DyNetVis - An interactive software to visualize structure and epidemics on temporal networks

Claudio D G Linhares
Faculty of Computing
Federal University of Uberlândia
Uberlândia, Brazil
claudiodgl@gmail.com

Jean R Ponciano
Faculty of Computing
Federal University of Uberlândia
Uberlândia, Brazil
jeanrobertop@gmail.com

Jose Gustavo S Paiva
Faculty of Computing
Federal University of Uberlândia
Uberlândia, Brazil
gustavo@ufu.br

Luis E C Rocha
Department of Economics
Department of Physics and Astronomy
Ghent University
Ghent, Belgium
luis.rocha@ugent.be

Bruno A N Travençolo
Faculty of Computing
Federal University of Uberlândia
Uberlândia, Brazil
travencolo@gmail.com

***Abstract*—The study of complex networks, especially temporal networks, increased over the last years. Understanding patterns, trends, and anomalies in these networks, as well as simulating and analyzing dynamic processes (e.g., infection spread dynamics in social networks), are not trivial tasks. Information Visualization techniques offer significant potential to assist the user in these analyses. This paper presents an extended version of *Dynamic Network Visualization (DyNetVis)*, a freely available and open-source interactive software to perform visual analysis of temporal networks. It provides four visualization techniques, structural, temporal, matrix, and community layouts, and a number of state-of-the-art methods to interact with each of these layouts. DyNetVis also implements dynamic processes, including standard epidemic models. It is a computational tool to study and explore networks in diverse domains.**

***Index Terms*—Temporal Network Visualization, Dynamic Networks, Dynamic Processes, Visual Scalability, Visual Analysis.**

I. Introduction

A growing number of research areas have been using complex networks as a tool to understand the structure and dynamics of complex systems [1]. Such analyses have provided novel insights in areas such as biology (e.g., interactions of proteins), computer science (e.g., email communications), and medicine (e.g., the interaction of brain cells) [2]. Complex networks are represented by interactions (edges/connections) between entities of a system (nodes). When such models include the information about *when* each connection occurred, they are called temporal (or dynamic) networks [3]. In some situations, such as the analysis of social network evolution, it gets more challenging with increasing network size [4]. One alternative is to analyze specific network properties, such as network communities, that are defined as groups of nodes that connect more between themselves than to other nodes [5].

IEEE/ACM ASONAM 2020, December 7-10, 2020
978-1-7281-1056-1/20/$31.00 © 2020 IEEE

Information Visualization studies techniques to help interpretation and reasoning in data through visual analysis and interactive processes [6]. There are several approaches for visualization of complex networks [7]–[9], however, it is still a challenging area in cases where the volume of data is large [10]. It is particularly difficult in temporal networks to find an appropriate layout that reduces visual clutter and enhances the analysis because of the network evolution. Finding an adequate way of displaying data on the screen, filtering relevant information, and interacting with the visual elements according to organizational principles remain a challenging research question [7].

Adequate visualization techniques provide means for quick and reliable identification of non-trivial patterns, trends, and anomalies in the network structure that would be difficult to find otherwise. Temporal network characteristics (e.g., idleness and bursts) make them useful to study dynamic processes through simulation models that estimate flow over the nodes, spreading of opinion, rumors, infections, and others [8]. Network visualization could assist the user, for example, on making decisions related to social distancing, tracing the infection, and designing vaccination protocols [8].

This paper presents an extended version of *Dynamic Network Visualization (DyNetVis)*, a free and open-source interactive software for visualizing structure and epidemics on temporal networks. It was greatly improved from a previous version [11] and now includes:

- Four interactive layouts, structural, matrix, temporal and community layouts;
- Several node positioning/ordering methods distributed on different layouts, including a state-of-the-art visual scalable strategy;
- Three edge sampling methods from literature;
- Network community detection through two state-of-the-art algorithms, which can be performed in all four layouts

provided by DyNetVis;
- Simulation and analysis of dynamic processes, including random walker, four infections spread models, and a novel node ordering strategy based on the infection path.

II. Related Work

Computational tools have been proposed to visualize complex networks, including some libraries for R and Python (programming languages), and softwares such as *Gephi* [12] and *Cytoscape* [13]. The most common layout is the node-link diagram (also known as structural layout [11]). *Gephi* and *DyNetViewer* [14] (a *Cytoscape* plugin) allow temporal network exploration through animated node-link diagrams that may consider, e.g., network communities or centrality measures. In contrast, *3D DynNetVis* provides filters and interactive tools to explore the network evolution through a 3D mapping over consecutive node-link diagrams [15]. Not least, PAOH [16] is an interactive system focused on visualizing temporal hypergraphs (a type of network where a single edge may connect several nodes).

