Brain Connectome Visualization for Feature Classification

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Abstract

Visual feature classification provides discriminating power through differential visual representation and feature visualization. This paper presents a new visual feature classification technique using the RYB color model. This technique is applied to a human brain connectome dataset. We visualize the brain regions of interest (ROIs) and their connectome links for three groups of subjects using intuitive color differentiation. ROI features detected this way can be useful for medical diagnosis and neuroimaging analysis.

Keywords: visualization, color model, brain connectome, feature classification, neuroimaging.

1 Introduction

Human connectomics [1] studies how the human brain is wired and how its function is affected by the connectivity pattern using multi-modal neuroimaging data. Research in this emerging field holds great promise for a systematic characterization of human brain connectivity and its relationship to cognition and behavior. The human brain is a complex network of approximately 10^{10} neurons linked by 10^{14} synaptic connections [2]. Given such an unprecedented complexity, we are facing critical computational challenges for comprehensive mapping and analysis of brain connectivity, across all scales. Research in this area has largely focused on extracting brain networks from structural, functional and diffusion magnetic resonance imaging (MRI) data [3][4]. The visualization and related visual analytics of this network has not been well studied [5].

In this paper, we focus on a specific visual connectomic analysis application: features classification for brain diseases. Visual feature classification applies feature visualization techniques to provide discriminating power for data classification. Carefully designed visual representations offers a way to more intuitively and effectively detect features that can best differentiate data groups for diagnosis and analysis [6].

2 Dataset and Brain Connectome

An overview of the brain connectome network construction process based on MRI and diffusion tensor imaging (DTI) data is shown in Figure 1. The pipeline is divided into three steps: (1) Generation of regions of interest (ROIs), (2) DTI tractography, and (3) connectivity network construction.

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ROI Generation: Anatomical parcellation is performed on the high-resolution anatomical MRI scan of each subject to obtain 68 gyral-based ROIs, with 34 cortical ROIs in each hemisphere. These ROIs can be further subdivided so that brain networks at different scales can be constructed.

DTI Tractography: The DTI data are analyzed and processed for fiber tracking using FACT (fiber assignment by continuous tracking). A spline filtering is applied to smooth the tracks.

Network Construction: Nodes and edges are defined in constructing the weighted, undirected network. The weight of the edge is defined as the density of the fibers connecting the pair.

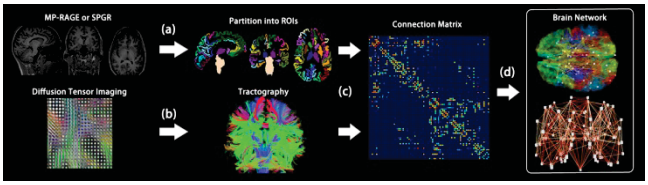

Figure 1. Creation of structural connectivity networks

In our study, the brain connectome data were collected for 134 subjects in 3 categories: HC (Healthy Control, 61 subjects); MCI (Mild Cognitive Impaired, 50 subjects) and AD (Alzheimer's Disease, 23 subjects). For each subject, 68 ROIs (34 in each hemisphere) were segmented and registered. Their connectome edges and their weights were also computed.

3 Visualization Method

The goal of the feature visualization here is to generate clear and intuitive visual representations that provide discriminating power for separating subjects in different classes. In our application, the classes are the three categories of brain connectome network data: HC, MCI and AD.

3.1 RYB Color Model

RYB is a color model based on Red, Yellow and Blue base colors. It is often considered a good model for physical mixture of pigments, or simulating color uses of painters [7], since color mix using RYB model is more intuitive in a way that the mixed colors still carry the proper amount of color hues of the original color components. For example, Red and Yellow mix to form Orange, and Blue and Red mix to form Purple. Thus, RYB model can create color mixtures that more closely resemble the expectations of a viewer. This suggests that we may use RYB color mix to represent the attribute values of three categories of data, and

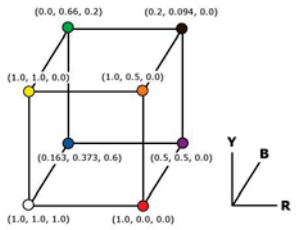

Fig. 2. RYB-RGB conversion [8]

expect the blended color to still show correctly the amount of bias towards certain attributes.

The resulting RYB color values, however, need to be converted to the RGB values for display. We adopt the approach proposed in [8], in which a color cube is used to model the relationship between RYB and RGB values (Figure 2). For each RYB color, its approximated RGB value can be computed by a trilinear interpolation in the RYB color cube.

