

# A taxonomic guide to diffusion MRI tractography visualization tools

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## Abstract

Visualizing neuroimaging data is a key step in evaluating data quality, interpreting results, and communicating findings. This survey focuses on diffusion MRI tractography, which has been widely used in both research and clinical domains within the neuroimaging community. With an increasing number of tractography tools and software, navigating this landscape poses a challenge, especially for newcomers. A systematic exploration of a diverse range of features is proposed across 27 research tools, delving into their main purpose and examining the presence or absence of prevalent visualization and interactive techniques. The findings are structured within a proposed taxonomy, providing a comprehensive overview. Insights derived from this analysis will help (novice) researchers, clinicians, and developers in identifying knowledge gaps and navigating the landscape of tractography visualization tools.

## KEY WORDS

diffusion MRI, taxonomy, tractography, visualization

## 1 | INTRODUCTION

Diffusion magnetic resonance imaging (dMRI) tractography, introduced in the late 1990s<sup>1,2</sup> gained significant traction during the 2000s.<sup>3</sup> It remains a prominent tool in both research and clinical domains within the neuroimaging community.<sup>4</sup> Its applications provide primary insights into how connectivity shapes brain function, development, and cognition, deepening the understanding of brain dysfunction in aging, mental health disorders, and neurological diseases.<sup>5</sup> In clinical settings, tractography has demonstrated its relevance in neurosurgical planning by enabling preoperative, non-invasive, three-dimensional (3D), in vivo depictions of white matter (WM) tract locations and trajectories.<sup>6</sup> Visualizing neuroimaging data stands as a fundamental method to assess data quality, interpret outcomes, and communicate findings.<sup>7,8</sup> Typically, these visualizations are generated through graphical user interface-based (GUI) tools. The process entails opening individual images, and for each instance, display settings are manually adjusted until the desired output is achieved. Moreover, currently, there are numerous code-based software packages available that often do not demand advanced programming skills, thereby enhancing accessibility.

The large number of available tools and software makes tractography visualization more accessible than ever.<sup>9</sup> Navigating this wealth of information, however, becomes increasingly difficult,<sup>9</sup> especially for novice researchers. This underscores the need for a comprehensive survey on

**Abbreviations:** dMRI, diffusion magnetic resonance imaging; WM, white matter; GUI, graphical user interface; WSL, Windows Subsystem for Linux; OS, operating system; CLI, command line-based interface; DTI, diffusion tensor imaging; HARDI, high angular resolution; CSD, constrained spherical deconvolution; ML, machine learning; HCP, Human Connectome Project; FA, fractional anisotropy; MD, mean diffusivity; AD, axial diffusivity; RD, radial diffusivity; BIDS, brain imaging data structure; ROI, region of interest; MLV, multiple linked view; 2D, two-dimensional; 3D, three-dimensional.

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tractography visualization tools. With this survey, we aim to assist (novice) researchers in making informed decisions about which tractography visualization tool to employ for their study, and to explore potential knowledge gaps for future research.

The structure of our survey is as follows. In Section 2, we will delve into the context of tractography visualization, and the papers that have inspired this survey. The collection process of the tools is elaborated in Section 3. Section 4 elaborates on the taxonomy for the survey, including examples. Finally, Section 5 presents the summary, including recommendations and limitations, and an outlook on future research in dMRI tractography visualization tools.

## 2 | BACKGROUND

The research field of tractography spans various disciplines, including physics<sup>10,11</sup> mathematics,<sup>12</sup> computer science,<sup>13</sup> biomedical engineering,<sup>14</sup> neuroscience,<sup>15,16</sup> and medicine.<sup>17,18</sup> Tractography can be used for different fibrous tissues (e.g., cardiac muscle, skeletal muscle),<sup>19</sup> however, its primary use has been within the central nervous system, specifically the brain's WM.<sup>20</sup> The process from data acquisition to tractography involves multiple steps with several assumptions and uncertainties. These factors can significantly impact the tractography's accuracy in representing the true axonal connections within the brain.<sup>4</sup> Causing tractography, despite the progress made in the last years, to remain a fundamentally ill-posed problem.<sup>17</sup> For a clear overview of common misconceptions, biases, and contemporary (organized) challenges in tractography we refer the reader to<sup>4,9,13</sup> and.<sup>17</sup> For detailed information regarding steps in the process, beyond visualization, readers are directed to surveys such as<sup>6</sup> and.<sup>20</sup> This review process will focus on visualization tools designed for tractography data and the related challenges.

Accuracy, validity, and reproducibility of discoveries have been a main challenge in neuroimaging research.<sup>4,21</sup> Encouraging transparent evaluation and independent replication of scientific output could offer a solution.<sup>7</sup> However, despite the increase of transparency and code sharing in neuroimaging analyses, there is a notable gap in sharing the code used to create figures such as brain renderings and spatial maps. This gap stems from the manual process involving GUI manipulation, including sliders, buttons, and overlays. The final visualization often is a screenshot with potentially added beautification through image processing software. As a result, it is challenging to replicate neuroimaging visualizations, even for the original authors.

### 2.1 | Terminology and origin

In scientific literature, tractography has been referenced using various terms, including 'fiber tracking' or 'fiber tractography',<sup>8</sup> 'dMRI tractography',<sup>9,22</sup> 'WM tractography',<sup>6</sup> and simply 'tractography'.<sup>7,23</sup>

In this survey, we will adopt the terminology proposed by Côté et al<sup>24</sup> in 2013. According to this description, 'tractography' refers to 'the process of generating streamlines of brain fibers. This is synonymous with fiber tracking in the central nervous system'.<sup>24</sup> Please note that tractography can also be applied to various other fibrous tissues, as previously mentioned.

Streamlines are continuous curves that follow the direction of a specific vector field.<sup>25</sup> They serve as a visual representation aiding scientists and engineers in comprehending complex phenomena. These curves are utilized across various disciplines, including electricity and magnetism, fluid dynamics, blood flow, materials science, etc.<sup>26,27</sup> In the context of tractography, fiber tracking generates curves that can be visualized as (illuminated) (thin) streamlines or -tubes.<sup>8</sup>

For a better understanding of the terminology used in the dMRI community, we encourage readers to refer to.<sup>24</sup> We reiterate the need for the dMRI community to strive for more consistent definitions regarding fiber tracking, especially regarding tractography (visualization) techniques that have been proposed.

### 2.2 | Related work

There are a handful of papers that include an overview of different tractography (visualization) methods. However, in none of these papers, the primary objective is a survey of the available tools. The survey of Isenberg et al<sup>28</sup> primarily focuses on visualization techniques rather than visualization tools. Further elaboration on this distinction will be provided later in this section.

The papers including tractography tool overviews can be subdivided into two categories: papers introducing a new tool and comparing it with existing ones,<sup>29,30</sup> and papers focusing on exploring neuroimaging techniques,<sup>7</sup> such as the human connectome,<sup>31</sup> dMRI<sup>23</sup> and dMRI tractography.<sup>22,32</sup> The tools and features included in the overviews vary per paper.

The former category involves comparing a proposed tool with the most similar<sup>29</sup> or freely available<sup>30</sup> applications found in the literature. Osorio et al<sup>29</sup> assesses (i.e., yes or no) whether the tools incorporate specific visualization features (e.g., 3D rendering, fiber color) and interactions (e.g., zooming, panning). The comparison detailed by Xie et al<sup>30</sup> extends beyond visualization and also incorporates a binary assessment, e.g., for

preprocessing and modeling. This evaluation also includes categorical (programming language) and numerical (installation size) features. The visualization techniques are a subset of the overview, resulting in a limited focus on these techniques.

In the latter category, Chopra et al<sup>7</sup> stand out as the only paper which primarily focusses on (neuroimaging) visualization, by comparing five binary features (voxel, vertex, regions of interest [ROI], edge, and streamlines). Besides that, for each feature it specifies the required data format, and for each tool its user-friendliness<sup>23</sup> and<sup>31</sup> both incorporate visualization features as part of their overviews. Additionally, Margulies et al<sup>31</sup> assesses multi-modality (functional MRI) and fiber tracking models (deterministic or probabilistic), whereas Soares et al<sup>23</sup> assesses features for quantitative analysis (e.g., ROI, histogram), quality control, and preprocessing (e.g., outlier detection, skull stripping). The overview of Kamagata et al<sup>22</sup> does not incorporate any visualization features. Instead, the tools are characterized based on its ‘available tracking models’ and ‘main purpose’.

