Pattern Visualization of Human Connectome Data

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Abstract
The human brain is a complex network with countless connected neurons, and can be described as a “connectome”. Existing studies on analyzing human connectome data are primarily focused on characterizing the brain networks with a small number of easily computable measures that may be inadequate for revealing complex relationship between brain function and its structural substrate. To facilitate large-scale connectomic analysis, in this paper, we propose a powerful and flexible volume rendering scheme to effectively visualize and interactively explore thousands of network measures in the context of brain anatomy, and to aid pattern discovery. We demonstrate the effectiveness of the proposed scheme by applying it to a real connectome data set.

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

1. Introduction
Recent advances in acquiring multi-modal neuroimaging data provide exciting new opportunities to study how the human brain is wired and how its function is affected by the connectivity pattern. Research in this emerging field, known as human connectomics [BSss], 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 [Wik]. Given such an unprecedented complexity, we are facing critical computational challenges for comprehensive mapping and analysis of brain connectivity, across all scales, from the micro-scale of individual synaptic connections between neurons to the macro-scale of brain regions and interregional pathways.

A large body of research has been devoted to extracting brain networks from structural, functional and diffusion magnetic resonance imaging (MRI) data [AB07, BBD¹¹, BSss, BS09, RS10, Spo11, CWS¹², FCD⁰⁸, GWK¹⁰, HCG⁰⁸, HKG⁰⁷, HSM¹⁰, MHO¹¹, CC11, CGM¹²]. The number of nodes in these networks varies from a few dozen to several thousand. Existing studies on analyzing these networks are primarily focused on characterizing them with a small number of easily computable measures that may be inadequate for revealing complex relationship between brain function and its structural substrate. To facilitate large-scale connectomic analysis, we propose a flexible volume rendering scheme to effectively visualize and interactively explore thousands of brain network measures, and to aid pattern discovery. We demonstrate the effectiveness of the proposed scheme by applying it to a real connectome data set.

Volume rendering supports the direct display of volume data sets through semi-transparent images and transfer functions. To highlight segmented volumes or multiple overlapping volumetric fields, existing methods typically modify traditional rendering procedure to traverse multiple segmented data sets. For example, in [HBH03], the segmented components are combined within each cutting slice in a 3D texture mapping algorithm. In [BA02] and [TSH98], a ray casting algorithm is modified to access boundaries of segmented objects during the ray casting process. In [CS01], the intermixing of multiple volumes are assessed at intensity level, opacity level and illumination parameter level at different stages of the rendering process. In our volume rendering algorithm, we apply a unique transfer function based volume intermixing by encoding the multiple volume intensity values within the same volume such that the transfer function can directly access the intermixing information. Since transfer function can be changed dynamically, this approach is more flexible in generating different visual effects interactively by simply manipulating the transfer functions.

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