ECOViz: Comparative Visualization of Time-Evolving Network Summaries

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ABSTRACT

How can we visualize, interact with, and 'learn' important structures of time-evolving networks? Given domain-specific attributes, such as node membership of functional brain regions, how can we use this domain knowledge to discover coherent structures and track their evolution over time? In this demo paper, we introduce ECOViz (for Evolving COmparative network visualization), a system that enables pairwise comparison of temporal graph summaries based on variations in data source and preprocessing parameters. Our system further allows the user to perform structural and temporal analysis of a graph through efficient querying and visualization of its summarizing subgraphs.

ECOViz performs the following tasks: (a) It generates a set of temporal structures for each graph of interest using a dynamic graph summarization algorithm offline; (b) It supports contrasting visual analysis of time-evolving network pairs by providing quantitative metrics on summary structure composition and temporal graph statistics; (c) It interactively visualizes the induced subgraph of each structure in a summary, at either a full time sequence or a time interval specified by the user.

In our demonstration, we invite the audience to use ECOViz to make comparisons between a variety of time-evolving functional human connectomes, and explore their salient temporal structures.

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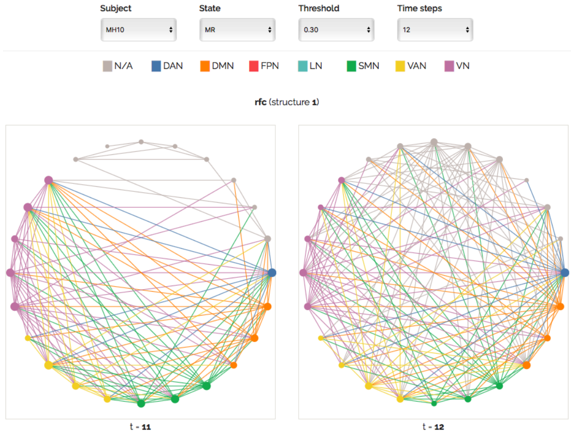
1 INTRODUCTION

Given a set of nodes of interest, how can we improve the discovery and visualization of salient structures in a time-evolving network? The objective of summarizing such networks is to identify structures that are notable in their topology and/or recurrence over time. Showing changes over time, however, demands further knowledge of the graph's underlying structure, and perhaps calls for an application-driven approach. For visualization in particular, preserving the mental map across snapshots is desirable when following *groups* of nodes [3]. This is applicable when a user seeks to find community-level patterns within a dynamic graph.



Subject: MH10
State: MR
Threshold: 0.30
Time steps: 12

Figure 1: Visualization of temporal summary structure: ranged full clique (rfc). Resting-state sub-networks of interest are indicated by node color (e.g., orange corresponds to the default mode network 'DMN', green to the sensorimotor network 'SMN').

Tracking evolution of communities in dynamic networks, ranging from modules in protein-protein interaction networks [18] to groups in scientific co-authorship networks [4], is of high relevance for domain scientists. Especially in scientific fields such as connectomics, which explores the functional and structural connectivity of the brain, visualization is a vital tool for pattern discovery [20]. Domain scientists may lack graph drawing skills, but their expertise on the data at hand can be used to augment automatic graph analysis and layout algorithms. How can we pair the specificity of domain expertise with the objectivity of graph summarization output to depict the structure and evolution of dynamic graphs? Instead of communicating results outside of the problem context, we respond in the domain-specific 'language' of the user.

In this demo paper, we introduce ECOViz, a system that supports interactive, comparative analysis of time-evolving networks by focusing on domain-specific summaries of their most salient structures. For more holistic understanding, ECOViz also allows the user to 'zoom in' on one time-evolving network and interactively explore its discovered temporal patterns. Our system assimilates domain knowledge in the following ways:

- **Domain-specific Summarization**: To assist the discovery of coherent structures, we employ 'semi-supervision' that takes domain expertise into account early in the exploration process. This is achieved using static graph decomposition that is biased towards an *egocentric* view of high-interest nodes. Figure 1 shows one temporal pattern (full clique ranging time steps 11 and 12) in the summary of a 'mindful rest' functional network of a human subject.

