

Functional Connectivity Glyphs for Brain Visualization

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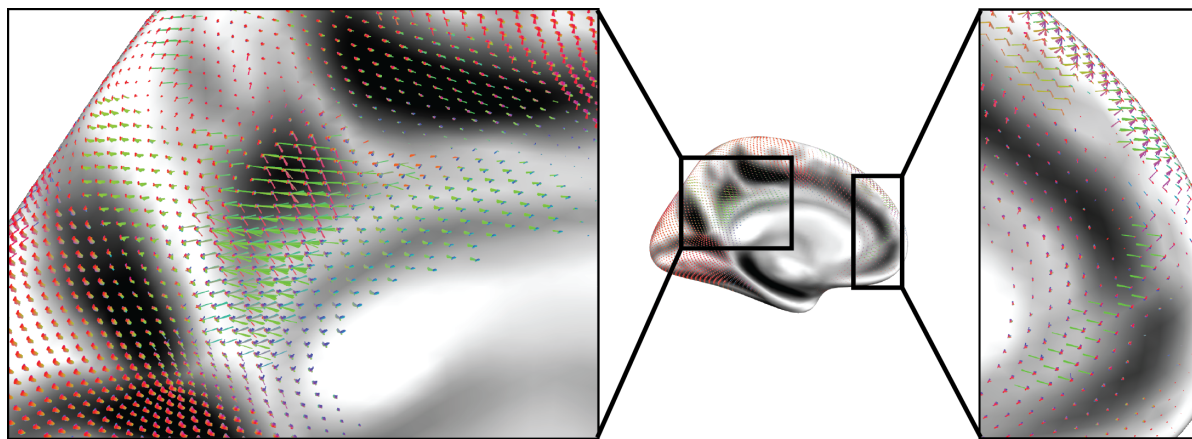


Figure 1: Detail views of the posterior (left) and anterior (right) parts of the medial wall of the cerebral cortex. The long-range interconnections between these two regions, characteristic of the “default-mode” network, can be seen as the green horizontally oriented vector glyphs pointing toward each other.

Abstract

The correlation of spontaneous brain activity, termed: functional connectivity, has become a valuable method in recent years for mapping brain organization. We present a novel approach to visualize functional connectivity that displays full connectivity between nodes on the cortical surface. Functional connectivity glyphs make it possible to visualize the entire functional connectome within a single image, thus enabling a detailed mapping of different cortical areas based on their connective fingerprint.

Categories and Subject Descriptors (according to ACM CCS): I.3.8 [Computer Graphics]: Applications—

1. Introduction

Understanding how brain organization underlies behavior is among the most challenging research questions in science today. One of the primary lines of research that addresses this question is investigating the human *connectome*—the complete set of connections in the human brain. *Functional connectivity* (FC), based on the correlation of spontaneous fluctuations in brain activity as measured with functional magnetic resonance imaging (fMRI), has

become a valuable method for mapping brain organization. The resulting FC data are of high dimensionality because they describe a connection strength between every pair of data points. Current visualization methods are only able to present one FC map at a time in the three-dimensional or surface-based space, requiring drastic reduction in the initial richness of the full connectivity data during presentation.

Glyphs, small iconic representations at each location in

a rendering, are a common visualization method for the display of spatially distributed multivariate data. We developed *functional connectivity glyphs*, which can show FC of the whole brain in a single image without requiring data reduction. Our method is a valuable tool for investigating functionally relevant boundaries in the cerebral cortex, and for describing overall brain organization.