Moreover, there are two reviews dedicated to dMRI (tractography) visualization techniques. These reviews primarily aim to provide detailed insights into the relevance of these techniques. For instance, Schultz et al<sup>8</sup> provides an overview of dMRI visualization strategies, such as gray-scale and color encodings, glyph representation, and renderings of fiber tractography. They mention the advantages and disadvantages of the techniques, including local glyphs and global fiber trajectories, and two-dimensional (2D) and 3D visualization techniques. Besides that, the importance of information transfer through visual encodings is also emphasized, such as symmetry, continuity, disambiguity in glyphs. Isenberg et al<sup>28</sup> conducted a survey focusing on dMRI tractography visualization techniques addressing the issue that dense line-based tractography datasets are often too large to understand directly. Various techniques are discussed, such as depth perception of fiber tracts, uncertainty representations, and the combination of fiber tract visualization with contextual rendering. As well as visualizations of additional data, fiber tract bundles, and spatially abstracted connectivity.

The dispersed nature of information across papers, each presenting a different variety of features and publications spanning from 2013 to 2023, highlights the need for a more unified and thorough analysis.

### 3 | APPROACH

It has become apparent that a wide array of tractography tools with varying characteristics exists. This section will detail the approach used to select the tools and features included in our survey. This survey will be on tractography visualization tools for neuroimaging only, we will therefore only include tools capable of visualizing streamlines of brain fibers, aiming to explore the diverse range of characteristics inherent in each tool.

#### 3.1 | Tools

We used a combination of venues, such as IEEE Xplore and PubMed, for searches to identify the tools included in this survey. Additionally, we utilized Google Scholar to identify additional research. The keyword searches used were a combination of ‘tractography’, ‘dMRI’, ‘neuroimaging’, ‘visualization’, ‘software’, and ‘tool’. To identify older research, we used backward citations in the already identified tools’ papers to find similar visualization tools. This resulted in a total of 49 visualization tools. As this is a survey on tractography visualization tools, our primary inclusion criterion was the tool’s ability to visualize tractography data, which may seem trivial. Some of these tools, however, only focus on visualizing the connectome,<sup>33,34</sup> glyphs,<sup>35</sup> quality control and statistical output,<sup>36</sup> or visualize through another platform.<sup>37,38</sup> A distinction can be made between clinical tractography tools (e.g., StealthStation by Medtronic<sup>39</sup>), which are often commercial, and research tractography tools (e.g., MRtrix<sup>3</sup><sup>40,41</sup>), which are typically non-commercial. Since our target audience primarily consists of (novice) researchers within the field of neuroimaging, we have decided to omit commercial tools. To be suitable for research the tool must be non-deprecated (i.e., maintained), established in the last 20 years (i.e., at least developed after 2005), and susceptible to external data. Deprecated tools fall into two categories: those not being updated for the framework they depend on (e.g., ABrainVis<sup>29</sup>) and those that are no longer available (e.g., Vist/e<sup>42</sup>). Lastly, there are platforms that integrate various tools under a single overarching system, which we refer to as ‘umbrella tools’. These platforms, such as Brainlife.io,<sup>43</sup> act as wrappers for existing tractography visualization tools such as Mrtrix<sup>40,41</sup> Fibernavigator<sup>44,45</sup> FSL<sup>46</sup> and DiPy.<sup>47</sup> In this survey, we have included the individual tractography visualization tools but excluded the umbrella tools to avoid redundancy. Table 1 gives an overview of the six criteria and the 22 tools that are in conflict with either or multiple criteria.

#### 3.2 | Features

The remaining 27 tools are analyzed based on the features included in the papers in Section 2.2, along with our own input.\* We did not include a strengths and weaknesses analysis of each tool, as such an assessment depends on a variety of factors, including the user’s expertise, the type of data being analyzed, and the specific goals of the visualization process.

**TABLE 1** Overview of the 22 excluded tool(s) due to unmet inclusion (i.e., exclusion) criteria.

Exclusion criteria	Excluded tool(s)
No streamline visualization	BRAINintrinsic, <sup>33</sup> CMTK, <sup>34</sup> dMRI-explorer, <sup>35</sup> PANDA, <sup>36</sup> Camino, <sup>37</sup> TractoR <sup>38</sup>
Commercial	StealthStation, <sup>39</sup> Brainlab, <sup>48</sup> Amira, <sup>49</sup> Inobitec, <sup>50</sup> ANDI-DTI, <sup>51</sup> NeuroNavigator, <sup>52</sup> Brainvoyager QX, <sup>53</sup> OsiriX <sup>54</sup>
Deprecated	ABrainVis, <sup>29</sup> Vist/e, <sup>42</sup> MRI Studio/DTI Studio, <sup>55,56</sup> Fiberweb, <sup>57</sup> MM-DTI <sup>58</sup>
Not accepting external data	BrainTutor 3D <sup>59</sup>
Umbrella tool	Brainlife.io <sup>43</sup>
Published before 2005	DTI-Query/CINCH <sup>60,61</sup>

In Table 2 we present an overview of the 27 tools and some general characteristics within this field, including the URL, tool types, open source, main programming language, operating system (OS), and interface options. In Section 4 we will elaborate on the two identified tool types: process and visualization tools. Of the 27 included tools 18 are open source. Tractography visualization tools exist for general-purpose OS such as Windows, Linux, and MacOS, as well as web and mobile applications. For Windows, some tools require the Windows Subsystem for Linux (WSL), a feature that allows users to run a Linux environment on their Windows machines. Additionally, for some web applications, it is possible to run or develop the tool on your local machine. With most tools designed for general-purpose OS. There are no mobile applications that meet all our criteria. C++ is the most prevalent main programming language, featured in 14 out of 27 tools, followed by C, Javascript, and Python, each featured in 3 tools. Please note that we only mention the main programming language, although some tools can be extended to support multiple languages.

We analyzed whether the tools have a GUI or a command line-based interface (CLI). A GUI is a user-friendly display that often includes the basic (processing) tools and necessary parameters, whereas the CLI can be used by (advanced) users to perform command-line batch processing. There are tools that do not have a self-contained GUI or require manual creation of visualizations. We consider tools to have a GUI if it is self-contained. Twenty-five out of twenty-seven tools offer a GUI, while 18 out of 27 tools provide a CLI. Finally, we conducted an analysis of the journal (and conference) types of the papers to explore the multidisciplinary nature of tractography. The journal types categories include ‘Biomedical’, ‘Computer Science’, and ‘Both’ (i.e., Biomedical and Computer Science) with 22, 7, and 3 papers, respectively. See Appendix A for the journals and conferences categorized within each type. Figure 1 illustrates an overview of the paper publication years. To get an overview of the total number of tractography-related tools, both included and excluded tools are visualized. Note that not all excluded tools have associated published papers. The plot is characterized by multiple peaks. We included four publications to give a plausible explanation for this pattern. Diffusion tensor imaging (DTI)<sup>10</sup> and high angular resolution (HARDI)<sup>87</sup> both are data acquisition techniques. Constrained spherical deconvolution (CSD)<sup>88</sup> is a mathematical model used for fiber reconstruction, and machine learning (ML) tractography<sup>89</sup> has sparked a renewed interest in tractography. Essayed et al<sup>6</sup> provides a more elaborate (chronological) overview of major publications within this domain. One can see that in the years following the introduction of a new technique, there is typically a lag before witnessing an increase in the publication of tool-related papers. This surge may be attributed to the integration of these techniques into new tools, as an effort to enhance accessibility for the broader research community.

## 4 | TAXONOMY

The taxonomy in this survey is aimed at assisting users with access to unprocessed or processed tractography data who seek guidance on the visualization of tractography data. Its structure revolves around three branches: tool types, types of visualization, and types of interactivity. An overview of the taxonomy can be seen in Figure 2.

This section presents a description and detailed examples for each of the three branches, supported by relevant literature. Additionally, it discusses the advantages and disadvantages of visualizations within each category. We aim to showcase a diverse range of tools to the best of our ability. We thoroughly examined all the visualization options and interactivity features for each tool, these details are summarized in Tables 3 and 4, respectively. The figures included have been generated using data from the Human Connectome Project (HCP) dataset,<sup>90</sup> unless stated otherwise.

### 4.1 | Tool types

The software tool landscape is diverse and challenging to navigate. What types of tools exist in tractography? This distinction is relevant for users in order to choose the right tool for their intended data usage. There are tools that focus on particular processing algorithms but lack visualization and interaction features.<sup>78</sup> Conversely, there are tools specifically tailored for visualizing brain data.