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- **Preprocessing-dependent Analysis**: While most real-world graphs are directly observed, many scientific domains (including neuroscience) infer graphs from measurements that are often in time series form. In response to the sheer volume of graph construction choices, we offer an interactive way to *evaluate* a comparison of preprocessing parameters. The contrasting data analysis interface includes data source selection provides complete flexibility in making inter- and intra-data comparisons.
- **Visualization of Communities**: To highlight communities of high-interest nodes (via domain-specific labels) and enable the extraction of richer insights, we provide quantitative meta-summaries of the structures and use colors to visually distinguish communities.

The paper is organized as follows. In Section 2, we introduce the application-specific data that motivated our system. Then in Section 3 we present our domain-specific graph summarization technique and in Section 4 we describe our system, ECOviz. Sections 5 and 6 give data analysis examples and our demonstration plan, respectively. Finally, Sections 7 and 8 contain related work and the conclusion.

2 CONNECTOMICS: DATA

While most real-world graphs are directly observed, functional brain networks are inferred from biological signals. Namely, blood oxygen level-dependent (BOLD) data from fMRI are a common source to computational models [9]. Fully connected, undirected graphs are typically constructed by computing the pairwise statistical dependence between all voxels (volume units of neurons). This step involves simulation over BOLD data to obtain per-voxel time series. Pearson's correlation coefficient – or another measure of association – is then computed pairwise between voxels. These values (in absolute terms) are filtered by a lower bound threshold, forming an unweighted graph.

In this demonstration, we use a dataset that consists of fMRI activity of 61 human subjects at both resting and mindful rest states. During the regular resting state (8 minutes), the thoughts of the subjects were allowed to wander about, while during the 'mindful rest' state the subjects were instructed to focus on their breath and actively not let their thoughts wander about.

Each fMRI session yields data using 100 ROI (region of interest) parcellation, each of which is accompanied by time series of length 240 timeticks (30 measurements per minute). Throughout the paper, we refer to ROIs as voxels or nodes. Out of the 100 voxels, 45 are part of resting-state networks of interest and labeled accordingly. The seven sub-networks of interest are: dorsal attention (DAN), default mode (DMN), fronto-parietal (FPN), language (LN), sensorimotor (SMN), ventral attention (VAN), and primary visual (VN) networks.

Time-evolving Graph Construction. We convert the time series per fMRI session to a time-evolving graph by extending the graph generation procedure described above. Specifically, instead of generating one connectome for the whole duration of the session (8 minutes), we split the time series into non-overlapping intervals of equal length and apply the generation process to each interval (i.e., each temporal snapshot is based on the statistical dependencies between time series during the corresponding interval). A uniform filtering threshold is applied to all the resulting networks for positive correlation values only. This leads to evolving snapshots of functional connectivity and allows us to track changes in thoughts (and their corresponding patterns) over time.

Two critical factors affect the construction of dynamic graphs: time interval granularity of the per-voxel time series and threshold value of the full association matrix. These choices can produce drastically different levels of sensitivity to noise for edge significance and aggregation [27]. As such, poorly constructed graphs can limit how well a summary captures true dynamics in the data. For instance, the full clique ranging time steps 11 and 12 in Figure 1 was found in a network formed with a threshold of 0.30 (correlation) and 12 time steps, yet its accuracy depends on how well the graph represents the subject's mindful rest state. We posit that prior knowledge of the biological signals, in the form of sub-network labels of voxels, can both indicate quality of graph construction and bolster pattern discovery in fMRI data.

3 PROPOSED METHOD: DOMAIN-SPECIFIC GRAPH SUMMARIZATION

Central to connectomics is finding novel patterns of activity between functional regions of the brain, with the goal of elucidating local and global organization. In contrast to the power law degree distribution found in many large-scale networks, the brain exhibits a small-world architecture, characterized by high local clustering and short global path lengths [9]. Superimposed on the structural tracts of the brain is a diverse, hierarchically organized functional network [21], whose typical inference was described in the introduction. We are particularly interested in mining the relatively unknown dynamics within and between specific modules (or sub-networks) of the functional network.

Current approaches in examining resting-state fMRI data include *model-dependent*, or focused on a single seed region of interest that is analyzed with respect to all other voxels, and *model-free* methods, or unsupervised techniques that include independent component analysis (ICA) [25]. While the former is simple and interpretable, it lacks the exploration of global brain patterns that the latter is capable of. To gain benefits of both methods, we use labels from resting-state networks, or functionally linked sub-networks that are highly active during rest, to inform our summarization algorithm.

