Interactive Visualization of Temporal Brain Connectivity Data based-on Frequent Feature Mining

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Abstract—**Medical data visualization is instrumental in assisting disease diagnosis and exploring brain function and structure. In this paper, we constructed a brain connectivity network using changes in BOLD signals at different time intervals and identified frequent characteristics to help doctors quickly pinpoint areas of interest. To study the changes in connectivity between brain regions, we visualize frequent sequences and compare them, highlighting important temporal features of patient brain areas. This makes the study and analysis of fMRI data more convenient and assists doctors in investigating abnormalities in the connections between brain functional areas.**

Index Terms—**Visual analysis, temporal graph comparison, brain connectivity data**

I. INTRODUCTION

Functional magnetic resonance imaging (fMRI) is a brain imaging method commonly used to study cognition in the brain, which can explore the neural basis of cognition and emotion [1]. This approach produced a wealth of data that revealed patterns of hemodynamic activity throughout the brain. It plays an important role in describing functional connections in the brain under various clinical conditions.

Brain neurons are interconnected to form vast and complex networks, and fMRI contains a lot of data. Some researchers carry out feature extraction on the obtained data and apply the data to automatic diagnosis of brain diseases and other fields [2] [3]. However, there are relatively few researches on the extraction of time series features, and no time attribute is added to the data for research. Graph models and mathematical tools are often used to describe and analyze network data. As the scale of network data increases, the visualization method changes from static graph to dynamic graph, and some visual metaphor methods also appear. Some researchers present link information by building abstract views, generating functional link matrices and anatomical views of the brain. And linking this information to anatomy helps neuroscientists locate spatial representations of brain regions [4]. But this analysis lacks comparisons of temporal features to help study changes in brain connectivity over time. We can see that there are few

methods for feature extraction for a large number of data, and visual results are only represented by one view, which is inconvenient for data exploration and comparison.

In this work, we mined time sequence features from the constructed brain connection network, used the extracted time series data to generate dynamic graphs, and introduced a new visual analysis framework for comparison between dynamic graphs. The visualization results are placed in a Web-based GUI with an optimized nested comparison layout that allows you to compare timing data without affecting the data topology. For exploratory data analysis, we use linked views for visualization by interactively exploring the relationships between the different dimensions of the dataset. Instead of relying on a priori model of complex relationships in high-dimensional data, researchers develop an understanding of the principles that describe the system.

In Section II, we review related research work. In Section III, we introduce application design ideas and datasets with temporal properties. In Section IV, we present the results of experiments on the data. In Section V, we conclude the paper and discuss future work.

II. RELATED WORK

The visualization of functional brain networks and feature extraction methods in brain networks are briefly described below.

In order to study the differences of brain networks in clinical studies, Gleicher et al. [5] proposed to overlay and display the adjacency matrix to facilitate visual comparison of data. However, due to the complexity of spatial structure changes and the extensibility of time dimension, a visual coding may not be suitable for all visualization tasks. The above methods are combined with the adjacency matrix visualization method to study the brain connection data. The multi-view hybrid visualization method can balance the advantages and disadvantages of a single visualization technology. "In Situ" supports a variety of visualization techniques such as vertex link graphs, adjacency matrices, and timelines to maximize insight and avoid misunderstandings [6]. The connection view

is adopted in the research [7], which can interactively explore the relationship between different dimensions of the dataset. This method allows researchers to explore and analyze the data. Therefore, we use the adjacency matrix overlapping to visualize the time series. Multiple views were used to explore and analyze changes in brain functional connectivity.

While advances have been made in disease prediction and other applications due to the development of AI technology, how to detect and validate specific brain connectivity features remains challenging. F Fei et al. [8] applied multiple threshold constraints to generate multiple connected networks and extracted frequent sub-networks from the generated connected networks. Yang et al. [9] proposed a comprehensive analysis method to compare blocky brain networks. Different from the previous methods, the researchers combined the two visualization methods of node-connection graph and adjacency matrix, used the clustering algorithm to divide the brain regions, and improved NodeTrix [10] to design and display the block-level brain network connection mode. On the basis of the above research, feature extraction is performed on the constructed brain network, and frequently changing regions are obtained to help amateurs quickly locate the brain regions of interest.

