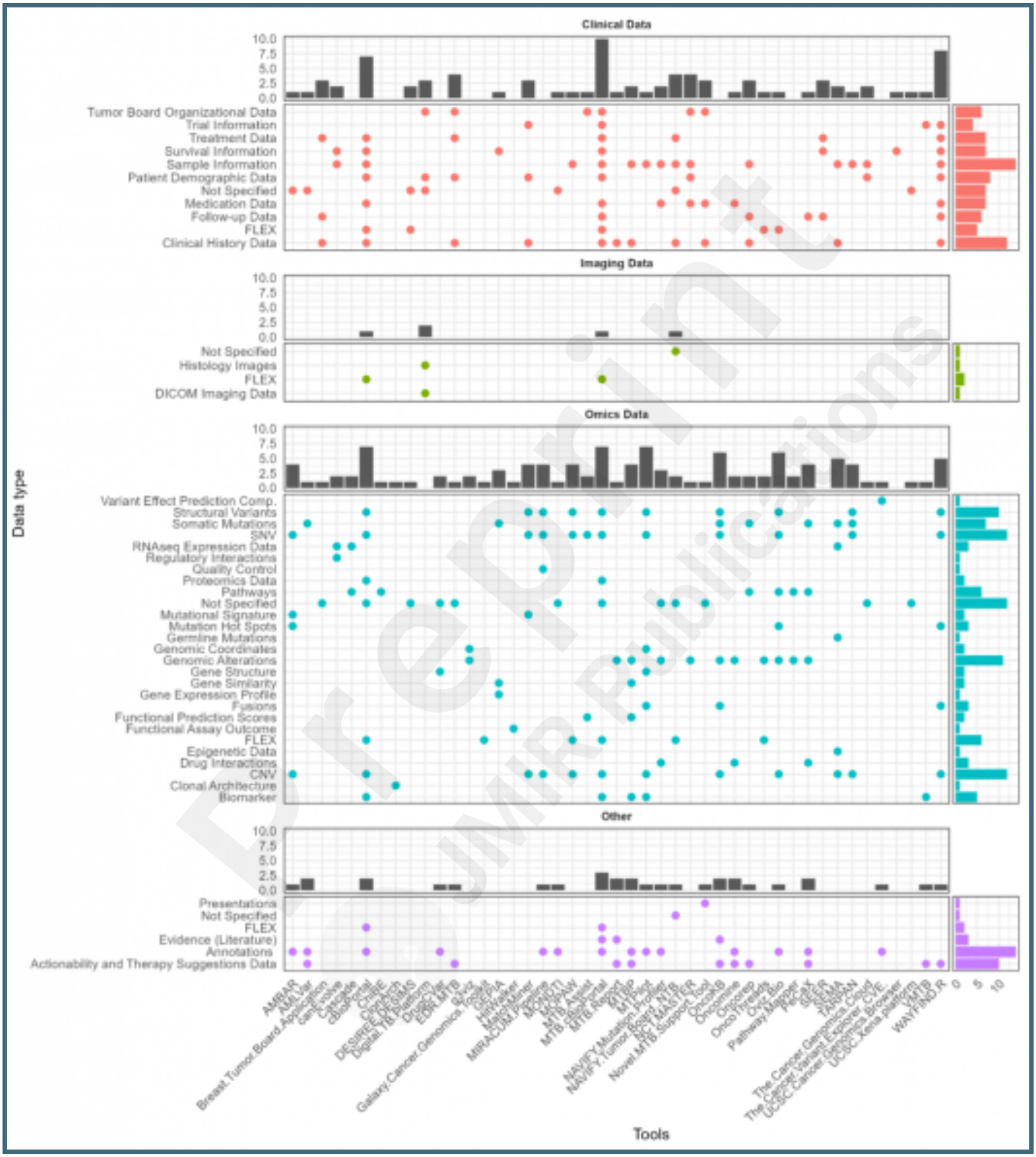
PRISMA flowchart.