We leverage TimeCrunch [22], a principled and parameter-free dynamic graph summarization algorithm. The algorithm (i) creates a set of subgraphs per static snapshot in the temporal graph; (ii) labels these subgraphs as structures based on the MDL principle (e.g., star, full clique, bipartite core); (iii) stitches static into temporal structures; and (iv) compiles a summary of top structures using again the MDL principle at the graph level. The resultant network summary consists of temporal patterns from the cross product of a *static vocabulary* that captures connectivity patterns (full clique, near clique, full bipartite core, near bipartite core, star, chain) and a *temporal vocabulary* that captures recurrence patterns (ranged, periodic, constant, flickering, oneshot). For instance, a graph may have a summary with several oneshot stars, a flickering bipartite core, and a periodic full clique.

In order to benefit from domain knowledge consisting of the nodes of interest (i.e., those belonging to specific sub-networks,

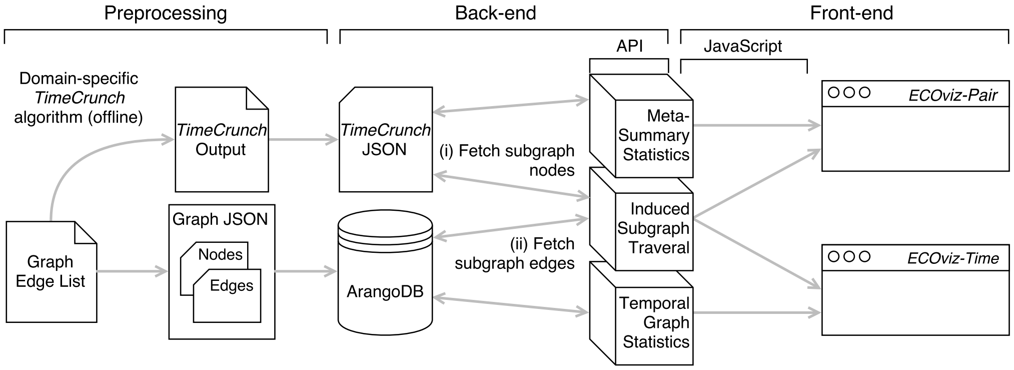


Figure 2: Full pipeline of graph summary visualization system. Major components include offline preprocessing, ArangoDB & Flask API back-end, and web interface (JavaScript) front-end.

such as the DMN in the brain), we propose a domain-specific subgraph extraction routine for the TimeCrunch [22] pipeline. Specifically, instead of using the original clustering routine of TimeCrunch, which is tailored towards real large-scale graphs with power-law degree distribution, we extract labeled nodes' *egonets*, or induced subgraphs of an *ego* node and its neighbors, as subgraphs for TimeCrunch and its static graph counterpart, VoG [15, 16]. We mainly employ egonets to simulate the model-dependent approach discussed previously, which uses seed ROIs for analysis of fMRI functional networks. Egonets also provide natural communities that partitioning algorithms targeting high-degree hub nodes – ill-suited for the small-worldness of brain networks – may overlook. Their use in analysis of heterogeneous social networks, which also have small-world properties, improved network abstraction [19].

4 SYSTEM OVERVIEW

In the following subsections, we discuss in detail the components of ECOviz. A pictorial overview of our system and its various components is given in Figure 2. Particular emphasis is placed on how resting-state network labels are utilized across the length of the entire pipeline.

4.1 Domain-specific Summarization

As described in Section 3, in place of the subgraph generation in TimeCrunch and VoG, we utilize an egocentric approach to partitioning the graph. This is achieved by using voxels of particular interest to neuroscientists as seed nodes. Specifically, the 'interesting' voxels are the ones that participate in well-known sub-networks, such as the default mode network (DMN) and other networks presented in Section 2. Irrespective of the labeled node's network of origin, we use its egonet as a subgraph input to TimeCrunch, resulting in a static total of 45 egonets per functional network. These labeled nodes are indicated in the 'labeled/total' ratio and 'entropy' columns of the summary tables (see Figures 3, 4). The former gives the number of labeled nodes per extracted egonet, and the latter is a measure of label diversity per egocentric community (e.g., a value of 1 means that the nodes are uniformly distributed among the sub-networks of interest).