III. MATERIALS AND METHODS

In this study, we designed a Web-based interactive visual interface (Fig.2). The method is expected to help researchers analyze brain connectivity data, allowing them to compare differences between samples from multiple dimensions.

A. Dataset

In this study, time series data of brain functional connectivity were obtained by processing ADHD-200 dataset. The two groups of data were respectively from children with normal brain function development (TDC for short) and children with ADHD. Subjects were all in a resting state when fMRI data was collected. The processed time series correlated with brain regions. Each set of data, combined with the AAL template, was divided into 116 anatomical regions containing 172 time series.

B. Feature Extraction

The connectivity features between brain regions are very high dimensional, and it is expensive to verify many computational models proposed in complex brain network studies. Therefore, we use machine learning technology to extract features from brain connectivity data.In the frequent sequence screening process, the same step size is set to divide the data into a certain number of time segments, the BOLD signal changes of nodes in adjacent time segments are calculated, and then the nodes that have asynchronous changes of blood oxygen concentration in the same time period and meet the linear correlation are found. Arrange the matrix in order of time segments to form a network of brain connections. Next, we look for nodes that occur more frequently in the brain connectivity network, and extract the previous node and the last node of the node to form frequent sequences.
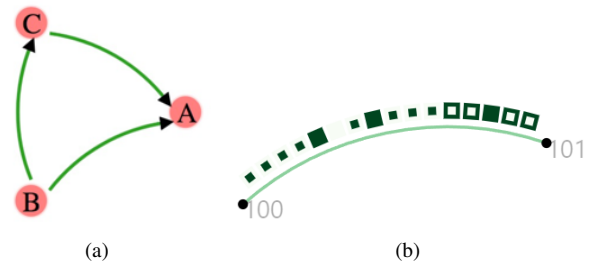

Fig. 1: The arrow in (a) points to the direction of time change, that is, the direction of the four fingers of the left fist. The black nodes in (b) represent the divided brain regions. The number of each node corresponds to the serial number of the partition in the AAL template. There are two overlapping squares on the connection line between them. When the color of the square is green, it means that the two regions are connected at a certain time, where the outer square is the patient time series data, and the inner is the control group.

In order to verify whether the extracted features are discriminant, SVM was used to classify the extracted features. The results showed that there were significant differences in feature distribution between normal subjects and patients.

C. Visual Design

1) Colorwall: We do a motion picture comparison in the Colorwall area. In this view we filter the data based on embedded visualization techniques and also add a design to assist comparison. For data visualization, choose a method where two squares overlap. By choosing the same hue on both squares, the user can easily compare the mapping values between the squares by observing only the difference in brightness between the inner and outer areas of the squares. Because of the time series data, we use the arc of the curve to represent the direction of time(Fig.1).

As dynamic networks become more complex, we need to design the layout. Grouping nodes visually simplifies the page and facilitates the analysis of the data. In order to ensure that the visual dynamic graph can avoid visual confusion, we group the time series data. Nodes in a group are deployed in Force mode to prevent node overlap. Layout allows users to intervene and adjust, further preventing overlapping of data visualization results.

2) Anatomy: In this panel, we generate anatomical images of the brain, and we can study and analyze the connectivity between brain regions in three dimensions. We processed the time sequence data to generate a functional connection matrix, and drew a 3D brain corresponding to the aal template. A dot is drawn to mark the corresponding location of each functional area, and the lines between functional areas indicate the degree of correlation between brain functional areas. Part of the region connection is based on the clustering results in Colorwall region.

3) List: This area contains options such as sample switching, brain region selection, and layout adjustment. Frequent

areas were listed in descending order of occurrence, allowing the researchers to focus on more diverse areas.