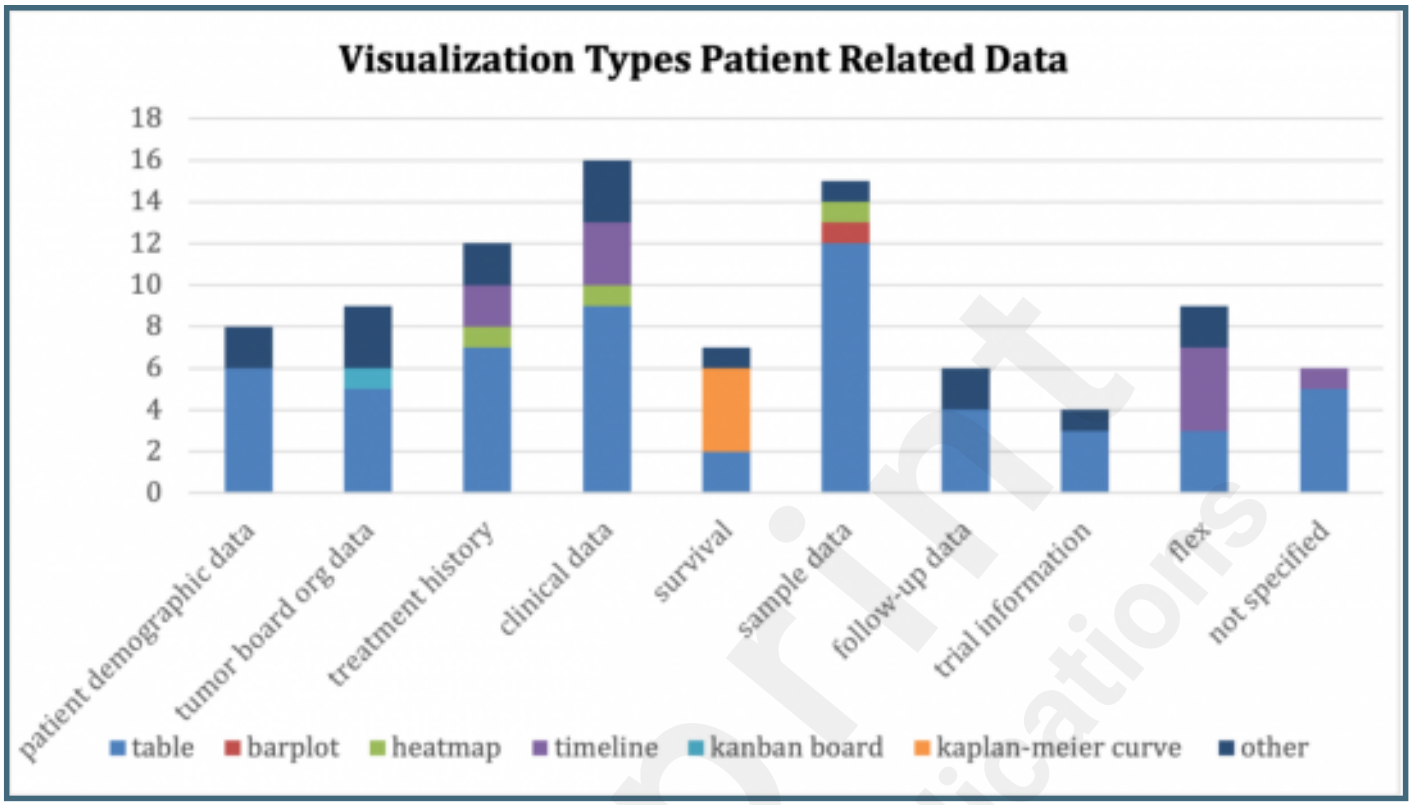
Publication distribution by year.



