ARTICLE IN PRESS

YNIMG-10423; No. of pages: 18; 4C: 3, 4, 5, 6, 7, 8, 9, 10, 11, 14

NeuroImage xxx (2013) xxx–xxx

Contents lists available at SciVerse ScienceDirect

NeuroImage

journal homepage: www.elsevier.com/locate/ynimg

Review

Visualizing the human connectome

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A R T I C L E   I N F O

Article history:
Accepted 26 April 2013
Available online xxxx

A B S T R A C T

Innovations in data visualization punctuate the landmark advances in human connectome research since its beginnings. From tensor glyphs for diffusion-weighted imaging, to advanced rendering of anatomical tracts, to more recent graph-based representations of functional connectivity data, many of the ways we have come to understand the human connectome are through the intuitive understanding these visualizations enable. Nonetheless, several unresolved problems persist. For example probabilistic tractography lacks the visual appeal of its deterministic equivalent, multimodal representations require extreme levels of data reduction, and rendering the full connectome within an anatomical space makes the contents cluttered and unreadable. In part, these challenges require compromises between several tensions that determine connectome visualization practice, such as prioritizing anatomic or connectomic information, aesthetic appeal or information content, and thoroughness or readability. To illustrate the ongoing negotiation between these priorities, we provide an overview of various visualization methods that have evolved for anatomical and functional connectivity data. We then describe interactive visualization tools currently available for use in research, and we conclude with concerns and developments in the presentation of connectivity results.

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Introduction

When investigation of the human brain was limited by what the eye could see, its structure, albeit elaborate, was within our mental

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1053-8119/$ – see front matter © 2013 Published by Elsevier Inc.
http://dx.doi.org/10.1016/j.neuroimage.2013.04.111

Please cite this article as: Margulies, D.S., et al., Visualizing the human connectome, NeuroImage (2013), http://dx.doi.org/10.1016/j.neuroimage.2013.04.111

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grasp. But the resurgence of interest in connectivity, like that of cytoarchitectonics a century ago, has established a new dimension of information to assimilate. As our data grow in intricacy, the images we create reflect how we bestow them with significance — because implicit (and often explicit) in our visualizations of the human connectome are the categories, metaphors, and abstractions that we use to make it comprehensible.

An analogous transition in visual metaphors was underway with the emergence of mass transit systems over a century ago. Much like the complexity of the brain, the unfamiliar transport systems presented a challenge of how to effectively communicate their structure to the public. Early London Underground maps found comfort in familiarity, and wove the train paths unobtrusively into the contours of the existing cityscape (Fig. 1, *top*). It was only decades later that the crisp, emblematic form – subsequently mimicked the world over – came into being (Fig. 1, *bottom*). In emphasizing the relative connections, rather than the underlying terrain, the resultant image offered the viewer an intuitive mapping of the *relevant* information. Maps never show us everything about a place or a space; their value is rather in the cartographer's insight to enunciate selected features over others.

Every map has a context — and when the content is overflowing with innumerable data dimensions, the task of creating *intuitive*, *informative*, and *candid* images becomes all the more challenging. The mapping of connections in the human brain has been a visual tale of increasing complexity, continuously pulled between various priorities of data presentation. Our illustrations and figures narrate the transition from describing the brain as a three-dimensional object to describing the proximity of areas in terms of the strength of connections. These two basic models of brain space, though there are more, are the basis for the territorial battles for defining space. The result in any connectome image is a content-dependent balance of *anatomical clarity* versus *connectomic complexity*.

Connectivity mapping has also been forced to struggle with evolving methodologies — analytic tools that in some cases may have overstated their actual information content. Controversies surrounding the veracity of paths derived from diffusion weighted imaging-based tractography (Dyrby et al., 2007; Hubbard and Parker, 2009; Jbabdi and Johansen-Berg, 2011) or functional connectivity derived using controversial analytic approaches (e.g., Saad et al., 2012; Smith et al., 2011) run the risk of visualizations that make the underlying data appear deceptively tangible. The aim of an image, from this perspective, is to accurately show the uncertainty in the data (Allen et al., 2012b) — be it statistical or methodological. Given the high information content of connectivity data, *prioritizing honest depictions of uncertainty*, *while also rendering the wealth of available data in an intuitive form*, is a formidable challenge.

