A Survey of Macroscopic Brain Network Visualization Technology*

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Abstract — Brain science, as an important branch of Neuroscience, is a discipline that studies the structure and function of brain nervous system of human and other mammals. With the invention of new technologies such as brain imaging, light microscopes and brain electromagnetics, brain science is gradually unraveling the mysteries of human emotion, intelligence and behavior. In this wave, data visualization punctuates the landmark advances in brain science since its beginning. This survey reviews the recent literature on brain network visualization (aka connectome) from the fields of both connectomics and visualization. In particular, we focus on the macroscopic-level brain network visualization techniques, that reveal the structural and functional connectivity of the whole brain, in comparison to microscopic-level neuronal connectivities. We also discuss the interactive visualization tools currently available for viewing the brain networks. Finally, we conclude with a number of ongoing challenges in macroscopic brain network visualization.

Key words — Brain network, Connectomics, Visualization.

I. Introduction

Connectomics is a division of neuroscience that studies connectome, i.e., the map of the neuronal system in the brain and all its connections among neuronal structures. The goal of connectomics is to create a complete representation of such map by understanding the brain’s wiring mechanism[1]. It is believed that the representation of connectome can help to increase our knowledge of how functional brain states emerge from their underlying anatomical structure[2].

Studies of the connectome, also know as the brain network, are becoming increasingly popular in the fields of neuroscience, computer science and neurology. Modern brain connectivity and brain network data have typical big data properties, because of the large variety of features recorded and represented. According to the taxonomy of brain networks, three types of connectivity can be distinguished. First, structural or anatomical connectivity usually represents the physical connections between neural elements by a “wiring diagram”. Second, Functional connectivity concentrates on “the temporal correlation between spatially remote neurophysiological events”[3]. Finally, effective connectivity concerns the causal interaction between distinct units within the brain nervous system[4].

In Ref.[2], Sporns et al. differentiated among macro-, meso- and micro-scale connectomes. Several image modalities have been invented and employed in connectomics since 1920s, among which Electroencephalography (EEG)[4] is the oldest noninvasive functional neuroimaging technique. While EEG records electrical brain activity from a bundle of electrodes on the scalp, Magnetoencephalography (MEG) measures magnetic fields outside the head which are induced by electrical brain activity[5]. EEG and MEG provide functional connectivity information on the macroscale, as well as some newer image modalities such as functional Magnetic resonance image (fMRI)[6] and Positron emission tomography (PET)[7]. The structural information on the macroscale can be obtained by image modalities such as Single-photon emission computed tomography (SPECT) and Magnetic resonance imaging (MRI)[8]. At the macroscale, the spatial resolution is typically in the range of millimeters and the temporal resolution ranges from milliseconds to minutes (see Fig.1). The mesoscale connectome describes con-
nectivity in the range of micrometers, and lighting microscopy (LM) techniques are the typical image modalities for imaging of living cells. Most of LM techniques focus on structural information of single neurons, with sufficient resolution for the identification of major cell parts, such as dendrites, somas, axons, and also boutons as possible locations for synaptic connections\[1\]. At the finest microscale, the connectome involves mapping single neuronal cells and their connectivity patterns. Electron microscopy (EM) techniques enable imaging of neuronal tissue at the nanometer scale. However, the sample preparation and image acquisition in EM is labor-intensive and time-consuming, and the size of the acquired dataset is up to multiple terabytes.

With the invention of new imaging technologies, brain science is gradually unraveling the mysteries of human emotion, intelligence and behavior. Modern brain science research has generated massive data sets and many brain computation models, closely linked with the progress of information science, especially the big data analysis and artificial intelligence. As our data grows in complexity, visualization of brain imaging data can support the analysis of brain structures and their structural and functional connectivity in a new manner. The visualization of brain network connectivity punctuates the landmark advances in the human connectome research since its beginnings\[9\]. The study of the human brain using both scientific and information visualization techniques has become indispensable and important means of modern brain science.