**TABLE 2** Overview of the general features of the 27 included tools<sup>a</sup>. Including the tools's name (within brackets the tractography-specific software), literature references, URL(s), tool types (visualization or process), open source, main programming language, operating system (Linux, windows, MacOS, web, mobile), and interface types (GUI and CLI). Indicating the presence (✓) or absence (–) of open source and the interface types.

Tools/Features	Literature	URL(s)	Tool types	Open source	Main programming language	Operating system	Interface	
							GUI	CLI
AFNI (FATCAT)	62 63	<a href="https://afni.nimh.nih.gov/">https://afni.nimh.nih.gov/</a>	Process	✓	C	Linux/ Windows/ MacOS	✓	✓
AFQBrowser	64	<a href="https://github.com/richford/AFQ-Browser">https://github.com/richford/AFQ-Browser</a>	Visualization	✓	JavaScript	Web <sup>b</sup>	✓	✓
BioImageSuite	65	<a href="https://bioimagesuiteweb.github.io/webapp/">https://bioimagesuiteweb.github.io/webapp/</a>	Visualization	–	C++	Web <sup>b</sup>	✓	✓
Brainnetome DiffusionKit	30	<a href="https://github.com/brainnetome/diffusionkit">https://github.com/brainnetome/diffusionkit</a>	Process	–	C/C++	Linux/Windows	✓	✓
Brainsuite BIDS App	66	<a href="https://brainsuite.org/">https://brainsuite.org/</a>	Process	✓	Python	Linux/ Windows/ MacOS	✓	✓
DiffusionToolkit (TrackVis)	67	<a href="https://trackvis.org/dtk/">https://trackvis.org/dtk/</a>	Process	–	C++	Linux/ Windows/ MacOS	✓	✓
DiPy/FURY	47 68	<a href="https://github.com/dipy/dipy">https://github.com/dipy/dipy</a> <a href="https://fury.gl/latest/index.html">https://fury.gl/latest/index.html</a>	Process	✓	Python	Linux/ Windows/ MacOS	–	✓
DSI Studio	69	<a href="https://dsi-studio.labsolver.org/">https://dsi-studio.labsolver.org/</a>	Visualization	–	C++	Linux/ Windows/ MacOS	✓	✓
DTI-TK	70	<a href="https://dti-tk.sourceforge.net/">https://dti-tk.sourceforge.net/</a>	Process	✓	C++	Linux/MacOS	✓	✓
DTI Web	71	<a href="http://trueta.udg.edu/DTI/">http://trueta.udg.edu/DTI/</a>	Process	–	Java	Web <sup>b</sup>	✓	–
ExploreDTI	72	<a href="https://www.exploredti.com/">https://www.exploredti.com/</a>	Process	–	Matlab	Linux/ Windows/ MacOS	✓	–
Fibernavigator	44 45	<a href="https://github.com/chamberm/fibernavigator">https://github.com/chamberm/fibernavigator</a>	Process	✓	C++	Linux/ Windows/ MacOS	✓	–
FiberStars	73	<a href="https://github.com/lorifranke/FiberStars">https://github.com/lorifranke/FiberStars</a>	Visualization	✓	JavaScript	Web <sup>b</sup>	✓	–
FreeSurfer	74 75	<a href="https://github.com/freesurfer/freesurfer">https://github.com/freesurfer/freesurfer</a>	Process	✓	C++	Linux/ Windows <sup>c</sup> / MacOS	✓	✓
FSL	46	<a href="https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSL">https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSL</a>	Process	–	C/C++	Linux/ Windows <sup>c</sup> / MacOS	✓	✓
MedInria	76	<a href="https://med.inria.fr/">https://med.inria.fr/</a>	Visualization	✓	C++	Linux/ Windows/ MacOS	✓	–
MIBrain	77	<a href="https://github.com/imeka/mi-brain">https://github.com/imeka/mi-brain</a>	Visualization	✓	C++	Linux/ Windows/ MacOS	✓	–
MITK-DI	78	<a href="https://github.com/MIC-DKFZ/MITK-Diffusion">https://github.com/MIC-DKFZ/MITK-Diffusion</a>	Visualization	✓	C++	Linux/ Windows/ MacOS	✓	–
Mrtrix3	40 41	<a href="https://www.mrtrix.org/">https://www.mrtrix.org/</a>	Process	✓	C++	Linux/ Windows <sup>c</sup> / MacOS	✓	✓

(Continues)

TABLE 2 (Continued)

Tools/Features	Literature	URL(s)	Tool types	Open source	Main programming language	Operating system	Interface	
							GUI	CLI
NeuroTrace	79	<a href="https://gitlab.com/Besm/neurotrace">https://gitlab.com/Besm/neurotrace</a>	Visualization	✓	C#	Windows	✓	-
OpenWalnut	80	<a href="https://openwalnut.org/">https://openwalnut.org/</a>	Visualization	✓	C++	Linux/Windows	✓	✓
pyAFQ	81	<a href="https://yeatmanlab.github.io/pyAFQ/">https://yeatmanlab.github.io/pyAFQ/</a>	Process	✓	Python	Linux/Windows/MacOS	-	✓
QIT	82	<a href="https://github.com/cabeen/qit">https://github.com/cabeen/qit</a>	Visualization	-	Java	Linux/Windows/MacOS	✓	✓
Slice:Drop	83	<a href="https://slicedrop.com/">https://slicedrop.com/</a>	Visualization	✓	JavaScript	Web	✓	-
SlicerDMRI	84	<a href="https://dmri.slicer.org/">https://dmri.slicer.org/</a>	Process	✓	C++	Linux/Windows/MacOS	✓	✓
Surf-Ice	85	<a href="https://github.com/neurolabusc/surf-ice">https://github.com/neurolabusc/surf-ice</a>	Visualization	✓	Pascal	Linux/Windows/MacOS	✓	✓
VistaSoft	86	<a href="https://github.com/vistalab/vistasoft">https://github.com/vistalab/vistasoft</a>	Process	✓	Matlab	Linux/Windows	✓	✓

<sup>a</sup>To the best of our knowledge at the time of submission, our information was collected from software manuals, websites, and published literature.

<sup>b</sup>Tool can also be run or developed locally.

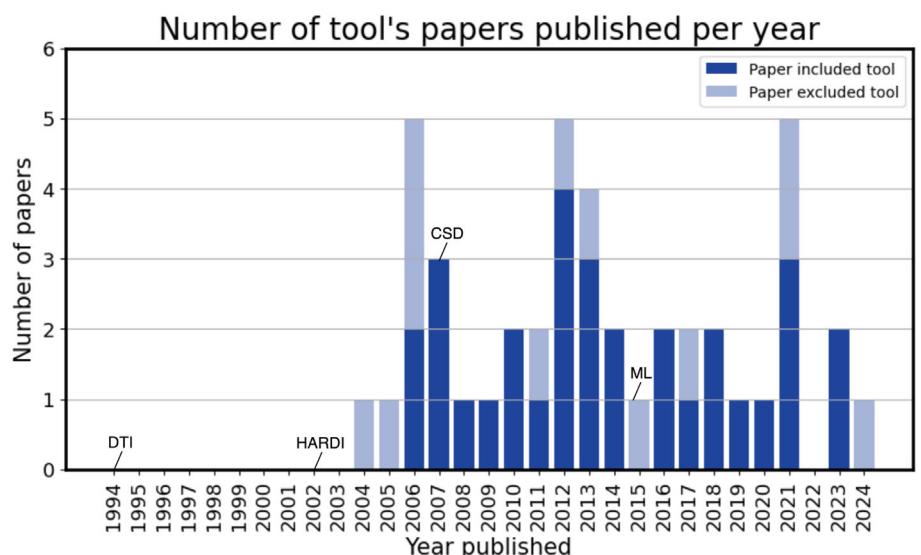
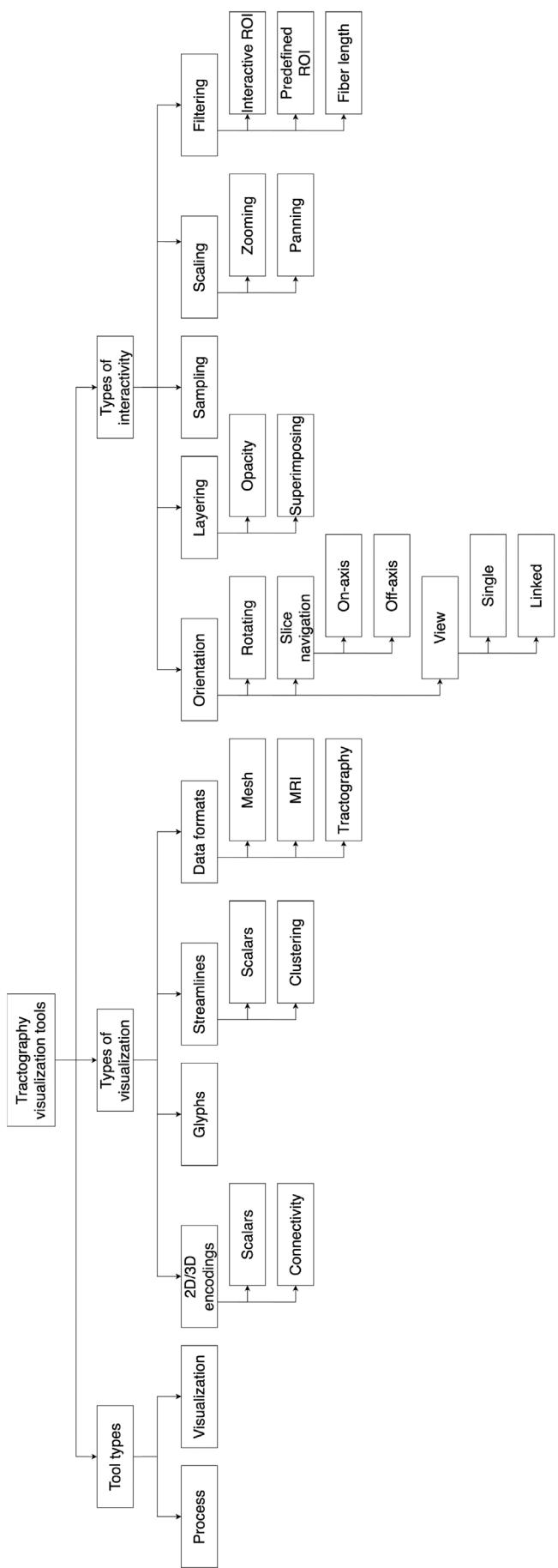