2. Related Work

2.1. Functional Connectivity Visualization

FC is based the correlation in spontaneous brain activity measured with fMRI. While many methods for analysis of such data exist (for reviews, see [LSS12, MBL*10, vd-HHP10]), visualizations are generally reduced to single brain images depicting a single probabilistic connectivity map using scalar values. As the visualization limitations require that connectivity results are sparse, numerous analytic approaches for data reduction have been developed (e.g., seed-based FC to describe connectivity of specific selected regions [BYHH95, MKU*07, SMD05], and independent component analysis (ICA) to describe large-scale networks [BDDS05, DRB*06, DLBDS*06]). ICA has been proposed for visualizing three networks simultaneously by using one color for each on the same surface [MN06], but seed-based FC forms the analytic basis for the majority of interactive visualization tools [BMH*11, Cox96, EFAK11, SR12, vDVF*10]. For instance, the FC interactive analysis software, *BrainCove* [vDVF*10], is developed at the intersection of visualization and visual analytics, and uses multiple synchronized views with different levels of abstraction and interactive selection techniques. Nonetheless, *BrainCove*, like other similar seed-based FC tools, requires that users iteratively concentrate on different aspects of the data, much like exploring a dark room using a searchlight.

While interactive software may enable the user to interact with FC data, they still do not solve the limitations of current forms of data presentations. Graph-based network mappings enable the visualization to devote the spatial layout to the numerous connections, rather than brain anatomy [ICTH12, MMM11]. However, such methods also require the data to be reduced from the original resolution to a smaller number of regions to improve clarity and reduce computational complexity.

2.2. Glyph Visualization for Diffusion-Weighted MRI

Glyphs are widely used for the visualization of directionality information in diffusion-weighted imaging (DWI) data (e.g., [SK10]), and form the basis for subsequent anatomical tractography methods. DWI data yield a map of multivariate

profiles of diffusion speeds, which are considered a reflection of white matter fibers influencing the random diffusion of water. Directionality of DWI data can be displayed using colors, however, complex glyph representations can be used to represent the probability of diffusion in any given direction. Our approach here is to apply similar methods to display the directional information of FC data.

3. Methods

3.1. Data and preprocessing

fMRI data, acquired while participants were asked to relax, were preprocessed according to [MGH*13]. An anatomical scan was used to create three spatial representations of the cortical surface with the software *Freesurfer* [DFS99, FSD99], which is documented and freely available online (<http://surfer.nmr.mgh.harvard.edu>). The cortical surface, a semi-inflated surface, and a spherical representation each consist of 10242 corresponding nodes (Figure 2). The two hemispheres are created as separate surfaces. Since these surfaces are spatially overlapping in their inflated and spherical representations, we apply a constant offset between them, placing the surfaces as close as possible to each other without overlap. We calculated FC between pairs of nodes using Pearson correlation of the time-series of the surface-sampled functional data. The resultant 10242 x 10242 (for one hemisphere) or 20484 x 20484 (for both hemispheres) connectivity matrices, and the set of surfaces serve as input for our software. The software allows interactive manipulation of a correlation threshold, which is used to calculate which nodes are considered connected.

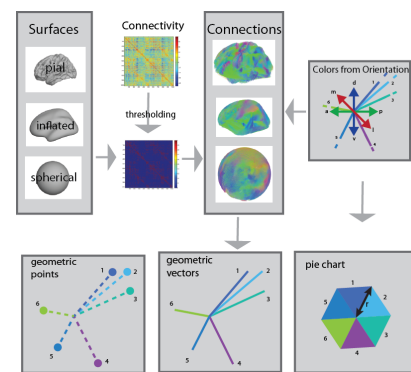


Figure 2: We calculate FC between each pair of nodes on a set of cortical surface representations. Thresholding yields a set of connections that are colored by orientation. Colors and geometry of connections are then used to calculate diverse glyph representations at each node.

3.2. Glyphs

We aim to differentiate cortical areas based on their unique connectional profiles; glyphs should thus enunciate the

unique aspects of each set of connections. We employ small iconic renderings of FC information at the location of each node, enabling the user to visually distinguish between different patterns of FC by integrating across neighbors. To create the glyphs, we use the relative position of all connected nodes to derive color and position of one point, line, or triangle for every connection.

3.2.1. Color

To calculate the color of the display primitives, we use the orientation information of the connections, as previously implemented with DWI data [DTP*91]. For each connected node, we normalize the connection vector, and use the absolute value of the x, y and z components as red, green and blue components, respectively. We then show the connectivity information of each node on the surface by drawing three types of glyphs, which differ in how the colored primitives are spatially distributed on the screen. In the very limited space, the glyphs differ in their ability to represent connectivity compactly or with anatomical accuracy.