The left part of Fig.2 summarizes the categories of brain networks according to different spatial resolutions. Such big number of varieties, classifications and imaging modalities leads to the complexity in designing the visualization and visual analysis techniques for brain networks. Corresponding to the study of visualization, we summarize five levels of research topics (right part of Fig.2) from neuron level to individual level, in defining the brain network visualization research. In the finest level, neuron-level brain connectivity visualization mainly presents the datasets on the mesoscale and microscale. The structural information of a single neuron, such as microscopic soma, dendrite, and axon captured by LM techniques, is visualized, as well as the synapse connections captured by EM techniques. Voxel level brain data visualization presents a coarser granularity of brain connectivity information by rendering and interacting with the three-dimensional brain images. The main image modality used in this visualization level is the MRI.

To visualize the global connectivity structure of the whole brain, researchers often use the neural fiber tracing techniques (aka tractography) on brain imaging data to synthesize the connectivity information of individual voxels into continuous streamlines at the nerve fiber level. The direction of each streamline is tangent to the primary eigenvector of the voxel tensor at the voxel location, through which the main direction of the corresponding fiber is represented. Most vector field visualization techniques serve at this level.

Connectivity level brain network visualization discretizes neural fibers into intra-brain connections and further map them to the network structure between the brain regions. These network structures are mainly divided into two types, namely the structural brain network and the functional brain network, which correspond to the anatomical connectivity and functional connectivity, respectively. Different from the three aforementioned levels which mainly rely on the theory and methodology of the scientific visualization, network connectivity level visualization often depends on methods of information visualization. Finally, individual level brain network visualization focuses on the grouping and inter-group comparisons of the human subjects’ brain network. The main research at this level focuses on the visualization and visual comparison among the brain networks of different classes of
subjects, and the brain networks of the same individual in different mental states and life stages.

According to the scope of the brain visualized, we divide the above five levels of brain network visualization into two major categories, i.e., macroscopic and microscopic brain network visualization. Macroscopic visualization mainly focuses on the visualization of high-level brain networks, while microscopic visualization mainly focuses on the visualization of the structure of neuron, such as soma, dendrite, axon and synapse. Although the voxel level visualization also employs the dataset produced by the MRI modality, which is classified to the macroscale connectome by Sporns et al.\cite{2}, the main goal of these studies is to develop novel visual metaphors to visually encode the complex information binding to a single voxel. Therefore, we categorize the nerve fiber level, connectivity level and individual level visualization as the macroscopic brain network visualization studied in this survey. To this end, we review the state-of-the-art macroscopic brain network visualization techniques in the field of both connectomics and visualization. We describe the current brain network visualization techniques to visualize both the anatomical and functional connectivity from different imaging modalities. In Section III, we will further present and discuss the interactive visualization tools currently available for use in research and engineering domains. We finally conclude with a number of challenges in the ongoing macroscopic brain network visualization research.

II. Macroscopic Brain Network Visualization

1. Nerve fiber level

The voxel level visualization (categorized in microscopic visualization) mainly shows the local distribution of the connection in the whole brain. At the nerve fiber level, nerve fiber tractography is often used to connect the connectivity information of individual voxels into continuous streamlines to visualize the global connection structure of the brain. The direction of each streamline is tangent to the primary eigenvector of the voxel tensor at the voxel location, as a result the streamline can represent the corresponding nerve fiber. A three-dimensional vector field is formed by collection all the brain nerve fibers. Therefore, the visualization methods of vector fields attracted much attention at this level.

Firstly, traditional nerve fiber tractography techniques generate definitive streamlines, also known as deterministic tractography, which can be displayed using a variety of visual glyphs. The mostly fundamental method uses a three-dimensional linear representation\cite{10}. The later advanced visualization methods introduced the models of computer graphics and GPU accelerating algorithm to represent the nerve fibers. Petrovic et al. invented tuboid, a fully-shaded streamtube impostor constructed entirely on the GPU from streamline vertices to represent the connectivity between different brain regions\cite{11}. Tuboids require little to no preprocessing or extra space over the original streamline data. Text labeling technique for tuboids that appear attached to the surface of the tubes provides adaptive, aesthetically pleasing labels (Fig.3(a)). Merhof et al. used textured triangle strips and point sprites to obtain a tube-like appearance of streamline representation\cite{12}. By employing GPU programming, they achieved real-time rendering of dense bundles encompassing a high number of fibers with high visualization quality (Fig.3(b)). Peeters et al. presented a curled hair model to show extra tensor properties along the fibers in DTI dataset\cite{13}. They also used line illumination and shadowing of fibers in order to improve the perception of their structure (Fig.3(c)). Also, Zhang et al. employed streamtubes and streamsurfaces to represent structures with linear diffusion and planar diffusion, respectively\cite{14}. The research on traditional nerve fiber tractography mainly focuses on three-dimensional rendering models and computational methods that generate interactive and appealing visualization for further surgery planning. Visual efficiency and interactivity are the two main goals to be addressed by these proposed methods.