FIGURE 1 Overview of the included (dark blue) and excluded (light blue) tool's papers published. The apparition of four major milestones (e.g., DTI, HARDI, CSD, and ML-based tractography) is added to the figure for timeline reference.

In this first subsection, we differentiate between two types of tractography visualization tools: those processing data from start to finish (including visualization) and those designed solely for visualizing processed data (e.g., streamlines). We will classify these tools as ‘processing’ and ‘visualization’ tool types, respectively. A tool can either have tool type ‘process’ or ‘visualization’.

#### 4.1.1 | Processing tools

In literature, processing tools are often described as a ‘pipeline’,<sup>46</sup> an ‘all-in-one solution’,<sup>30</sup> or as a ‘suite of tools for neuroimaging analysis’.<sup>74,75</sup> Figure 3 illustrates an example of a processing tool.



**FIGURE 2** Overview of the taxonomy with three branches: tool types, types of visualization, and types of interactivity. Each branch consists of different levels within the taxonomy.

A major challenge for researchers is the complex pipeline of image processing steps required to transform raw data into quantitative analyses.<sup>78</sup> Ensuring interpretations and final results requires a thorough examination of intermediate processing steps.<sup>46</sup> Fibernavigator, for instance, offers real-time parameter adjustments of processing steps, bridging the gap between processing and display. Two potential consequences of processing tools are that the tool might become too intricate for users, and the shift onto processing techniques, neglecting the importance of visualization.

#### 4.1.2 | Visualization tools

A high-quality viewing tool is essential for anyone working with data. Visualization tools often focus on specific aspects, such as tractography visualization, such that it can be used by researchers with limited technical expertise.<sup>64</sup> Despite its significance, the development of display or viewing tools is infrequently published, mainly because it rarely introduces new scientific advancements.<sup>46</sup> An example of a visualization tool is illustrated in Figure 4.

### 4.2 | Types of visualization

This section categorizes visualization properties into four subgroups: glyphs, streamlines, 2D and 3D encodings, and data formats. Please note that none of these visualization types are exclusive to tractography; they are used and have been applied in many other research fields as well. Glyphs represent multi-dimensional local data using attributes such as shape or color.<sup>8</sup> On the other hand streamlines, in the context of tractography, represent global brain fiber trajectories. The reduction of multi-dimensional tractography data to 2D or 3D images is classified as 2D and 3D encodings. This reduction occurs in two distinct types: connectivity and scalar visualizations. Besides tractography data, MRI and meshes are recurring types of brain imaging data in tractography visualization tools. In this section, we will provide more in-depth details and examples about each of the subgroups.

#### 4.2.1 | Glyphs

Glyphs, in the context of visualization, function as iconographic or geometrical depictions of different variables within a dataset.<sup>92</sup> Unlike other visualizations, they allow the representation of multi-dimensional information at a local point by encoding various dimensions into attributes, such as shape or color.<sup>8</sup> Representing multi-dimensional data is a common task in data visualization,<sup>93</sup> and the use of data glyphs, dates back to the 1950s.<sup>94</sup>

Glyphs in tractography tools appear in various shapes, such as sticks, cylinders, spherical harmonics, and ellipsoids,<sup>31</sup> see two examples in Figures 5 and 7 (middle). However, a primary drawback of glyph representations lies in their emphasis on local information, making it challenging to infer global structures, such as fiber trajectories. It has been proposed that compared with ellipsoids, boxes, and cylinders make it easier to identify the main directions due to their sharper edges.<sup>8</sup> For a more extensive analysis of the different types of glyphs and their use in tractography we refer the reader to the survey of Schultz et al.<sup>8</sup>

#### 4.2.2 | Streamlines

Streamlines are typically represented as thin lines, illuminated streamlines, or tubes.<sup>8</sup> See two examples in Figures 6 and 7 (right). Initially, streamlines were used in solid mechanics and fluid dynamics as hyper-streamlines, this visualization method has integrated additional visual components such as color and texture.<sup>8</sup> Streamlines contain spatial information about fiber trajectories. However, challenges that may arise are visual clutter caused by excessive streamlines, missing relevant structures caused by too few streamlines, and improperly placed streamlines could lead to wrong interpretations and conclusions.

**TABLE 3** Overview of the presence (✓) or absence (–) of visualization techniques within the included tools<sup>a</sup>.

Features/tools	AFNI	AFQBrowser	BioImageSuite	DiffusionKit	Brainsuite	DiffusionToolkit	DiPy/ FURY	DSI- studio	DTI- TK	DTI- web	ExploreDTI	Fibernavigator	FiberStars
Data format	Tractography	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Mesh	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	–
MRI	✓	–	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	–
Streamlines	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Scalars	–	–	✓	–	–	–	–	–	–	–	✓	✓	✓
Glyphs	–	–	✓	✓	✓	✓	–	✓	✓	✓	✓	✓	–
2D/3D encodings	Connectivity	✓	–	✓	✓	✓	–	✓	✓	–	✓	–	–
Scalars	✓	–	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

<sup>a</sup>To the best of our knowledge at the time of submission, our information was collected from software manuals, websites, and published literature.**TABLE 3** (Continued)

Features/tools	FreeSurfer	FSL	MedInria	MIBrain	MITK-DI	Mrtrix3	NeuroTrace	OpenWalnut	pyAFQ	QT	SlicerDrop	SlicerDMRI	Surfice	VistaSoft
Data format	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Streamlines	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Glyphs	–	–	–	✓	✓	✓	–	✓	✓	–	–	–	–	–
2D/3D encodings	–	✓	✓	–	✓	✓	✓	–	✓	–	✓	✓	–	✓
Scalars	✓	✓	✓	–	✓	✓	✓	–	✓	✓	✓	✓	–	✓

<sup>a</sup>To the best of our knowledge at the time of submission, our information was collected from software manuals, websites, and published literature.