4) Plot: In this view, we draw line plots that represent the changes in the BOLD signal. We decomposed the time series data to get the trend items of the two groups of data, and then smoothed the trend items to reduce the influence of outliers. Calculate the absolute value of the difference between the two groups of data to get the curve difference.

IV. RESULTS

Attention-deficit hyperactivity disorder (ADHD) is one of the most common developmental disorders in children, and children often have symptoms such as impulsiveness, inattention and hyperactivity [11], [12]. In recent years, cognitive functional magnetic resonance imaging (fMRI) and resting-state fMRI have been widely used to examine abnormal brain function. The detection of abnormal conditions in the resting state can be applied to mental and developmental disorders such as ADHD, Alzheimer's disease and depression. In some literature studies, it has been shown that the functional connectivity of the default mode network (DMN) in ADHD patients can either increase or decrease.

In this study, we were able to select the regions of the brain we were interested in and get the visualizations. Among them, the related regions of cerebellum are one of the most different regions in our feature mining results. The visualized results were obtained by selecting the functional brain regions mentioned above. As is shown in Fig.3. Number 110 corresponds to the Vermis_3 area in the AAL template. It can be seen from the colorwall region in the figure that there is connectivity between this region and the other four regions, and there is a large connectivity difference between patients and normal people. Taking the time sequence data between Vermis_1_2 (No. 109) and Vermis_3 (No. 110) as an example, the time direction is from Vermis_3 to Vermis_1_2. In the process of time change, ADHD patients were connected at the first four time points, while TDC were more connected at the later time points. In the Plot area, by comparing the trend curve and observing the difference curve, we can find that there are also large differences in values between samples. We can intuitively see the difference in BOLD signal between patients and normal people(Fig.3d). This difference can also be identified simultaneously in the anatomical view, which shows that functional connectivity in the brains of ADHD patients is generally lower than that of TDC. As described in reference [13], cerebellar functional connectivity disorders may be one of the pathological and physiological causes of ADHD cognitive impairment. At the same time, we found significant connectivity differences in the cerebellar region between ADHD patients and the control group in our comparative study.

V. CONCLUSION AND FUTURE WORK

In this study, we mainly designed an application for visual comparison of fMRI data. By processing the time series data generated by fMRI for visualization, we can study the changes of dynamic graphic data and highlight the difference between two sets of different data. We use AI technology to classify brain diseases, mine frequent features, highlight important time series features in patients' brains, and assist doctors in diagnosing diseases. Our work then suffers from some deficiencies in the handling of complex networks, manifested in the removal of excessive features to simplify the content, and the possibility of obscuring highlighted points by connecting lines in anatomical views. In the future, optimized algorithms will be used to reasonably filter temporal information and better visualize the connectivity of anatomical views.