![Fig. 3. Deterministic tractography of diffusion tensor imaging dataset. The streamlines are represented using different computer graphic models. (a) The tuboid and its text labeling\cite{11}; (b) A hybrid strategy to obtain a tube-like streamline appearance that combines textured triangle strips and point sprites\cite{12}; (c) A curled hair model to show extra tensor properties\cite{13}; (d) Line-based ambient occlusion with Phong illumination\cite{19}](image)

An important consideration of traditional nerve fiber tractography is the depth perception of fiber tracts. It can be difficult to perceive the spatial structure and the spatial relationship between fiber tracts, because of the two dimensional projection for display and the denseness of the fiber tracts itself. Illuminated stream lines/tubes can...
alleviate the problem somewhat by employing a realistic shading model, which also increases quality and realism of the resulting images (Fig.3(a–c)). Klein et al.[15] proposed distance-encoded contours and shadows for tubes as visual cues for depth ordering. Everts et al.[16] then presented illustrative line rendering with depth-dependent halos based on the observation that line-based techniques outperform tube-based renderings in showing more details of fibrous structures (Fig.4(c)). Inspired by global illumination models in computer graphics, specifically ambient occlusion[17], Díaz García and Vázquez[18] proposed ambient occlusion halos around the fiber tracts to enhance the illustrative results by removing clutter and revealing fibers shapes and orientations. Eichelbaum et al.[19] improved upon these approaches with line-based ambient occlusion technique that improves spatial and structural perception of line renderings (Fig.3(d)).

Secondly, high-dimensional multivariate data are often attached to the nerve fiber streamline data. One simple example is for the fiber bundle names, see Fig.3(a). The visualization of these additional data became a hot issue in recently. A large number of studies have discussed how to model and visualize the uncertainty of nerve fiber tracking results. Probabilistic tractography yields a probability flow field by sampling the same nerve fiber multiple times using Monte Carlo method and counting the ratio of streamlines running through individual voxels. The uncertainty visualization of probability flow field is a hot topic in recent years. The main approaches include the visual encoding of the flow field probability using color channels, such as different color scale[20], transparency[21], and saturation[22]. Besides, Rick et al. present probabilistic flow field information through enhanced 3D depth perception by using virtual reality[23].

Thirdly, bundling and abstraction are another research topics for nerve fiber visualization due to the difficulty of real-time and accurate visualization of the massive amounts of nerve fibers in human brain. Unlike traditional deterministic tractography that emphasizes on photo-realistic rendering of streamline, bundling and abstraction methods often employ a hierarchical method to aggregate nerve fibers into nerve fiber bundles and draw abstractly according to the connection and geometric orientation. Enders et al.[24] presented wrapped streamlines to intuitively represent white matter tracts (Fig.4(a)). Röttger et al.[25] presented the BundleExplorer as a GPU-based focus and context rendering framework for diffusion data. They proposed a combination of a fiber encompassing hull and line rendering to provide insight into inner-bundle fiber configurations as well as to enable bundle crossing exploration (Fig.4(b)). The aforementioned two methods employ direct metaphors (wrapping surfaces and fiber encompassing hulls) that represent the bundle of nerve fibers to highlight their independent characteristics, on the other hand, indirect bundle mapping can also be employed to represent dense nerve fibers with a typical method of depth-dependent halo mapping (Fig.4(c))[17]. The dense nerve fibers can be clustered into multiple nerve fiber bundles according to their geometric orientation. Then the nerve fibers within the same bundle can be drawn in the same color using just a few hint lines, and silhouette and contours are used to improve the definition of the cluster borders (Fig.4(d))[26]. Everts et al.[27] achieved fiber abstraction by analyzing the local similarity of tract segment directions at different scales using a stepwise increase of the search range, which results in a better understanding of the brain’s three-dimensional fiber tract structure.