3.2.2. Glyph types

Point glyphs: We draw a point g for each connection between points p and q . The point is slightly shifted from the glyph position p by adding a three-dimensional offset based on the analogous connection vector in one of the surface spaces $q_d - p_d$, which is scaled with a small scaling factor s :

$$g = p + s \cdot (q_d - p_d) \quad (1)$$

This results in a small map of the thresholded connectivity for each node at its location. Using node representations in a surface space that is independent from the space used for the glyph position makes arbitrary combinations of rendered surface and glyph shape possible. As all spatial representations can result in the overlap of connections, we also enable a projection from the spherical to a planar circular representation:

$$g_s = p + s \cdot \frac{((q_s - p_s) \cdot xy \cdot (q_s - p_s) \cdot z + r_s)}{2 \cdot r_s} \quad (2)$$

Here, p_s and q_s represent the mapped point and the connected point in spherical space. xy selects only the x and y component of the relative position vector, scaled with the z component. Since r_s represents the radius of the sphere, which is centered around the origin, the z component is shifted to the positive range. The resulting projection is similar to a polar map projection, and is free from overlapping connections (Figure 3).

To better indicate the direction of connections, we draw colored *vector glyphs* by connecting the node position with the above mentioned points using a line. This facilitates navigation between connected areas, and emphasizes long-range connections (Figure 3 & 1). To optimize screen use, we also sort the connections' colors according to their hue, and render each connection as a triangular section of

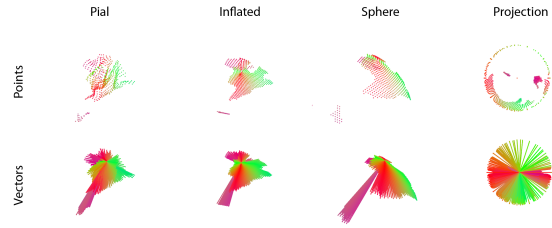


Figure 3: The glyph geometry is influenced by surface geometry (from cortical geometry to the overdraw-free unwrapped projection). Drawing point glyphs diminishes overdraw, while drawing vector glyphs emphasizes long-range connections.

a circular disc. We term the resulting glyphs, which indicate the distribution of connections, *pie chart glyphs*. While these glyphs discard the termination points' geometric information, they visually group similar connections, and facilitate the observation of FC changes across nodes. Pie chart glyphs always face the camera during interactive manipulation of the viewpoint.

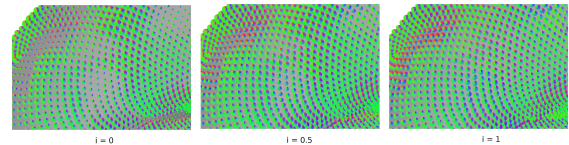


Figure 4: The radius of the pie chart glyphs is linearly interpolated between conveying the number of connections (left) and a constant radius (right).

The relative size of point and vector glyphs is determined by the geometry of the selected surfaces and a scaling factor s , which is interactively adjusted to limit overlap with neighbors. For pie charts, the radius r is also interactively interpolated between constant radius r_n and a radius r_a , which makes the glyph area proportional to the number of connections at that node, by manipulating an interpolation parameter i (see also Figure 4):

$$r = i \cdot r_n + (1 - i) \cdot r_a \quad (3)$$

3.3. Implementation

To enable the rapid interactive display of many glyphs, we integrated our method in the software *braingl* (code.google.com/p/braingl), using hardware shaders for the quick display of geometry. This enables interactive manipulation of viewpoint, threshold, scaling factor, and glyph style. For the pie chart glyphs, the connections are filtered and sorted by color hue before visualization. We tested our software on a workstation with an 8 core CPU

with 3.4 GHz, 16 GB RAM, and a NVIDIA GeForce GTX 590 graphics adapter.

To clarify the renderings, correct occlusion relations with the folded cortical surface are important. Since the glyphs are mostly inside the cortical surface, we offset them towards the camera by a small distance. This renders glyphs on the front of the visualization visible, while preventing the drawing of glyphs located behind the cortical surface.