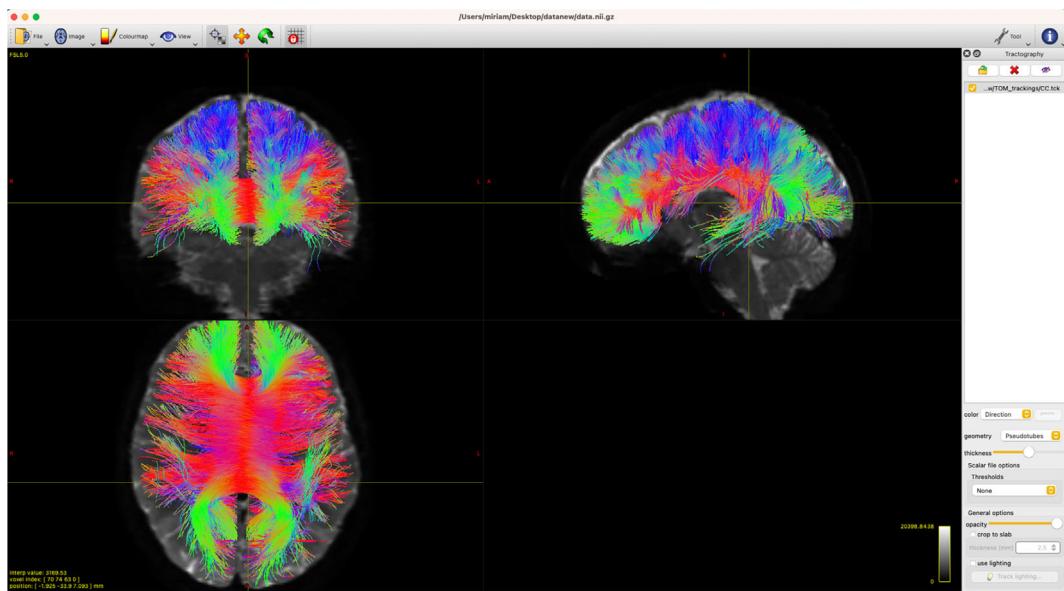
**TABLE 4** Overview of the presence (✓) or absence (–) of interactivity techniques within the included tools<sup>a</sup>.

Features/tools	AFNI	AFQBrowser	BioImageSuite	DiffusionKit	Brainsuite	DiffusionToolkit	DIPY/ FURY	DSI studio	DTI- TK	DTI web	ExploreDTI	Fibernavigator	FiberStars
Scale	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Panning	✓	–	–	✓	–	–	–	–	–	–	–	–	–
Orientation	Rotating	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Linked view	–	✓	✓	✓	✓	✓	–	✓	✓	–	✓	✓	–
Slice navigation	–	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	–
Layering	Opacity	✓	✓	✓	✓	–	✓	✓	✓	–	✓	✓	–
Superimposing	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	–
Filtering	Predefined ROI	✓	–	✓	✓	✓	–	✓	✓	–	✓	✓	–
Interactive ROI	✓	–	–	–	–	✓	✓	–	✓	–	✓	✓	–
Fiber length	–	–	–	–	–	–	–	–	–	–	✓	✓	–
Sampling	–	–	–	–	✓	–	–	✓	–	–	✓	–	–

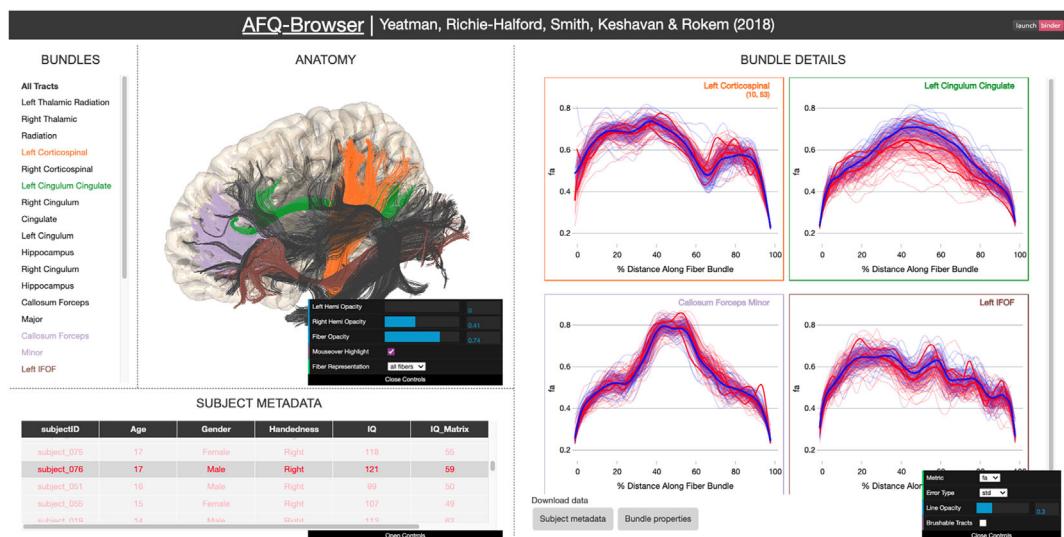
<sup>a</sup>To the best of our knowledge at the time of submission, our information was collected from software manuals, websites, and published literature.**TABLE 4** (Continued)

Features/tools	FreeSurfer	FSL	MedInria	MRIbrain	MITK-DI	MriTrix3	NeuroTrace	OpenWalnut	pAFQ	QIT	Slicer:drop	Slicer:DMRI	Surface	VistaSoft
Scale	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Orientation	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Layering	✓	✓	✓	✓	✓	✓	✓	–	✓	✓	✓	✓	✓	–
Filtering	✓	–	✓	–	✓	–	✓	–	✓	–	✓	–	✓	–
Sampling	–	–	✓	–	–	–	–	–	✓	–	✓	–	✓	–

<sup>a</sup>To the best of our knowledge at the time of submission, our information was collected from software manuals, websites, and published literature.<sup>b</sup>Off-axis slice navigation.



**FIGURE 3** An example of a processing tool is GUI. The top header provides options for file, image, colormap, view, tool, and information adjustments, with additional alternations available for panning and rotating. The left panel features three linked views, displaying streamlines of the corpus callosum superimposed on the MRI. The right panel allows the addition of files for superimposition. The bottom panel presents various visualization options, including thickness and opacity adjustments. Tool: MRtrix3.<sup>40,41</sup>

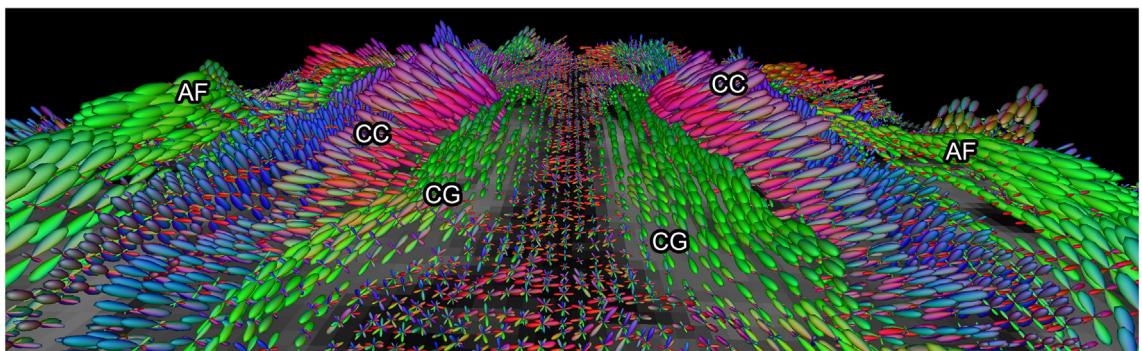


**FIGURE 4** An example of a web-based GUI of a visualization tool. The selected bundles are highlighted in the main panel. The opacity and fiber representation can be adjusted. On the bottom, the subject metadata is presented in tabular format. A selected subject is highlighted in the bundle details line plots. Tool: AFQ-Browser,<sup>64</sup> dataset:<sup>91</sup>

#### Clustering and scalars

Dense tractograms can be simplified by clustering streamlines. QuickBundles,<sup>95</sup> for example, is an efficient clustering algorithm for streamlines implemented in DiPy/FURY, see Figure 8.