![Image](https://example.com/image.png)

**Fig. 4.** The visualization of nerve fiber bundle. (a) Wrapped streamlines[24]; (b) A fiber encompassing hull and line rendering from the BundleExplorer[25]; (c) Depth-dependent halo mapping[17]; (d) 49 illustrative clusters using hint lines, silhouette and contours[26].

Finally, interaction design dedicating to lower visual complexity and high performance in exploring massive neural fibers also attracts some interest. Chen et al.[28] introduced a novel interaction method that augments the 3D visualization with a 2D representation containing a low-dimensional embedding of the DTI fibers. The proposed embedding preserves the relationship between the fibers and removes the visual clutter that is inherent in 3D renderings of the fibers. Blaas et al.[29] presented an effective approach that offers facilities to aid the user in selecting fiber bundles of interest using multiple convex objects. Schultz et al.[30] suggested a novel visualization metaphor that supports the visual analysis of classical streamlines from fiber tracking by integrating context from anatomical data. The whole brain nerve fiber connectivity map typically uses a Focus + Context visualization method that highlights selected nerve fiber bundles in the foreground and coarser granularity in the background to present other nerve fibers and brain structure.

2. Connectivity level

The research at connectivity level focuses on brain network structures between the regions of interest inside the
whole brain. The nerve fibers will be firstly discretized into inter-brain connections and further be constructed to form the brain network structure. As mentioned before, structural brain network and functional brain network are the main categories of the brain network structures (Fig.5)[31]. According to its definition, effective brain network can be understood as an extend of functional brain network, therefore, we treat the visualization methods as the same category. In a brain network, the nodes represent the structural Regions of interest (sROI) or the functional Regions of interest (fROI), which are generally extracted according to a certain physical map or a functional map, respectively. The connection between nodes is the inter-region nerve fiber connection for structural brain network, while it is the inter-region activation timing dependency for functional brain network. The brain network usually is a undirected weighted network, since the connections are of weight but no direction.

For functional brain network visualization, due to the complexity of potential connections between fROIs and unconstrained mappings between real and logical brain space, graph layout algorithms are often introduced to map functional brain network to logical space (usually in 2D space) to optimize the aesthetics of layout. Salvador et al.[35] depicted a neurophysiological architecture of functional magnetic resonance images of human brain by using a dimensionality reduction method (such as MDS) to map the real brain space into a two-dimensional logical space. It makes the visualization more clear to be understood by the compromise between the authenticity of the structural layout and the legibility of the functional layout (Fig.6(c)). Analogously, Achard et al.[36] created undirected graphs of functional brain networks directly after thresholding the wavelet correlation matrices. They constructed a more clear topological map of a small-world human brain functional network (Fig.6(d)).

New visual metaphors except the classical node-edge that represent the brain network connectivity are invented and introduced in brain network visualization. The adjacency matrix is another common visual metaphor used in functional brain network visualization. As shown in Fig.7(a)[37], each row/column of the matrix can represent a functional region of interest in brain space, while the filled color of each cell can represent the strength of the neural connectivity between two regions of interest.
The detailed visual design of the matrix cell can also be used to compare the differences between individual structural/functional brain networks (see Section II.3). The adjacency matrix metaphor is more suitable for the functional brain network visualization because of the higher complexity of the functional connectivity than structural connectivity. Sanz-Arigita et al.\cite{38} used a matrix-based graph analysis on resting-state condition fMRI data to study connectivity changes in early Alzheimer’s disease (AD) (Fig.7(b)). Besides, ChordMap (Fig.7(c))\cite{39} and NodeTrix (Fig.7(d))\cite{40} metaphors were introduced by McGonigle et al. and Yang et al., respectively, to simultaneously represent and visualize the brain network connectivity and the hierarchical structures of the brain.