For this demo, we extracted temporal summaries from 132 functional brain networks spanning: 11 human subjects, two rest states (resting and mindful rest state), and six combinations of preprocessing parameters (thresholds of $\{0.30, 0.45\}$ and time interval granularity of $\{12, 16, 24\}$) for the time-evolving graph creation.

4.2 Interactive Visualization

To support divergent modes of data analysis, the system provides two visualization views. ECOviz-Pair focuses on comparison between pairs of summaries differing in data source (i.e., subject and rest state) or preprocessing method (i.e., threshold value and time interval granularity). ECOviz-Time gives the user a more detailed narrative of how each structure evolves over time. While the views share a protocol for fetching structure connectivity, they differ in their interactivity and set of supporting features. Users interact with both views through selection of drop-down menus, each controlling a single parameter, at the top of the screen.

Preprocessing-dependent Analysis: A key feature of the system is to enable scientists to not only make inter-data comparisons, but also explore how tuning preprocessing parameters affects the summary structures found. As graph generation depends on these hyperparameters, we treat them as a set of settings that the user may toggle at will. Thus, the summarization results serve as implicit feedback about graph generation quality.

In ECOviz-Pair, we focus on the notion of summary diversity as an informal benchmark. To this end, three meta-summary charts are shown to the user: percentage of structures by structure type, node count by structure participation count, and top 10 node IDs by structure participation count (see Figure 3). The charts are displayed in a two-column format – users may either compare rest with mindful rest state of a single subject (Figure 5), or independently select parameters for each column (Figure 3).

As ECOviz-Time (Figure 4) offers a sequential view of how temporal structures evolve, we also display a chart that captures the sparsity of each functional network over time. This is intended to provide context to whether temporal changes in structure density are due to preexisting network structure. More concretely, a structure becoming denser over time could be due to preprocessing – the chosen time interval granularity may have produced networks with skewed temporal distributions of edges. For example, the

Subject 1	State 1	Threshold 1	Time steps 1	Subject 2	State 2	Threshold 2	Time steps 2
R01	R	0.30	12	R01	MR	0.30	16