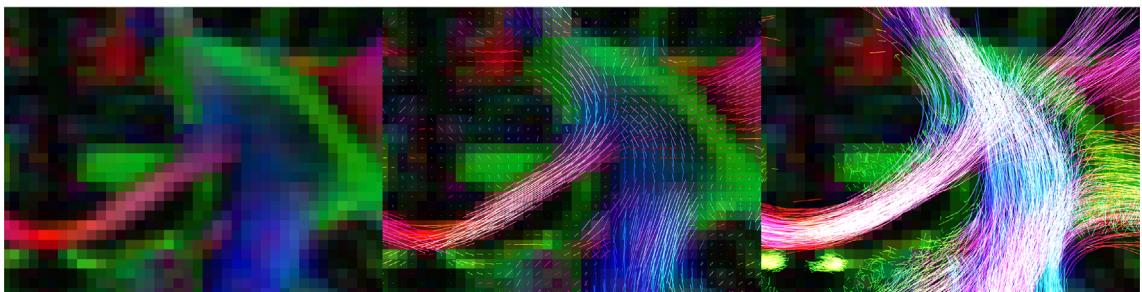
Furthermore, streamlines have the capability to leverage visual channels, such as color and width, to convey additional information, such as scalar values from metrics. Using shape, ExploreDTI has integrated hyper-streamtubes for visualizing specific local fiber tract properties. Hyper-streamtubes are streamtubes with variable widths and can be used to visualize specific local fiber properties, such as uncertainty. In Figure 9, the 95% cone of uncertainty<sup>96</sup> is visually encoded both in color and width. For more information about the visualization of uncertainty, we refer the reader to<sup>97–99</sup> and.<sup>100</sup>



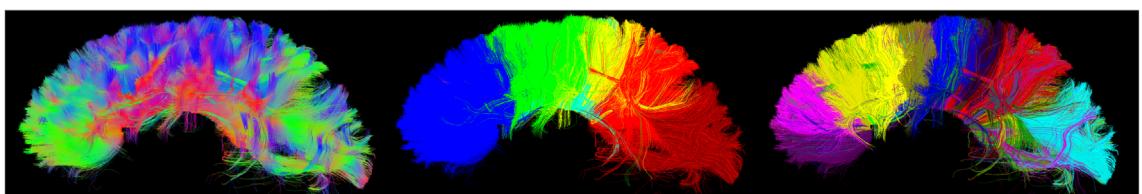
**FIGURE 5** Glyph visualization using slice-based rendering combined with bump-mapping revealing the underlying macro-structure (axial view). Tool: dMRI-explorer.<sup>35</sup>



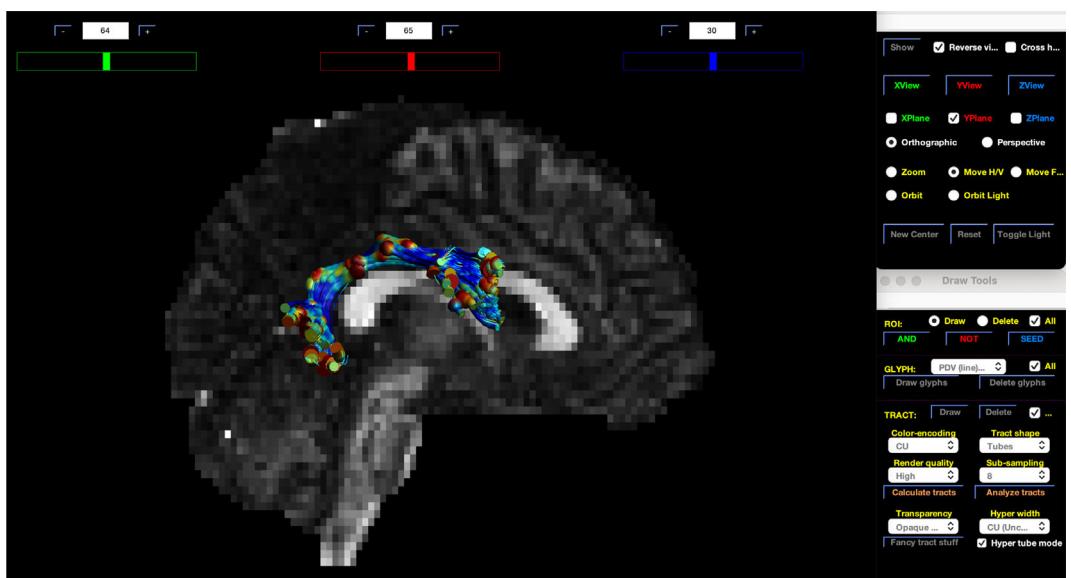
**FIGURE 6** Photorealistic rendering of the cingulum bundle rendered as streamtubes. Tool: Surf-Ice.<sup>85</sup>



**FIGURE 7** Directionally-encoded fractional anisotropy map (or RGB map, left), with diffusion peaks extracted from CSD (middle) and associated streamlines (right). Tool: Fibernavigator.<sup>44</sup>



**FIGURE 8** Clustering of the corpus callosum. Left: no clustering. Middle: 5 clusters. Right: 10 clusters. Tool: DiPy/FURY<sup>47,68</sup>.



**FIGURE 9** Visualization of the right arcuate fascicle. Both color and width visually encode the cone of uncertainty, defined by ExploreDTI. Blue representing a low uncertainty and red high uncertainty. Tool: ExploreDTI,<sup>72</sup> dataset: in vivo example dataset ExploreDTI.<sup>101</sup>

#### 4.2.3 | 2D and 3D encodings

Understanding multi-dimensional tractography data can be challenging, underscoring the necessity for dimensionality reduction. Visual encodings in 2D and 3D have been designed to analyze the connectivity between brain regions and scalar information.

##### Connectivity

Examples of connectivity visualization include the connectivity network or connectivity graph, connectivity matrix, chord diagram, and radial plot. While most visualizations are in 2D, the connectivity network is in 3D. Graph theory-based network analysis examines the overall topology properties of the entire network, avoiding the analysis of numerous individual tracts.<sup>102</sup> A connectivity matrix, also known as a structural network, is built from structural connectivity data by quantifying the number of fibers linking cortical regions in the brain.<sup>102</sup> A special type of connectivity matrix, is the connectome. The connectome is the connectivity analysis of all parts of the cerebral cortex,<sup>103</sup> understanding this structure and function is a primary objective in neuroscience research.<sup>47</sup> Connectivity matrices and chord diagrams offer concise visualizations of intricate relationships within the brain.<sup>104</sup> Radial plots are used in Fiberstars due to their effectiveness in detecting outliers among the mapped scalars and properties.<sup>73</sup>

##### Scalars

Scalars are commonly represented in 2D to provide a more simplified view, using techniques such as feature maps, line plots, histograms, and heatmaps.

Scalar maps in dMRI refer to images that represent scalar values assigned to each voxel in the brain (Figure 7, left), providing information about diffusion characteristics. Common scalar maps include fractional anisotropy (FA), mean diffusivity (MD), axial diffusivity (AD), and radial diffusivity (RD). FA measures the degree of anisotropy in water diffusion, indicating the directionality of fiber tracts. MD represents the overall magnitude of diffusion. AD measures diffusion along the principal axis, while RD reflects diffusion perpendicular to the principal axis. These scalar maps can aid in understanding neurological conditions by highlighting abnormalities or differences in white matter tissue microstructure.

AFQBrowser and DiPy/FURY use line plots to extract statistic values along bundles, known as tract profiles. Additionally, DiPy/FURY, among other tools, offers functionality to showcase the spatial distribution of a track by counting streamline density per voxel, depicted as a density heatmap. Histograms can aid in analyzing the data distribution, helping to determine if additional (pre-)processing steps are required.

#### 4.2.4 | Data formats

Multiple file formats exist for tractography (i.e., TCK,<sup>41</sup> TRK,<sup>67</sup> VTK,<sup>105</sup> TRAKC,<sup>106</sup> FIB,<sup>44,80</sup> and DPY<sup>107</sup> among others). Large community efforts<sup>108</sup> are currently ongoing with the main goal of standardizing those file formats.<sup>†</sup> Osorio et al<sup>29</sup> emphasized the importance of mesh and

MRI volume representations for a more comprehensive anatomical context in visualizing tractography data. The files (e.g., NIFTI, DICOM, Analyze, .mat, .csv, .vtp, .tko) used for each data format vary widely based on the tool. Chopra et al<sup>7</sup> provided insights into various file types associated with each tool per feature.

A recently introduced standard for organizing and sharing neuroimaging data is the Brain Imaging Data Structure (BIDS).<sup>109</sup> More and more dMRI visualization complies with these established standards over the years, which in turn facilitates streamlined data organization and exchange within the neuroimaging community.

#### *Tractography, MRI, mesh*

The importance of tractography has been extensively discussed in Sections 1 and 2 of this paper. Tractography serves as a crucial tool in understanding intricate neural structures within the brain, showcasing its clinical significance. However, its inherently ill-posed nature requires the development of new techniques to enhance its accuracy and reliability.

In addition to the primary focus on dMRI, many neuroimaging tools and software platforms are also designed to handle various other types of MRI data, including T1-weighted MRI and functional MRI. T1-weighted MRI provides detailed anatomical information about brain structures, while fMRI offers insights into brain activity and functional connectivity.