In particular, the structure of functional brain network is usually time-varying. Inspired by the way people comprehend and manipulate physical cubes, Bach et al.\cite{41} introduced matrix cube metaphor (Fig.8(a)) for dynamic networks. The third dimension of time is added to the two-dimensional adjacency matrix, and specifically designed interactions are used to guide the user to discover the important two-dimensional visualizations that emphasize specific aspects of the dynamic network suited to particular analysis tasks. They also proposed small multipiles (Fig.8(b))\cite{42} and time curves (Fig.8(c))\cite{43} metaphors consecutively in their subsequent research work. The multipiles metaphor is based on the physical analogy of piling adjacency matrices, each one representing a single temporal snapshot, while the proposed ‘piling’ metaphor presents a hybrid interface to help neuroscientists investigate changes in brain connectivity networks over several hundreds of snapshots\cite{42}. Time curves is a general approach for visualizing patterns of evolution in temporal data. It pays more attention to show the time-varying characteristics of dynamic network structure. By mapping a set of timing networks into curves that connect multiple nodes, the time-varying similarities between dynamic functional brain networks or individual differences are highlighted\cite{43}.

3. Individual level

Finally, the individual level visualization of brain network mainly focuses on the research of grouping and intergroup comparison of human brain networks, with the major aim of assisting neuroscientists on the mechanism of some certain diseases. In contrast to the aforementioned four levels, the main work at this level is about visual comparison of brain networks among different individuals, or among different states and phases of the same individual. In other words, researchers paid more attentions on functional brain network at this level.

Fair et al.\cite{44} reported their research findings that, over development, the organization of multiple functional networks shifts from a local anatomical emphasis in children to a more distributed architecture in young adults. As shown in Fig.9(a), regions in children are largely organized by their anatomical location, but over age anatomically clustered regions segregate (top row), while the more distributed adult functional networks in children are in many ways disconnected and they integrate over development (bottom row).

Grouping according to the individual attributes is usually employed before visualization and visual analysis of functional brain networks. Daianu et al.\cite{45} analyzed anatomical connectivity based on 3-T diffusion-weighted images from 111 subjects, which are categorized in 4 groups, to better understand how AD affects brain con-
nectivity. They performed whole brain tractography based on the orientation distribution functions, and compiled connectivity matrices showing the proportions of detected fibers interconnecting 68 cortical regions. Fig. 9(b) shows the asymmetries in anatomical connectivity in healthy elderly (top left), early (top right) and late mild cognitive impairment (bottom left), and AD (bottom right), where the colors encode p-values from their regression model comparing the left and right hemisphere connectivity matrices.

The main difficulty in the visualization and group comparison of individual-level brain networks is the alignment of network nodes in different individuals. So far, the measurement of the brain network at the microscale (typically for EM) and mesoscale (typically for LM) is still confined to a very small sub-region of the whole brain, therefore, the individual level brain network visualization and analysis are performed mainly based on the dataset acquired at the macroscale. The same set of brain network nodes of the whole brain atlas for all individuals is classified to reduce the complexity and difficulty of comparing macroscopic brain networks. Zalesky et al.\(^46\) proposed a Network-based statistic (NBS) to identify differences in brain networks. Fig. 9(c) shows their visualization to present the comparison between the results of the network-based statistic approach (bottom row) and the results of link-based FWE control method (top row). The orange nodes correspond to connections that are part of the contrast (which is absent in Fig. 9(c), refer Ref.\(^46\) for more details) and correctly identified as true positives, while the red nodes correspond to connections that were not part of the contrast but incorrectly identified.

Recently, the research of individual level brain network visualization mainly focus on two issues: 1) how to visualize the grouping of brain networks; and 2) how to visually compare the brain networks of different groups. As shown in Fig. 10(a)\(^47\), the strength of selected connections between network nodes of the same group of individuals is averaged and then mapped to the visual channels, such as color and width, of the edges of the brain network. However, this method does not show the distribution of the connection strength within the group. Wang et al.\(^48\) proposed a solution inspired by scientific visualization that superimposes individual brain networks in the same group to form a volumetric dataset, and then visualize such dataset using volume rendering to show the connection strength distribution (Fig. 10(b)). Visual clutter may occur due to the high density of connections of human brain networks when we employ the node-edge metaphors. Alpers et al.\(^47\) systematically studied the user analysis abilities of node-edge and adjacency matrix metaphors in a variety of visual comparison designs, and reported that the use of adjacency matrix metaphor and their superimposed design can significantly improve the user analysis ability. Shi et al.\(^49\) also analyzed the visual comparison performance of graph-based brain network visualization, and proposed an integrated framework to orchestrate computational models with comprehensive data visualizations on the human brain network, which greatly improves the performance of visual comparison of the brain networks (Fig. 10(c)).

