Visualizing Communities in Dynamic Mouse Brain Networks

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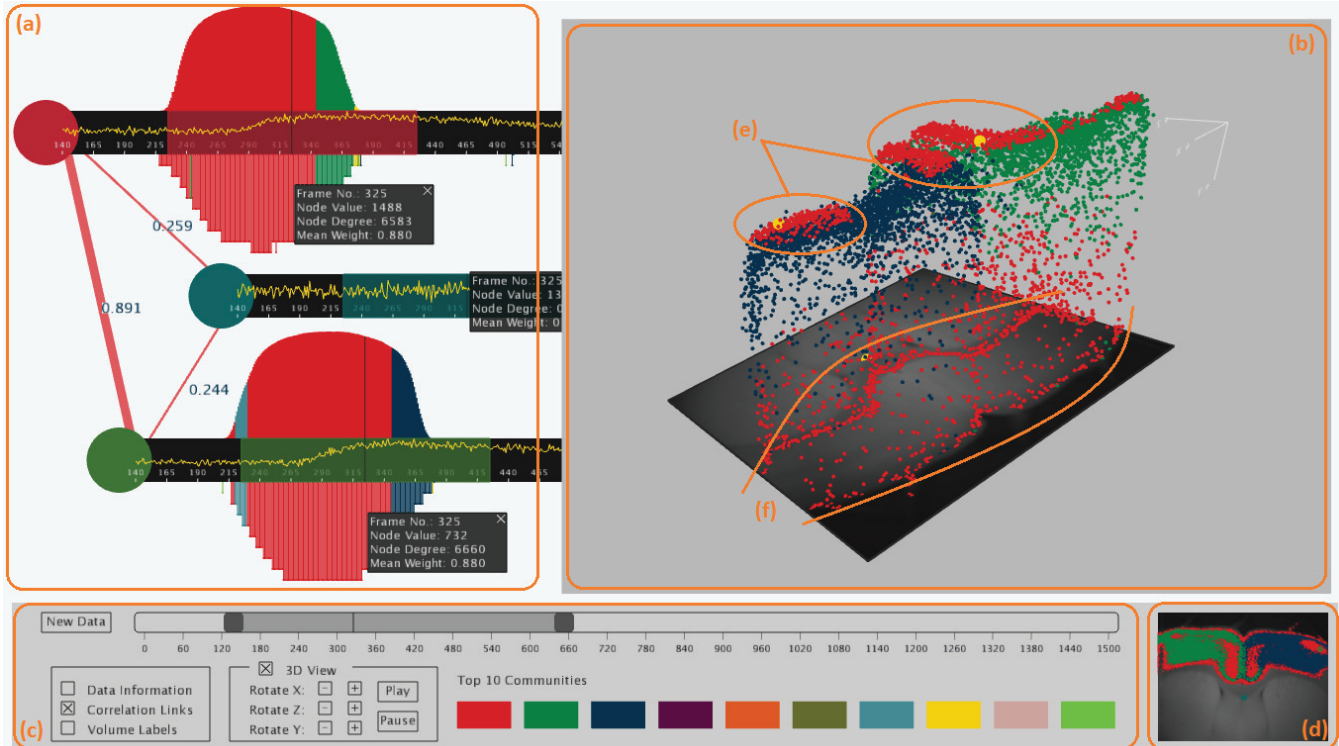University of Illinois at Chicago   University of Illinois at Urbana-Champaign

Figure 1: (a) Individual Statistical Visualization Model. (b) Space-Attribute Cube. (c) Control panel. (d) 2D image for displaying the community structure of the mouse brain correlation networks at the highlighted time point.

ABSTRACT

Community structure analysis reveals the properties of social networks. The application of this analysis to evolving communities in dynamic networks can help understand how social interactions between individuals dynamically change and how the brain networks grow. Visualizing these communities becomes challenging since the time dimension is an important component in dynamic networks. The problem is still more complex as the biological neural networks have physical structures, and communities are used to explore functional groupings. Our interactive visualization technique is used for exploring the community structure of dynamic mouse brain correlation networks and behaviors of individual nodes in the networks through time.

Keywords: Neural networks, dynamic communities, information visualization.

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Index Terms: H.5.2 [Information Interfaces & Presentation]: User Interfaces – Graphical User Interfaces (GUI).

1 INTRODUCTION

The analysis of social networks is a complex topic. It is used to understand relationships among individuals and groups within a network, and the behaviours or attributes of themselves. Visualization has always played a central role in social network analysis [3]. A good visualization is able to provide detail at all levels, from the broadest connection patterns down to the behaviour of individual members. Applying a social network model to mining and analysis of biological data sets is valuable in helping scientists understand relationships and functional connectivity within biological networks. Biological architecture is an important feature in analyzing biological networks.

Our research goal is to utilize social network modelling algorithms on biological data to uncover interactions among individual neural elements across time and space during the evolution of communities. The biological networks can be identified through the application of a Pearson correlation method then passing this data to a community analysis algorithm. Our prototype visualization tool is developed specifically to provide a visualization method that highlights the functional connectivity among cells or neurons of large biological time-series imaging data.