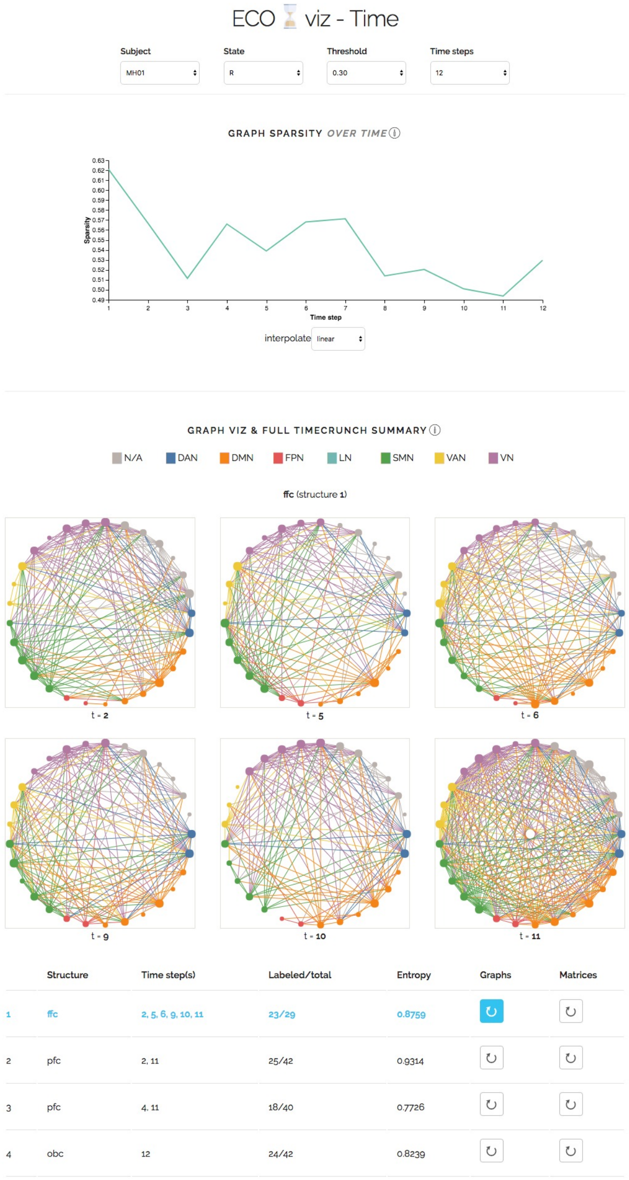
ffc (structure 1) at time step 3

ffc (structure 1) at time step 2

	Struct	Time step(s)	Lab/tot	Entropy
1	ffc	3 5 7 12	18/37	0.7605
2	rfc	4 5 6	17/47	0.7462
3	ffc	3 8 10	18/43	0.8521
4	ffc	3 4 8	16/34	0.7765

	Struct	Time step(s)	Lab/tot	Entropy
1	ffc	2 5 6	23/43	0.8937
2	pfc	7 16	24/44	0.8648
3	pfc	1 6	16/42	0.8846
4	pfc	5 13	11/35	0.7268

Figure 3: ECOviz-Pair contrasting data analysis view.



Subject	State	Threshold	Time steps
MH01	R	0.30	12

	Structure	Time step(s)	Labeled/total	Entropy	Graphs	Matrices
1	ffc	2, 5, 6, 9, 10, 11	23/29	0.8759	↻	↻
2	pfc	2, 11	25/42	0.9314	↻	↻
3	pfc	4, 11	18/40	0.7726	↻	↻
4	obc	12	24/42	0.8239	↻	↻

Figure 4: ECOviz-Time graph sequence of temporal summary structure: flickering full clique (ffc). Chart depicting graph sparsity over time is positioned above structure visualizations.

series of graph snapshots in Figure 4 appear to reach peak density at time step 11 (bottom-right cell), yet the network-wide sparsity chart above suggests that it is a global trend. This illustrates how the temporal summary chart can highlight local, structure-specific trends in sparsity from those in the background.

Visualization of Communities: The main component of the system is a visualization of the summary structures, either at a particular time interval or a full time sequence. Since TimeCrunch mines for a predefined vocabulary of static structures, which includes cliques, bipartite cores, stars, and chains, we use this base representation of the labeled structure in the visualization. Doing so also allows the user to evaluate how well a structure's connectivity aligns with its label.

Most apparent in the visualization is the colored node representation of resting-state network labels. As the nodes within each structure are ordered primarily by label and secondarily by node ID, ordering across time intervals is maintained. This enables the user to track a static map of the nodes across multiple time intervals, aiding in detecting edge evolution within the structure. We further apply these resting-state network labels to the adjacency matrix view of ECOviz-Time by grouping rows and columns by node label to highlight community dynamics.

4.3 System: End-to-End

Following offline execution of TimeCrunch on all functional networks, each of the summaries contains a list of structures, which describes the temporal structure type (e.g., full clique), node participation (i.e., of which nodes the structure contains), and time step participation of each structure. To depict the structure's connectivity, the system pairs node data from the summary with edge data from the original functional network. Providing real-time access to this data requires efficient storage and traversal of user-requested graphs. We chose *ArangoDB*, a multi-modal NoSQL database, as a solution to scalably fulfill these needs.

Once the system has stored network edge lists into ArangoDB and processed TimeCrunch output into JSON, the web server may begin receiving user queries. As structure visualization must support single and sequential time step requests (for the two views), a dedicated graph traversal API is utilized. The user chooses from a list of summary structures – fetched from the TimeCrunch JSON shown in Figure 2 – with their spatial and temporal properties. For each requested structure-time step pair, the graph traversal API fetches the participating node IDs from the TimeCrunch JSON (step 1 in back-end section of Figure 2). Next, the ArangoDB database is queried for the induced subgraph of these nodes (step 2 in back-end section of Figure 2). As the graph visualization JavaScript depends on this connectivity data, it makes either a single or multiple asynchronous requests (per visualization reload) to this API, depending on the front-end view.

Data flow of ECOviz-Pair and ECOviz-Time separates within JavaScript, with the links between the back-end APIs and front-end views diverging (front-end portion of Figure 2). The induced subgraph traversal API is shared among both views, while the meta-summary statistics and temporal graph statistics APIs are exclusive to ECOviz-Pair and ECOviz-Time, respectively.