### III. Softwares in Brain Network Visualization Community

There have been multiple applications and software packages that are designed to process, visualize and visually analyze brain network datasets. Some lists of them are found at wikipedia.org\(^\ast\ast\ast\). In this section, we enumerate some typical and popular tools used in brain network visualization community.

An early and probably the most popular software package is Diffusion Toolkit (DTK, http://trackvis.org), which is designed for diffusion imaging data processing and tractography\(^50\). DTK is implemented in C++, using Qt (https://www.qt.io/) for the graphical user interface and Visualization Toolkit (VTK, https://www.vtk.org/) for the visualization core. It can handle large whole brain tractography datasets including Diffusion tensor imaging (DTI) data, High angular resolution diffusion imaging (HARDI) data, Diffusion spectrum imaging (DSI) data and Q-ball imaging data. Two components, diffusion

\(\ast\ast\ast\) https://http://trackvis.org

\(\ast\ast\) https://en.wikipedia.org/wiki/List\_of\_neuroimaging\_software

\(\ast\ast\*) https://en.wikipedia.org/wiki/List\_of\_functional\_connectivity\_software
toolkit itself and the visualization program called TrackVis (Fig.11), are comprised in the software package and are cooperating in reconstruction, fiber tracking, analysis and visualization of brain tractography data. Some of the most striking examples of tractography can be found in their subsequent articles, such as Ref.[51].

Fig. 10. New approaches to visual analytics of individual level brain networks. (a) Visual representation of the average strength of connections[47]; (b) Visual representation of the strength distribution of connections by superimposing individual brain networks in the same group[48]; (c) The framework for the visual exploration of multi-label brain networks and the visual comparison among brain networks across different subject groups[49]

Fig. 11. A snapshot of TrackVis

Chen et al.[28] developed an effective interaction mode (Fig.12) that combines 3D, 2D, and statistical views to broaden the user’s exploratory space, which was designed to enable efficient browsing, manipulation, and quantitative analysis of DTI fiber tracts. Intuitive interactions such as rotation, lens viewing, coloring, slicing, and selection are provided in a three-dimensional view (left side of Fig.12), as well as a traditional fiber tracts visualization. Specially, their two-dimensional point embedding (right side of Fig.12) of the DTI fibers preserves the relationship between the fibers and removes the visual clutter that is inherent in 3D renderings of the fibers. Later, Jianu et al.[52] proposed two-dimensional neural maps (Fig.13) for exploring connectivity. Rather than using two-dimensional point embedding as aforementioned, the planar path representation (bottom panels in Fig.14) may be more intuitive and easier to use and learn.

Fig. 12. A snapshot of DTI fiber exploration system from chen et al.[28]

Fig. 13. An interactive analysis system using linked views and planar tract-bundle projections[52]

Fig. 14. The graphical user interface of OpenWalnut

Most of softwares in research community may largely aim either at visualization researcher or the neuro-scientist, who own expert knowledge. Such softwares are usually designed to answer a certain set of questions and handle certain data sets from different imaging modalities, with accordingly designed graphical user interfaces. In open source community, softwares may be designed to be used with different signals, modalities and data types, aiming at a general purpose of data processing workflow.
and interactive rendering and explorability user interface. 3D Slicer is a free open source software application for medical image computing, which not only supports versatile visualizations but also provides advanced functionality such as automated segmentation and registration for a variety of application domains. OpenWalnut is another open source software package in brain network visualization community. It has a modular design and a built-in pipelining engine with drag-and-drop graphical user interface (Fig.14). OpenWalnut integrates several well-known toolkits, such as Eigen (http://eigen.tuxfamily.org), OpenSceneGraph (http://www.openscenegraph.org) and BioSig (http://biosig.sourceforge.net), etc., to utilize their strengths and make itself more extensible and flexible. Due to the large scale of the amount of connectivity data, Eklund et al. implemented a GPU accelerated interactive interface for exploratory functional connectivity analysis. The connectivity analysis was written in Open computing language (OpenCL, https://www.khronos.org/opencl/). The correlation map of all voxels in fMRI data can be updated in real-time, which greatly facilitates the analysis of the connectivity patterns in the brain. The interactive tool was implemented in the MeVisLab (https://www.mevislab.de) software environment, which also supports an intuitive pipeline editing with abundant data processing, interaction and visualization components.