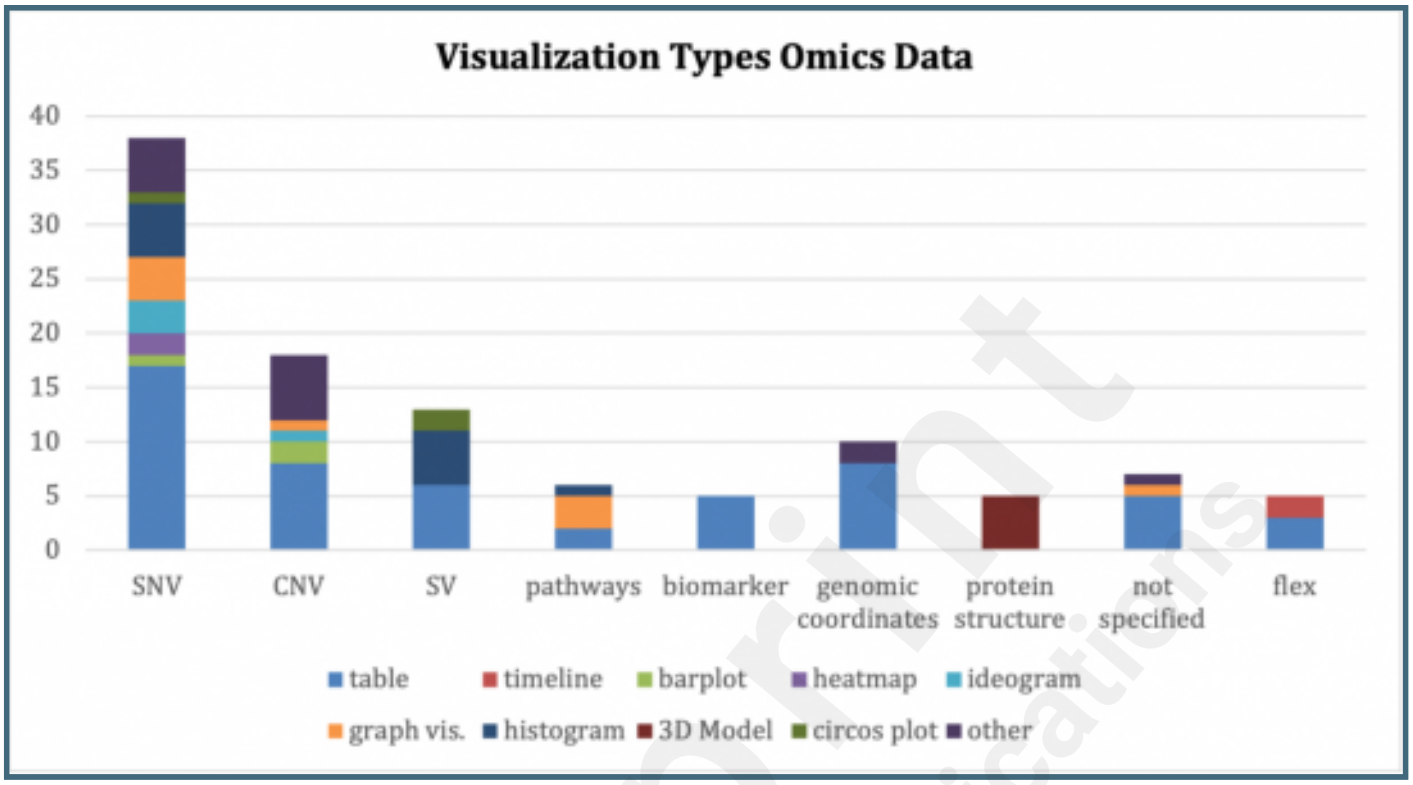
Data Type Overview. Filled fields represent the existence of visualization for the data type. FLEX rows represent generalized visualization solutions for the category that can be primarily used through user-defined data.



Distribution of data types and visualization strategies for patient-related data.



Distribution of data types and visualization strategies for omics data.



Distribution of data types and visualization strategies for miscellaneous data.