Besides anatomical context, meshes can be used to visualize voxelwise data onto the surface, see Figure 10. However, this poses a significant challenge due to the lack of a direct match between voxel locations and mesh vertices. A solution is to interpolate in order to estimate the intensity at the vertex location.<sup>85</sup>

### 4.3 | Types of interactivity

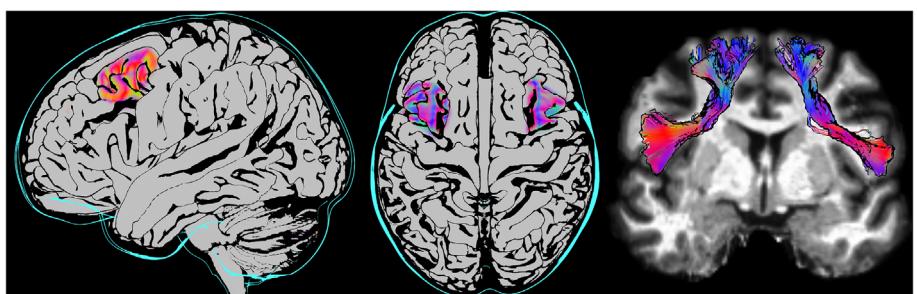
The tools provide a variety of data interaction techniques including scaling, layering, filtering, sampling, and orientation adjustments. Zooming offers a change in scale, with panning proving useful for a detailed exploration. Layering diverse data types can add contextual details, where opacity adjustment can facilitate effective management of the superimposed visualizations. Filtering enables the selection of specific fiber lengths or ROI using predefined files or interactive interfaces. Sampling helps manage the abundance of generated streamlines by sampling a percentage. Users can view tractography data from various angles through rotation, slice navigation, and linked or single views. In this subsection, we will explore the various options interactivity encompasses allowing the user to navigate and explore tractography data.

#### 4.3.1 | Sampling

The usefulness of streamline visualization relies on the quantity and arrangement of curves. An excessive number of streamlines can result in visual clutter, while an inadequate amount might result in overlooking crucial structures.<sup>111</sup> Sampling techniques offer a solution by selectively displaying a percentage of the streamlines, effectively managing the visual complexity.

#### 4.3.2 | Filtering

Researchers have the option to filter an ROI through predefined files or interactive selection methods. This approach allows the isolation of streamlines within specific areas of interest, thereby enabling a region-focused analysis.



**FIGURE 10** Mesh of the cortex showing end points of the bilateral frontal aslant tract rendered using an illustrative approach.<sup>110</sup> Tool: Fibernavigator.<sup>44,45</sup>

### Interactive and predefined ROI

Interactive ROI filtering involves manual selection (of pixels). Alternatively, researchers can use predefined 2D or 3D shapes (i.e., fiducials or geometric primitives) such as rectangles, cuboids, spheres, disks, and seeds. An example is provided in Figure 11. These filters are adjustable within the GUI using logic statements such as AND and NOT. Both manual selection and predefined shapes enable researchers to observe and analyze how the selection of an ROI influences the included streamlines.

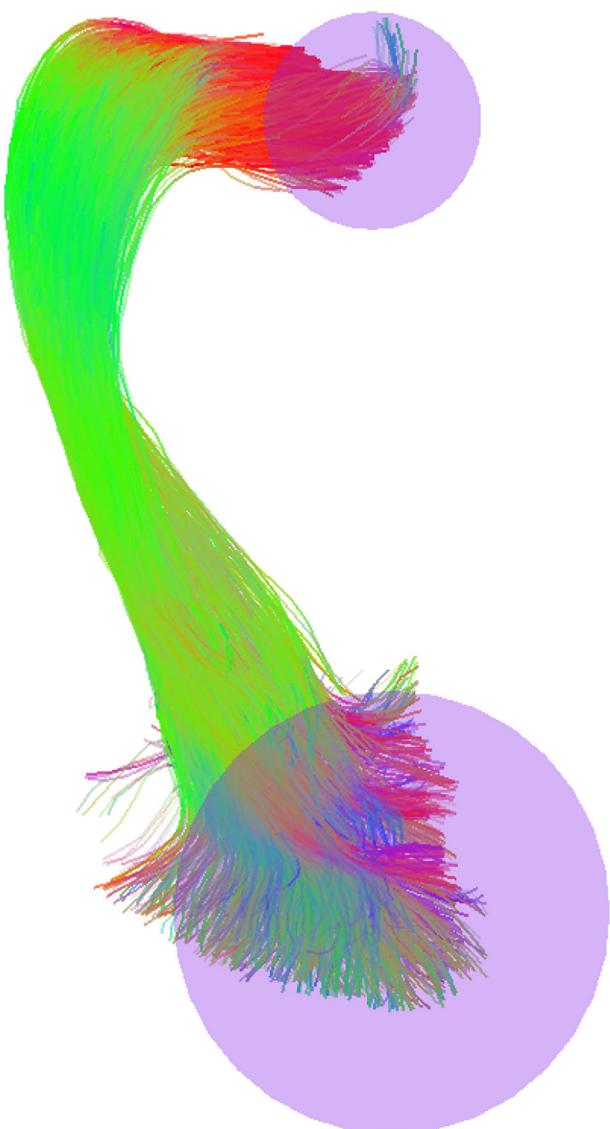
When filtering a ROI using a predefined file, a binary mask or an atlas is commonly used. Tools such as Surf-Ice perform a ROI analyses by pooling data from voxels located within a specific region of an anatomical atlas.<sup>85</sup> This predefined file, which contains the information about the ROI, needs to be either included in the command line or uploaded to the respective tool.

### Fiber length

A less studied, but important brain feature is the length of tractography streamlines. Assessing streamline lengths in tractography is biologically relevant to understand shorter or longer connections within tracts.<sup>112</sup>

#### 4.3.3 | Layering

Transparency allows overlay, facilitating visualization techniques such as occlusion to become useful.<sup>113</sup> Examples of layering are illustrated in Figures 4, 9, and 10.



**FIGURE 11** Optic radiation selection using a set of two inclusion ROIs (purple). Tool: Fibernavigator<sup>44,45</sup>.

### Opacity and superimposing

In the literature, transparency and opacity, as well as superimposing and overlay, are used interchangeably. Transparency and superimposing are commonly used together. Studies suggest that using transparency resolves occlusion issues and enables overlaying planes for direct comparison.<sup>113</sup> However, limitations exist, such as the restricted number of layers that can be superimposed. Additionally, challenges such as false colors and fragmented shapes can arise from the use of transparency and overlay techniques.<sup>113</sup>

### 4.3.4 | Orientation

This section focuses on discussing interactive features that enhance visual orientation, providing users with new perspectives and insights of the data.

#### *Rotating and slice navigation*

The ability of rotation allows the change of dynamic information while preserving shape and viewing data.<sup>114</sup> Slice navigation, on the other hand, includes the options of on-axis and off-axis navigation. On-axis refers to navigation along the x, y, and z dimensions, while the off-axis denotes the tool's ability to display slice-wise information at arbitrary oblique cuts through the data. Why is this useful? For example to display streamlines in their most suitable anatomical context.<sup>40,41</sup>

#### *View*

There are two types of views available: multiple-linked views (MLVs) and single views. The exploration process within a tool allows users to modify various parameters, thereby altering the visual output. For instance, these changes can affect the displayed information, its quantity or resolution, and even transform the display type. MLVs enable users to quickly view scenarios, compare dimensions, and investigate attributes like dependencies and sizes,<sup>115</sup> see Figure 12.

### 4.3.5 | Scaling

Numerous articles in the field of visualization underscore the importance of observing diverse scale levels, a concept frequently implemented in interactive applications. This practice is commonly known as multiscale viewing, which we will refer to as scaling.<sup>116</sup>

#### *Zooming and panning*

The concept of focus+context in Information Visualization stresses the importance of displaying data across multiple scales: users should be able to zoom in for detailed examination while maintaining an overview and understanding of the broader data context.<sup>116</sup> However, there exist tractography visualization tools able to zoom but lacking the ability to pan. As a result, users must zoom out to rotate to a different area, restricting smooth exploration and navigation.