A third tension of human connectome visualization is the balance of *complexity and simplicity*, otherwise stated as *thoroughness and readability*. What is the most effective and appropriate scale to chunk the data? The meaningful unit could be a parcellation of local modular regions, large-scale independent networks, or each and every unsmoothed voxel. The meaningful unit could be individual fibers, bundles, or something in between. A meaningful unit may be a hypothesis about the role of a specific region or connection, and its significance might dynamically alter from moment-to-moment or across the lifespan. The way we define it, the scale we chose, has consequences for the subsequent visual story we will need to convey. Visual simplicity may often be desired, but not necessarily at the cost of genuine information loss.

The aim of this review will be to provide a critical overview of connectivity visualization methods for the human neuroimaging community, calling attention to gaps and weaknesses, as well as innovations from other fields that may benefit our own. Pfister et al. (2012) recently reviewed connectomics for a scientific visualization audience, and provided a thorough overview of the methodologies and specific challenges across a wide range of neuroscientific fields. While the review provides a valuable introduction to connectivity for a visualization audience, no overview yet exists aimed at the unique concerns of the human neuroimaging community, although there is growing interest in visualization-focused publications (Allen et al., 2012b; Irimia et al., 2012b; Pyka et al., 2010).[1] Reviewing the progress and current limitations, we will begin by presenting the literature related to functional and anatomical connectivity visualization, characterizing both the predominant trends and selected innovations. Research practice itself will be the focus of the following section, where we review software for the exploration of connectivity data. The final discussion on data presentation and publication considers how we currently present connectivity results and how we could in the future. We will address the impact of connectome visualization on its interpretation, online publication tools for data presentation, and domains that hold promise for innovating novel techniques.

Of glyphs and paths, matrices and graphs

The building blocks of connectome visualization are symbolic units. For anatomical connectivity these units express directional information at each voxel; for functional connectivity they may be any number of data reduction steps that result in describing a statistical relationship between regions. From these fundamental elements, various analyses produce individual connections, which together form the connectome. At each stage of data transformation, opportunities for visualization arise, each with their own emergent challenges for maintaining clarity and faithfulness to the underlying data. The following section will follow that path from data unit to connection to connectome, and finally to the added complexity of visualizing dynamics and multimodality. With each new technique, there will be options and opportunities to prioritize certain aesthetic values and information content over others, with rarely an optimal context-independent solution. The result is that the connectome emerges as a product of these choices.

Anatomical connectivity

The most visually arresting connectivity images arguably belong to the anatomical family. Composed of a variegated nest of interwoven fibers, diffusion weighted imaging-based tractography continues in many ways to stay at the forefront of computer visualization research. From the get-go, the methodological origins of anatomical connectivity were dependent on innovative visualization. To demonstrate that the anisotropy of water diffusion using diffusion-weighted MRI (DWI) reflects the orientation of white matter, the pioneering publication relied on red and blue to represent two orthogonal directions (see Fig. 4 from Douek et al., 1991). Rather than each voxel only containing a single scalar value of information (Fig. 2a), two independent values could simultaneously be represented (for an example of three dimensions, see Fig. 2b). The following two decades of research into anatomical connectivity using DWI are the further exploitation of the limited space of the voxel.

Glyphs

In order to visualize the richness of information contained in multidirectional DWI data, it is necessary to show more dimensions than possible with only the display of scalar values or the three dimensions that color easily affords. This first became apparent for diffusion tensor imaging (DTI), where diffusion is modeled as a tensor of rank two (with six degrees of freedom) at each voxel. In order to display these tensors, *glyphs*, generally defined as small *localized visual representations of multivariate information*, in the shape of ellipsoids were used (Fig. 2c; and see Fig. 7 from Basser et al. (1994)). The ellipsoid

[1] Another example and resource is the Beautiful Brain project from Brainhack 2012: http://www.brainhack.org/wiki/doku.php?id=beautifulbrain.

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