4. Results

Hardware shaders enable the drawing of all glyphs with fluent frame rates (> 10 Hz). We determined the FC threshold and minimum connection length of short edges interactively (Figure 5). Lowering the threshold enabled visualization of more subtle FC-based structures (with only prominent networks remaining for correlation values above 0.7), but had greater computational demands. For minimum connection length, additional details appeared up to 20 mm, while higher values appeared to remove known FC.

We found the pie chart glyphs especially helpful to visual-

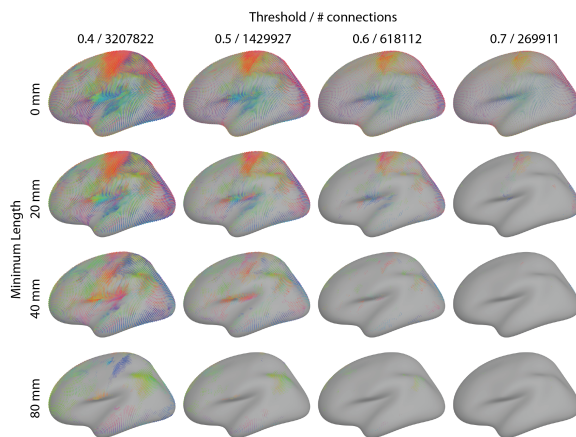


Figure 5: Two free parameters determine the included connections: minimum connection length and correlation threshold. Increasing the minimum connection length removes local FC. The threshold determines the level of FC detail.

ize weaker, more local changes in connectivity, such as between language- and motor-related areas (Figure 4). It was also possible to distinguish gradients and sharp boundaries between areas defined by unique connectivity profiles.

Across all glyphs, it was possible to distinguish the sensory brain networks (motor & visual; Figure 6). Other networks, such as the default-mode networks are also distinguishable (Figure 1), especially using a lower threshold and high minimum connection length emphasizing long-range connections. The vector glyphs assisted in distinguishing areas with

long-range connections from surrounding locally connected areas.

5. Discussion and Conclusions

Glyphs enable visualization and presentation of a full, thresholded FC matrix without requiring data reduction to individual networks. Interactive exploration of the parameter space is made possible through low computational demand, enabling real-time display of changes in parameters. The optimal parameters are a tradeoff between emphasizing different aspects of FC: long range over local connectivity, overdraw against complete information, directional detail against overview of subtle changes, etc. For example, using the anatomically correct cortical surface space makes the colors sensitive to local variation in folding, whereas the inflated or spherical space maximizes color variance. The latter relates color changes to the connectivity profile, rather than topographical orientation.

The limiting factors to transfer of information remain screen

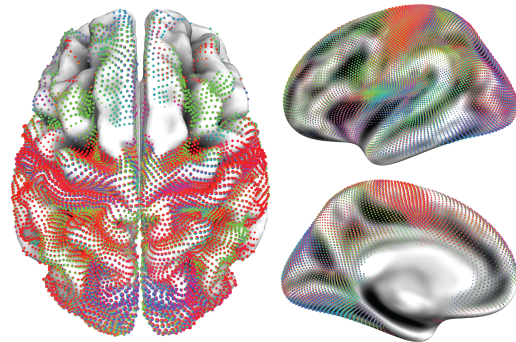


Figure 6: In a whole-brain visualization using pie chart glyphs, several networks area identifiable: the motor network is the red belt spanning across the middle of the cortex, due to its interhemispheric connectivity with prominent x -components. The visual network is a collection of red-blue glyphs in the posterior regions. A multitude of other cortical subdivisions with similar FC fingerprints are visible.

and print resolutions. The space that can be afforded for the depiction of a glyph determines how much detail can be shown. Further improvement of the rendering efficiency and clarity seems possible using level-of-detail (LOD) techniques, which could render different representations of the local connectivity profiles depending on the glyph size on the screen.

The application of our technique to visualize complex connectomic differences between groups, as well as pathological changes in the brain, is promising. While analytic developments continue to address the challenge of mapping the connectome, we believe our method to offer a crucial complementary tool for enabling researchers to understand it.

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