5 DATA ANALYSIS: EXAMPLES

Here, we showcase the differing functions supported by the contrasting (ECOviz-Pair) and temporal (ECOviz-Time) data analysis views in terms of their functional network visualizations. The two views provide a more comprehensive glimpse at the data at hand, specific to the user's chosen purpose.

5.1 Contrasting Data Analysis

Within the ECOviz-Pair interface, there are two modes of data selection: a single set of drop-down menus controlling subject, threshold, and number of time steps, as well as a double set of menus each with an additional option for rest state (see Figure 3). The former automatically displays rest state on the left column and mindful rest on the right. The latter gives the user total control over the combinations of parameters to compare on either column. In the remainder of this subsection, we describe example use cases specific to each drop-down mode.

In the single set drop-down mode, the user is only concerned with making comparisons between resting and mindful rest states within the same subject. We demonstrate this in the pair of one-shot bipartite cores (obc) selected in Figure 5, with resting state on the left visualization and mindful rest on the right. In the resting state, there is an evident division between the SMN and other functional brain regions on either side of the bipartite core. There appears to be less segregation among nodes of the same label in the mindful rest state, which applies to both unlabeled nodes – which do not belong to sub-networks of interest – and labeled nodes in the DMN, LN, and VN. Interestingly, both rest states feature a relatively high-degree unlabeled node on the left side linking to nodes on the right. This observation could lead to further exploration of the unlabeled nodes by domain experts. As the TimeCrunch summarization algorithm is parameter-free, interpretation of trends in the summary structures depends on the user's application context.

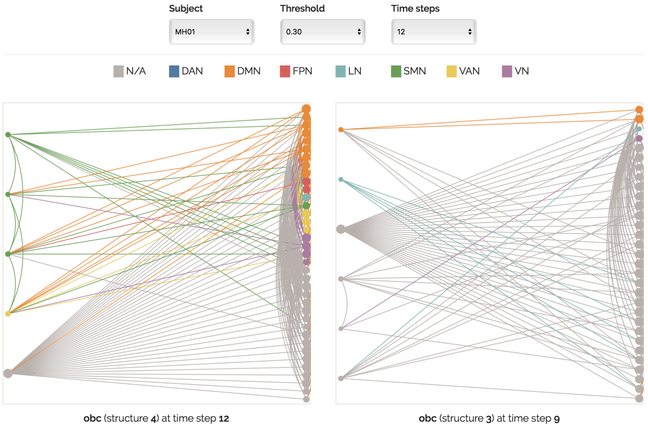

Subject: MH01
Threshold: 0.30
Time steps: 12

Figure 5: ECOviz-Pair temporal data analysis view of two one-time bipartite cores (obc). For the selected subject, the left structure corresponds to resting state and the right structure to mindful rest.

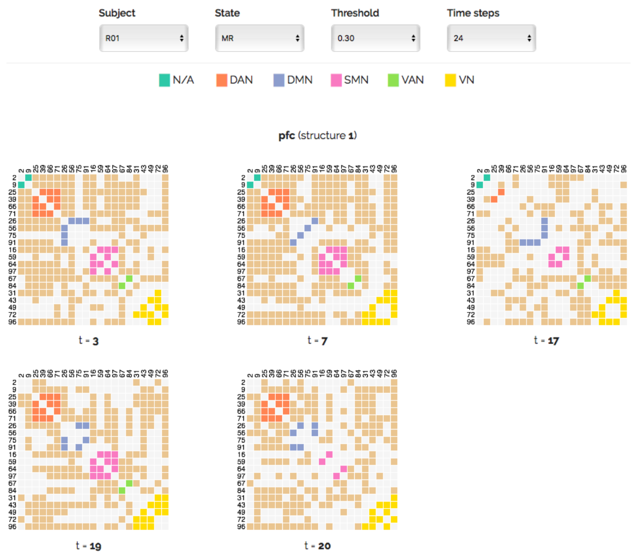
The double set drop-down mode, which is shown in Figure 3, offers full flexibility to the user in terms of variable(s) to compare, making it possible isolate effects of preprocessing method. The three meta-summary charts in ECOviz-Pair provide high-level insight on the structure and node composition of the TimeCrunch summaries. In Figure 3, we compare the effects of modifying temporal granularity within a single subject. On the left column, each voxel's time series is partitioned into 12 equal intervals, while the right uses 16. From the summary item proportion chart, coarser granularity results in a more temporally diverse summary – with the majority of the summary containing ranged, periodic, or flickering structures. The node count chart is more skewed right for coarser granularity, indicating more node overlap in structures. There is little variation in the top 10 node IDs, which suggests that temporal granularity has limited effect on the summary's most active nodes.