3.2 Connectome Visualization

A standard MRI brain (with ROIs registered) is used to visualize the differential features of the subjects in 3 categories. To reduce obscuration, only a hemisphere is visualized (with 34 ROIs). For each ROI, we first compute the average node weight within each category. This weight can be any attribute the user wants to visualize. In our examples, the in-degree of the node in the connectome network is used. Similarly, for each edge, we compute the average edge weight within each category. These edge weights are typically the DTI fiber density values.

The nodes are visualized by color rendering of the ROI surfaces, extracted from the ROI sub-volumes. The weights of each node in the three categories are assigned as the three color components in the RYB color model. The resulting RYB color is then converted to an RGB color which is used to display the ROI surface. The relative strength of each color component provides the visual bias in the resulting visualization, which can indicate potential discriminating ROIs (features), as shown in Figure 3(a).

The edges are also visualized using a color coded pattern. The thickness of the line indicates the total weight of the edge, and the length of each color segment is proportional to the weight of that category. Figure 3(b) shows the same hemisphere with edges embedded. In this case, a threshold is used to the total weight of the edges, and a slightly larger surface opaque is applied.

For comparison, we also implemented a simple technique using randomized patches. Here three colors, representing three categories, are assigned randomly to small patches of each ROI surface. The numbers of patches associated with the three color values are proportional to the three weights of the node. This creates a color pattern that can also exhibit visual bias towards the stronger weight. The results are shown in Figure 4, which clearly is not as effective as the RYB approach.

In summary, an appropriate color model can be very effective in conveying information for multiple attributes. More sophisticated hue-preserving color models may also be explored in the future [9]. One limitation of this approach is that it can only represent three categories at a time. But this is usually sufficient for medical applications. Moreover, muti-path feature visualization may be applied for larger number of categories.

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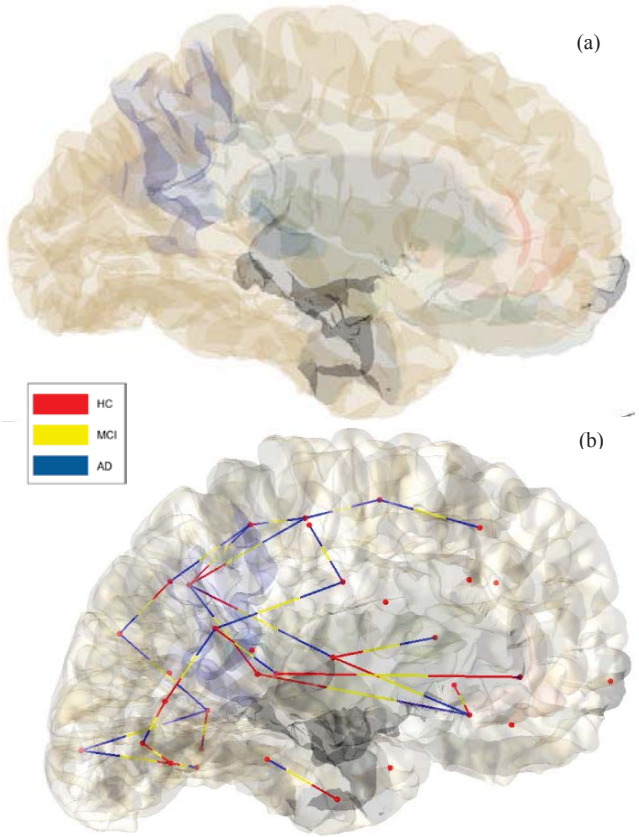

Figure 3. Brain connectome visualization by RYB model. (a) ROI rendering; (b) Network visualization.

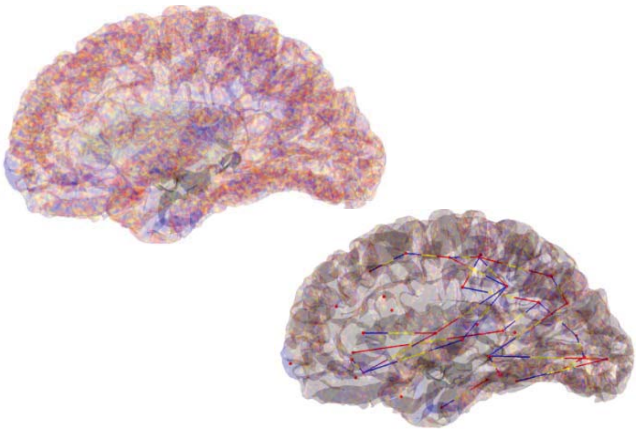

Figure 4. Brain connectome visualization by Randomized Patches