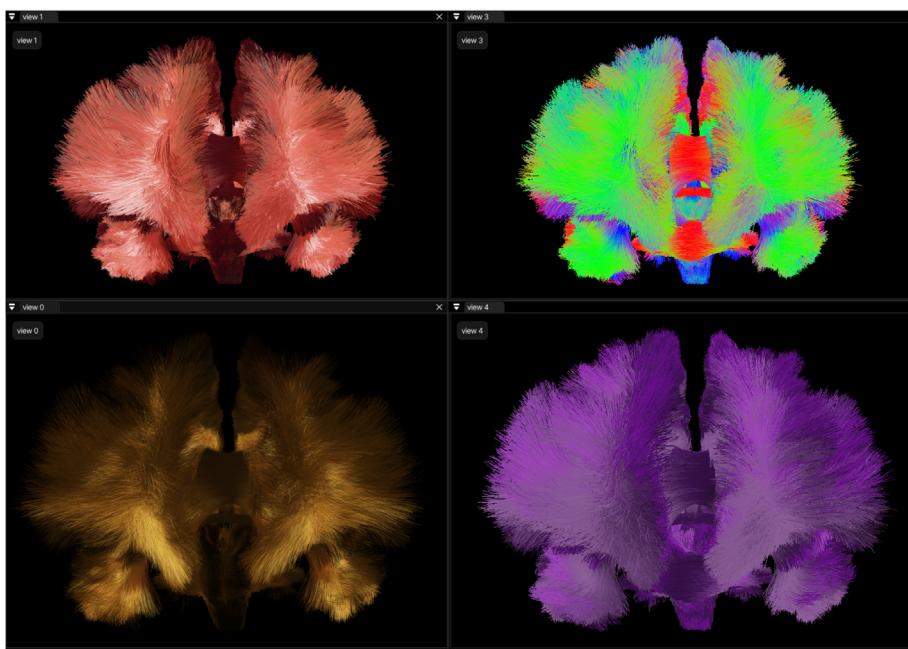
## 5 | SUMMARY

We have emphasized the significance of interactive data exploration and high-performance visualization in handling the challenges posed by large and complex multi-dimensional tractography data.

A list of 27 tractography visualization tools has been qualified based on a set of six criteria. These tools consist of a unique combination of features summarized in Tables 2, 3, and 4, serving as a starting point for a systematic exploration of different features within frameworks.

The taxonomy outlines three primary branches in tractography visualization. Firstly, it distinguishes between tools suited for users based on their intended data usage and programming proficiency. Secondly, it identifies a spectrum of visualization techniques including glyphs, streamlines, 2D and 3D encodings, and data formats. Thirdly, it characterizes different forms of interactivity, such as sampling, filtering, layering, orientation, and scaling.

This comprehensive overview aims to offer insights into the current landscape of visualization techniques in this domain. The survey revealed the large array of available tools, visualizations, and interactive techniques for visualizing tractography data. Despite the recent focus on processing techniques, there's a growing need for innovative reproducible visual analysis methods.



**FIGURE 12** The use of MLVs for multi-subject (and multi-metric) comparison. Tool: Neurotrace.<sup>79</sup>

## 5.1 | Recommendations and limitations

In a taxonomy, data is viewed as a representation of the world. As a taxonomy reflects a representation, the taxonomy is creator-dependent and static, capturing a moment in time. These two aspects make it sensitive to different views and perspectives, as well as to innovation and development over time (see Figure 1). This taxonomy serves as an initial proposal, leaving room for debate regarding the branches and subsequent levels within. The primary objective of this survey was to offer a clear and structured overview of the recent advancements in this field over the past two decades, specifically tailored for novice researchers in neuroimaging, as mentioned in Section 1. It would be of great interest for future research of tractography visualization tools to engage in multi-disciplinary discussions within the neuroimaging field to determine essential, lacking, or excessive features. While this survey has focused on the most prevalent features in tools, features such as color, multi-modality (e.g., ultrasound, EEG), and tool dependencies could enrich the analysis. For example, the ‘data formats’ sub-branch of visualization types could be expanded to include multi-modality or data types. The decision to exclude this aspect in the survey was due to the focus on the visualization aspect of the tool, as well as the vast array of file types used in practice.

The data collection process for this taxonomy was not self-evident. The level of documentation, including user manuals, tutorials, user support, wiki's, courses, workshops, screenshots, and videos, varies significantly across tools. It is advisable for each tool to create comprehensive documentation outlining all functionalities to ensure users understand its capabilities and how to utilize them. It would also be recommended for new tools to explicitly specify the features they include or exclude, for example, in a table format, either as an overview in the published paper or on the website. This upfront clarification would provide users with a clear understanding of the tool’s capabilities and limitations. The features highlighted in this survey could serve as an initial starting point to implement this practice in future media.

This concept could be taken to the next level by the development of a platform aimed at tractography advancements. A platform might better accommodate the dynamic nature of tractography software development. There have been efforts, such as the Common Toolkit ([www.commonkt.org](http://www.commonkt.org)), aimed at collecting common concepts in medical imaging software to increase collaboration and prevent redundant work in the field. We propose not merely merging common ideas, such as ‘umbrella tools’, but to create a platform that updates and provides an overview of the diverse range of tractography-related techniques, including processing, visualization, interactivity, statistical approaches, etc. Emphasizing the importance of clear, transparent, and easily accessible documentation. Currently, getting a comprehensive understanding of this relies on researchers publishing surveys. A centralized platform could provide this overview, without having to shift through numerous academic papers, hence, simplifying the analysis of (the latest) techniques, and the development of potential new tools.

Finally, we suggest that the community consider proposing an updated tractography dictionary to enhance consistency in the terminology used. As discussed in Section 2.1, the current terminology is relatively outdated, and with new advancements, more updated terminology is necessary.

We hope that these recommendations encourage the community to enhance the consistency and transparency of tractography visualization tools.

## 5.2 | Future work

Validating the accuracy and reproducibility of tractography visualization is crucial for establishing reliable scientific conclusions and achieving effective clinical outcomes.<sup>4</sup> As mentioned in Section 2, this remains a challenge within tractography visualization. To go beyond simply advocating for transparent evaluation and independent replication of scientific output,<sup>7</sup> we would like to propose a set of ideas.

We believe that the future of tractography visualization lies in ensuring and understanding the effect of techniques and parameters used throughout the multi-step process on the accuracy and reproducibility of tractography visualization. This is particularly important given the advancements and increasing complexity of newer approaches, such as machine learning-based tractography.<sup>117</sup>

While we understand the importance of both clinical and research tools, a tool dedicated to tractography education would be invaluable for novice researchers. Such a tool could focus on experimentation, allowing users to directly see the effects of their choices in later stages. We can draw inspiration from educational tools like VirtMRI,<sup>118</sup> designed for teaching MRI.

Additionally, enabling the option to download and import ‘figure settings’ would promote consistency and repeatability in visualizations, facilitating batch processes of images and collaboration through standardized parameters.

We hope that these suggestions for future work stimulate the community’s growth in validating the accuracy and reproducibility of tractography visualization.

## AUTHOR CONTRIBUTIONS

Miriam Laamoumi: Conceptualization, Methodology, Formal Analysis, Investigation, Writing—Original Draft & Editing; Tom Hendriks: Supervision, Methodology, Formal Analysis & Writing—Review; and Maxime Chamberland: Supervision, Conceptualization, Methodology, Formal Analysis, Writing—Review & Editing.

## CONFLICT OF INTEREST STATEMENT

The authors declare that there are no conflicts of interest regarding the publication of this paper.

## DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

## SUPPORTING INFORMATION

Additional supporting information may be found in the online version of the article at the publisher’s website.

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## ENDNOTE

\* Based on information found on the tool’s website, forum, or associated paper.

† <https://github.com/tee-ar-ex>

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## APPENDIX A

A JOURNAL TYPE.

**TABLE A1.** An overview of the journals (and conferences) with their type.

Journal type	Journal/conference name
Biomedical	Journal of neuroscience methods, <sup>30</sup> Brain connectivity, <sup>63</sup> The insight journal, <sup>65</sup> bioRxiv, <sup>66</sup> IEEE transactions on medical imaging <sup>69</sup> Medical Image Analysis, <sup>70</sup> MICCAI 2007, <sup>76</sup> ISMRM 2016, <sup>77</sup> Methods Inf Med, <sup>78</sup> Biomedical Engineering, <sup>80</sup> Aperture Neuro, <sup>81</sup> JCO Clinical Cancer Informatics, <sup>84</sup> Connectomics in NeuroImaging 2017, <sup>85</sup> Frontiers in neuroinformatics, <sup>44,47,75</sup> Neuroimage, <sup>41,46,74</sup> Proc. Intl. Soc. Mag. Reson. Med. <sup>67,72,82</sup>
Computer science	IEEE Visualization, <sup>45</sup> Journal of open source software, <sup>68</sup> ICCSA 2007, <sup>71</sup> PacificVis 2021, <sup>73</sup> International Workshop on Computational Diffusion MRI 2023 <sup>79</sup> , ACM SIGGRAPH 2013 <sup>83</sup> , Journal of vision <sup>86</sup>
Both	International journal of imaging systems and technology, <sup>40</sup> Computers and Biomedical research, <sup>62</sup> Nature Communications <sup>64</sup>