5.2 Temporal Data Analysis

As discussed in Section 4, ECOviz-Time focuses on temporal exploration of structures, showing the full sequence of time intervals that a structure appears in. Below, we detail two types of analyses that this view supports: *inter*- and *intra*-structure patterns.

The static layout of nodes across time intervals directs users' attention to trends in connectivity between structures. This is especially evident in Figure 1, where unlabeled nodes (colored in gray) shift from high intra-label connectivity to high inter-label connectivity between time steps 11 and 12. At time step 11, these unlabeled nodes are almost exclusively connected to each other, as the paucity of edges connecting them to nodes of other colors indicates. However, by time step 12, they have become heavily connected with nodes of dissimilar labels (including those within the DAN, DMN, SMN, VAN, and VN). This trend in connectivity may have been obscured in graph layouts that modify the layout of nodes between temporal structure snapshots.

Grouping nodes by label also facilitates more complex analysis of dynamics within resting-state network communities. The sequence of matrices in Figure 6 reveals how the adjacency matrix draws attention to intra-community patterns. We restrict our analysis on the four nodes within the DMN (colored in dark blue), which encompass nodes 26, 56, 75, and 91. At time steps 3 and 17, these nodes form stars centered around nodes 26 and 91, respectively. At time step 7 – between the two appearances of stars – the structure breaks into two sets of pairs (between nodes 91-26, 56-75). Finally, the DMN structure becomes a triangle at time step 19 (between nodes 75, 26, 91) and continues as a triangle at time step 20, though with a voxel replacement (between nodes *56*, 26, 91). Without the sequential matrix view, this fine of a granularity in pattern detection would likely be difficult to detect.



Subject R01

State MR

Threshold 0.30

Time steps 24

Figure 6: ECOviz-Time matrix sequence of temporal summary structure: periodic full clique (pfc). The DMN resting-state network reflects temporal patterns across the displayed time steps.

6 DEMONSTRATION PLAN

Prior to the demo, the system only requires an edge list of the dynamic or static network in question. Although this demo is specialized for functional brain network data and the preprocessing complexities that neuroscientists face, the system accepts any dynamic graph with a subset of nodes labeled by some criterion. Time-evolving networks must be partitioned into t edge lists, such that the i^{th} edge list contains edges present at time interval $i \in [1, t]$. Following data storage and TimeCrunch processing, the contrasting and temporal data analysis views are immediately available.

Contrasting Data Analysis: Regardless of single or double set drop-down mode, users interact with data source by modifying values of the desired drop-down menus. This automatically updates all supporting charts and the structure visualizations with the user's selections. In the case of double set drop-down mode, the system only updates the column referred to by the selected drop-down menu. To interact with the structure visualizations, users click on the button corresponding to the desired time step in the TimeCrunch summary table for the desired structure row. This updates the visualization with the chosen structure-time step pair.

Temporal Data Analysis: Users may visualize the full temporal sequence of a structure through two ways: graph visualization or adjacency matrix. To toggle each format, the user can click the button under the 'Graphs' and 'Matrices' column in the TimeCrunch summary table for the desired structure row (Figure 4). This refreshes the current visualization sequence with that of the structure selected by the user. In the adjacency matrix view, users may reorder the matrix by clicking, dragging, and dropping rows/columns – allowing for sorting criteria flexibility.

In both types of analyses, the user may hover over nodes in the structure visualizations to view node IDs. Proportion and entropy of resting-state region labels are also shown in the table underneath. We invite our audience to explore the spatial and temporal dynamics of their data through the interface.

7 RELATED WORK

Our work is related to visual graph analytics, and visualization techniques for temporal graphs.