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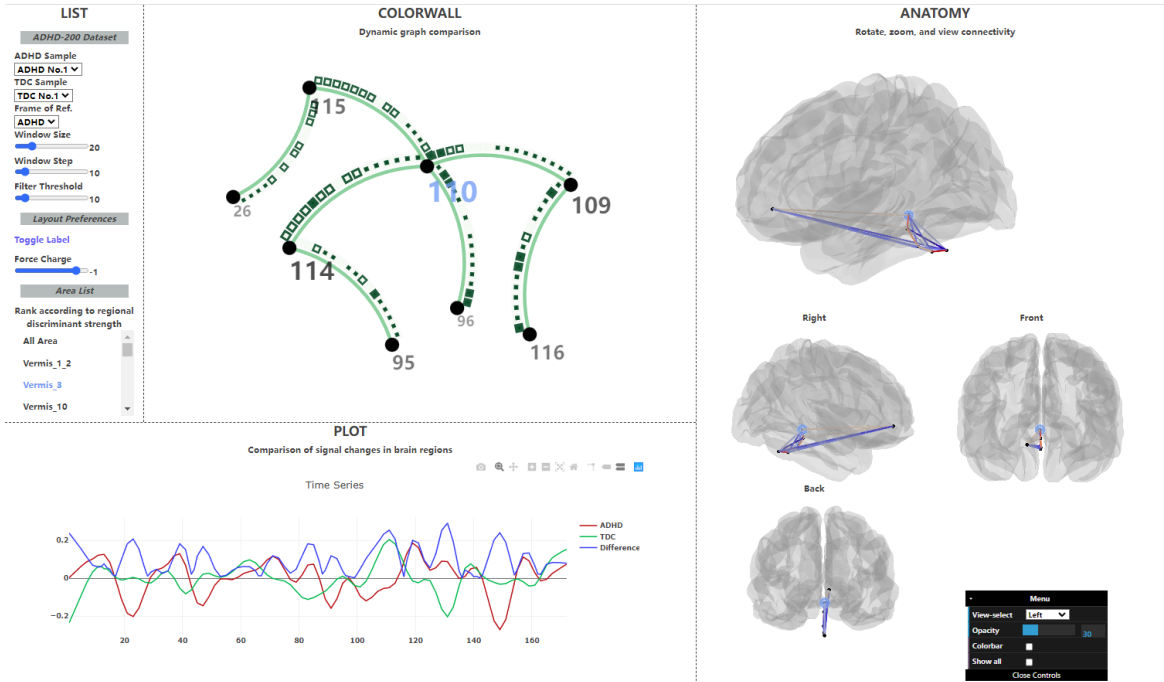
Fig. 2: Interactive interface overview.

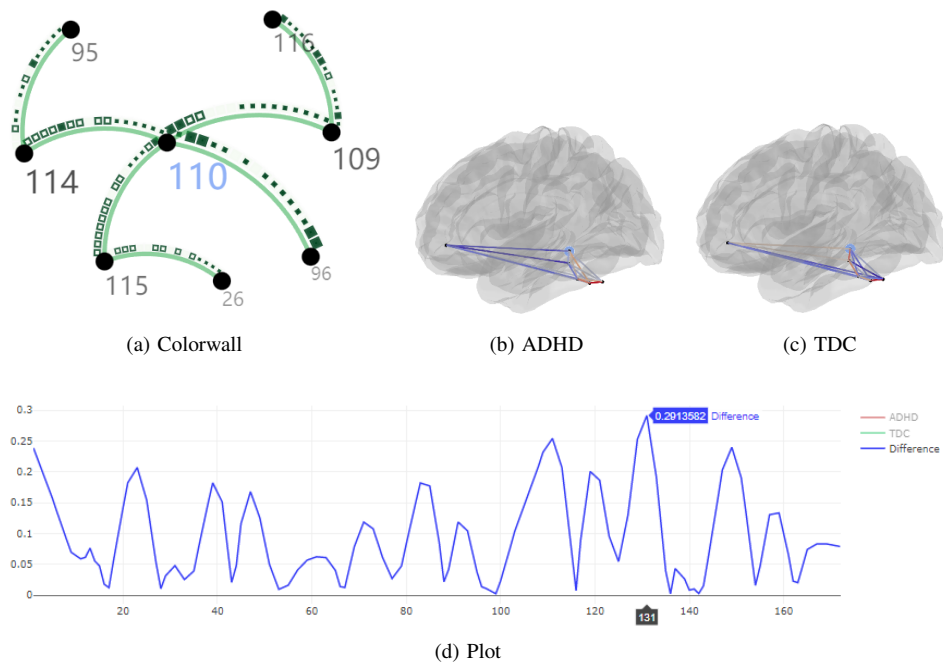(a) Colorwall

(b) ADHD

(c) TDC

(d) Plot

Fig. 3: (a) Comparison of the dynamic graphs of ADHD patients and TDC. (b) and (c) are 3D brain maps of ADHD patients and TDC, respectively. (d) Plot.