Previously described softwares in this section mainly focus on the visualization of structural connectivity, however, the inherent multi-modality of connectome datasets poses new challenges for data organization, integration and sharing, as well as knowledge based data processing, such as data mining, exploration and comparison. Gerhard et al. designed and implemented a set of extensible and also open source neuroimaging tools, called Connectome Viewer Toolkit. The plugin architecture of itself supports extensions with network analysis packages. The toolkit is written in Python, which also make it much easier to integrate and utilize the numerous existing powerful libraries, such as graph theory based analysis and other data mining algorithms, from scientific python community. The popular brain network visualization tool mentioned in Section II.2, called BrainNet Viewer, employ a graph-based network visualization to illustrate human connectomes as ball-and-stick models. The toolbox is notable for its diversity with both network mapping and surface-based data presentation. BrainNet Viewer is implemented using MATLAB with a friendly graphical user interface, helps researchers to visualize brain networks in an easy, flexible and quick manner.

Although impressive improvements in software distribution has been made in recent decades, there is still a wide gap between software developers and users. Issues of installation, configuration and running of softwares may be prone to occur due to complexity of operation system environments, including but not limited to software dependency, hardware driver version, etc. However, recent advancements in web technologies give promise of a change for the better. The improvements of JavaScript and WebGL make the developing of full-fledged three dimensional graphics applications that can run in a general web browser (e.g. Google Chrome) possible. Nowadays, a web browser based application can offer a friendly graphical experience comparable to most of traditional stand-alone desktop client. Meanwhile, the issues of burdensome configuration of runtime environment are also overcome because the applications will run in a web browser as a web service and some native JavaScript programs which execute on a built-in JavaScript engine. Haehn et al. contributed “The X Toolkit” (XTK), the first JavaScript-based framework for visualizing and interacting with medical imaging data using WebGL. The toolkit is geared towards powerful scientific visualization and provides a simple Application programming interface (API) which hides low-level elements of WebGL from users.

IV. Conclusions

In this survey, we first categorize the visualization techniques on interpreting brain networks into five levels, according to the diverging research targets ranging from a single neuron up to fibers, networks, and groups of brain networks. We focus on the macroscopic brain network visualization techniques where the whole brain network, including its structural connectivity and functional connectivity, attracts the most attention. As the massive brain imaging data nowadays is captured by a wide variety of modalities, it is intuitive to depend on the visualization to arrive at a thorough understanding of such digital data. In other words, learning how the human brain works is an important neuroscience goal, which leads to the emerging discipline of connectomics that analyzes the neuronal connectivity. However, visualizing the whole brain network is a challenging task due to the complexity of the human brain neuronal system, which has an estimated number of 10^{11} neurons and 10^{15} connections. Visual clutter may be prone to exist when we visualize such a whole brain network. Abstraction, projection, bundling, and many other techniques are widely employed to make the visualization result more readable. These challenges demand attentions on many research compromise, such as thoroughness/readability, aesthetic appeal/information content, and faithfulness/abstraction, etc. In addition, there also are ethical concerns if we dive into the brain connectivity research due to the uniqueness of the human brain compared with the other body blocks.

There are several software from the brain network visualization community offered as powerful tools for the
interactive exploration and analysis of neuronal connectivity. Advanced neuroinformatics tools are also required for the full-scale connectome mapping, analysis, and visualization, with intuitive interaction design on selection, rotation, moving and labeling, etc. The inherent multimodality, as well as the huge data volume, poses many new challenges on the data cleaning, storage, integration, registration, and organization. In the early stage of the brain network visualization research, scientific visualization methods, in combination with the image analysis techniques, were mostly used to emphasize the rendering and interactive exploration of faithful structural connectivity. More recently, the latest research has focused on introducing information visualization methods to visually display and analyze brain networks through novel visual metaphors, effective data mining algorithms, and accurate machine learning models. The construction of a general platform for the visual analysis of macroscopic brain network in multiple levels is also a promising research direction.

References


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