Several graph visualization frameworks, including Apolo [10], OPAvion [1], and NetRay [14] focus on anomaly detection at the node level, while others [7, 23] visualize the patterns in the adjacency matrices. Apolo [10] is a graph tool that supports attention routing. The user picks a few seed nodes and Apolo interactively expands their vicinities to enable sense-making. OPAvion [1] is an anomaly detection system for large graphs that mines graph features on Hadoop, spots anomalies offline by leveraging anomaly detection techniques, and interactively visualizes the anomalous nodes via Apolo. Shneiderman proposes simply scaled density plots to visualize scatter plots in [23], [7] presents random and density sampling techniques for datasets with several thousands of points, while NetRay [14] focuses on informative visualizations of the spy (distribution and correlation plots of web-scale graphs). Unlike these works, the system in this paper visualizes domain-specific summaries of time-evolving networks and supports pairwise comparison of the extracted summary structures.

Limiting node movement between temporal snapshots, or preserving the mental map, has long been believed to benefit dynamic graph visualization [6]. Early methods targeting this constraint include *supergraph* creation that encodes node layouts in all time steps [11], and simulated annealing that minimizes the cost function of inter-timeslice node movement [17]. Since our method aims to provide responsive user interaction through fast graph drawing, these solutions do not provide the necessary speed.

Despite consensus that temporal transitions should be interpretable, choice of presentation mode (i.e., animation vs. small multiples) is still under debate. Small multiples, a timeline-based display, result in faster response times among participants of dynamic graph analysis tasks [2, 12]. Qualitative responses also indicate that animation between frames leads to higher cognitive load when tracking multiple, simultaneous *community* transitions. However, accuracy in tasks that involved following *specific* nodes and edges improved in the animation case. Another experiment found that participants detected patterns across a wider window of time steps using small multiples as compared to animation [8]. Results show that the best approach depends on the user's task: *global* topological and temporal trends are easier to detect using small multiples; *local* ones are better suited for animation.

In giving users the ability to detect community dynamics, a major challenge lies in the display of both the node and community topology of dynamic graphs. Vehlow et. al [26] developed a method with node-link diagrams that overlay ribbons linking communities across adjacent time steps. This elegantly avoids the issue of edge overdraw by only displaying node-link diagrams at the junction of time steps. The animated radial layout proposed by Yee et. al [28] relies on polar projection of nodes in a radial layout to reduce low-level edge crossings, and animation between focal nodes to show high-level trends. These approaches offer principled ways to navigate the trade-off between showing detail and abstraction.

Apart from community and node-level dynamics, ECOviz must also show context from a known set of static structures. We choose radial and spine drawings [5] to reflect the respective forms of cliques and bipartite cores. To convey community dynamics within these structures, we also stratify nodes by domain-specific label, a user-defined semantic substrate [24]. These layout restrictions make previously discussed approaches of [26] and [28] unsuitable for ECOviz. Since our work uses small multiples for its more global community-level task, the edge crossings present in clique structures could benefit from a static layout such as hierarchical edge bundling [13].

8 CONCLUSION

In this paper, we leverage domain-specific insight in partially labeled data to produce interpretable summaries of dynamic graphs. Specifically, we propose a summary generation process that uses an *egocentric* view of labeled nodes to direct TimeCrunch towards exploring existing functional communities in the connectome. We also introduce a visualization-based system, ECOviz, to allow users to interact with the generated summaries and compare the results of different data sources. Via ECOviz-Pair we offer contrasting analysis between dynamic graphs' data source (e.g., resting vs. mindful rest state) and preprocessing methods for ease of *evaluation*, as well as more detailed exploration of a network's temporal patterns via ECOviz-Time. To better *express* structure connectivity over time, we maintain a static node layout according to the TimeCrunch encoded structure and node labels, producing a clearer visualization of dynamics within and between nodes of the same community.

Future steps include quantifying summary quality to automate the selection of preprocessing parameters for dynamic graph construction, assisting the user in detecting time interval granularity (instead of keeping intervals of equal length), and allowing the user to customize the summarization routine by allowing for introduction of new static graph vocabulary patterns (beyond cliques, bipartite cores, etc.). Though the task of exploring dynamic graphs for structures is largely unsupervised, the previous modifications would adapt to the user's data, creating a domain-specific graph summary that more effectively communicates findings to the user.

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