2 DATA ANALYSIS

In the study of the mouse brain, we choose to analyze flavoprotein autofluorescence [5] imaging data from a coronal slice preparation. All data are collected at 70 frames per second using a 2.5X objective (NA 0.1) and Retiga Exi camera for image collection. The image data has the dimension 172×30×2,000. We build weighted correlation networks based on these 22,360 pixels captured during 2,000 frames. Each pixel represents a group of neurons. A pixel can be considered as a vertex or node and the connection between a pair of pixels is the weighted edge representing the linear correlation coefficient value between the pair over a certain time window. By sliding the window one step for each iteration of time across the entire timeline as a same signal location, we obtain a time series of correlation networks.

In network analysis, communities are generally defined as groups of nodes which tend to have more and stronger connections with each other than with nodes outside. Modularity [4] is the most famous methods to find the structure of the communities. Louvain algorithm [2] can find high modularity partitions within large networks in a short time. It is an ideal suited to find snapshots of functional clusters of networks for our study. To understand how the interactions and the structure of clusters change over time, we use the Dynamic Community Inference (DCI) method [1]. This validated tool, is based on combinatorial optimization algorithms, to monitor the changing membership of individuals in a network.

3 VISUALIZATION DESIGN

The purpose of our visualization design is to discover the relationships among the resulting dynamic communities in both space and time. After analysing the data, we have the following properties that are critical in analysing the dynamic networks:

Raw Data Attributes are pixel coordinates and pixel value.

Node Degree is the number of edges connected to the node.

Mean Weight equals to Total Weigh/Node Degree.

Home Community is the community that individual belongs to.

Temporary Community is the community that the individual visits temporarily.
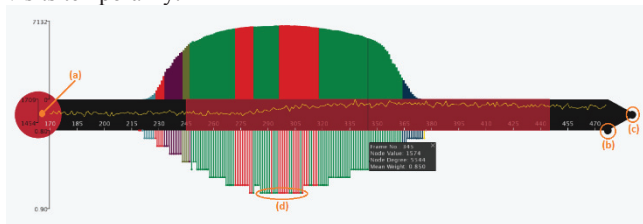

Figure 2: Individual Statistical Visualization Model. Click on (a) the center of the circle at starting point to drag the ISVM to anywhere in the main view. Drag the handle (b) in vertical changes the width (thickness) of the ISVM. Drag the handle (c) in horizontal changes the length of the ISVM. Click on (d) the points for mean weights value highlights the corresponding time point and causes a detail panel to pop up.

3.1 Individual Statistical Visualization Model

Based on those properties, we create an Individual Statistical Visualization Model (ISVM) for each member in the entire network. Basically, the layout is similar to a timeline chart depicting a time-series. In Fig. 2, the yellow line inside of the trunk represents the raw pixel's value over time. The solid colours above the trunk consists of bar graphs plotting the distribution of **node degrees** of the individual over time. The striped section below the trunk consists of point graphs representing the

distribution of its **mean weights**. Since the community identification is non-numeric data (i.e., A, B …), we colour encode it. Each individual has two identification codes: one identifies its membership – the **home communities**, represented by the colour above the trunk; the other one identifies the current community – **temporary communities**, where it resides at the particular point in time, represented by the colour below the trunk. If the element's two identification codes are identical then we display the same colour above and below. The member stays in its home community. If the individual is visiting its neighbouring community at time t then we display a different colour above (home) and below (visiting). From 300th frame to 320th frame in Fig. 2, the sequence of changes of the individual's home communities and temporary communities indicate how red neurons interact with green community.

3.2 Space-Attribute Cube

We create a 3D model (Fig. 1. (b)) to represent the spatial network. It is similar to but has important differences from the idea of space-time cube. In our 3D model, members can be represented in a cube as dots placed vertically according to one property value of the dynamic networks, such as node degrees and mean weights. We call this 3D model *space-attribute cube*. Colour in the space-attribute cube, like the ISVM, is used to represent the community structure.

The space-attribute cube can visualize the distribution of node degrees of all active individuals in space, and how the distribution is related with community structure. In Fig. 1. (b), we can see that neurons located in the center (e) have high node degree while neurons located in the outer ring (f) have very low node degree near to zero. One explanation is that red neurons near the outer ring have strong connections with the neurons in the center, but few connections with each other. In addition, the symmetrical structure (e) in the red community illustrates the connection between left and right side of the mouse brain.

4 CONCLUSION

In this paper, we present a new technique for visualizing dynamic spatial networks with multivariate features. The goal of our research is to explore patterns and relationships in dynamic networks to detect and predict the behaviours of both the individuals and communities, and uncover potential interactions in time and space. We currently apply our visualization method to the study of mouse brain in neuroscience domain. It illustrates how the interactive visualization design allows researchers to make new hypotheses based on the visual evidences and adjust the track of their exploratory research.

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