Pajek [17] is an interactive software designed for visualizing large temporal networks (in terms of number of nodes/edges) that provides an animated node-link diagram and a matrix-based layout. *DyNetVis* first version [11] is a freely available, multiplatform, and interactive software, that also provides two layouts, animated node-link diagram and temporal layout (also known as *Massive Sequence View (MSV)* [9]). *DyNetVis* also implements a variation of MSV called *Temporal Activity Map (TAM)*, which is focused on the node activity over time and thus allows complementary visual analysis.

III. Software description

DyNetVis is a freely available[1] and open-source[2] software developed in Java programming language to support multiple platforms. Our software has been successfully used for exploring networks in a variety of research areas, such as social network analysis [7], [11], healthcare [5], [7], [18], school [5], [19] and corporate environments [5], [11]. DyNetVis is also a powerful tool for simulating and analyzing dynamic processes (such as epidemics), as demonstrated in [8].

A. Layouts

DyNetVis implements four layouts. The *structural layout* (Fig. 1(a)) represents nodes as circles and edges as straight lines and can show the aggregated network (i.e., considering all timestamps at once) or highlight the temporal evolution through animation. This layout is useful, e.g., for understanding the network structure [11]. The *matrix layout* (Fig. 1(b)) employs a square and symmetric matrix to represent, in each cell, the edge between the involved node line and node column. In this layout, the temporal evolution is also considered by animation frames. This layout is useful, e.g., for comparative analysis between networks [10].

[1] www.dynetvis.com
[2] github.com/claudiodgl/DyNetVis

The *temporal layout* (Fig. 1(c)) is a timeline-based strategy [10] that places nodes vertically and timestamps horizontally, with vertical lines representing the connections (edges). This layout is useful, e.g., for edge distribution analysis [9]. The *community layout* (Fig. 2) is another matrix-based representation with columns representing nodes and lines representing network communities. It was developed to visually compare the performance of different community detection methods [5].

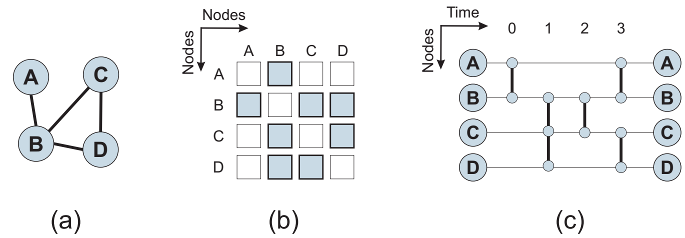

Fig. 1. Layouts for a network. (a) structural. (b) matrix. (c) temporal.

B. Methods and Features

The user may experience difficulty in exploring the network with any layout due to overlapping elements (nodes or edges) or the poor organization of these elements on the screen. One can, for example, reposition nodes and sample edges to improve layout readability. DyNetVis implements several methods for this purpose. Figure 2 presents an overview of all available methods and features of DyNetVis. For the *structural layout*, the software offers methods to organize the nodes in the layout (random, force-directed, circular, and hierarchical strategies [20]). For the *temporal layout*, DyNetVis implements: (i) the node ordering methods: random, appearance, lexicographic, degree [9], Recurrent Neighbors (RN) [11], and Community-based Node Ordering (CNO) [7]; (ii) the edge sampling methods: random, Accept-Reject (AR) [21], and Edge Overlapping Degree (EOD) [21]; (iii) the Temporal Activity Map (TAM) heatmap [11], that focus the analysis on the node activity over time and thus provide a new perspective of analysis. Not least, the *matrix layout* also contains several node ordering methods, such as trivial, RN, and a community-based ordering. If the method uses community detection, the user can choose between Louvain and Infomap algorithms (recommended in [5]), although others could be implemented as well. All methods and layouts indicated by golden circles in Fig. 2 are new features from this new DyNetVis version.

DyNetVis also implements models and tools for studying dynamic processes, especially epidemic dynamics (Fig. 2). The software includes a random walk model and four classic epidemic models (SI, SIR, SIS, and SIRS), where S stands for susceptible, I for infected, and R for recovered, which are the possible node states at a particular time [8]. The software was further improved with a novel node ordering strategy based on infection paths.

DyNetVis provides interactive tools that allow exploring the layouts by zooming, panning, and coordinating the analysis

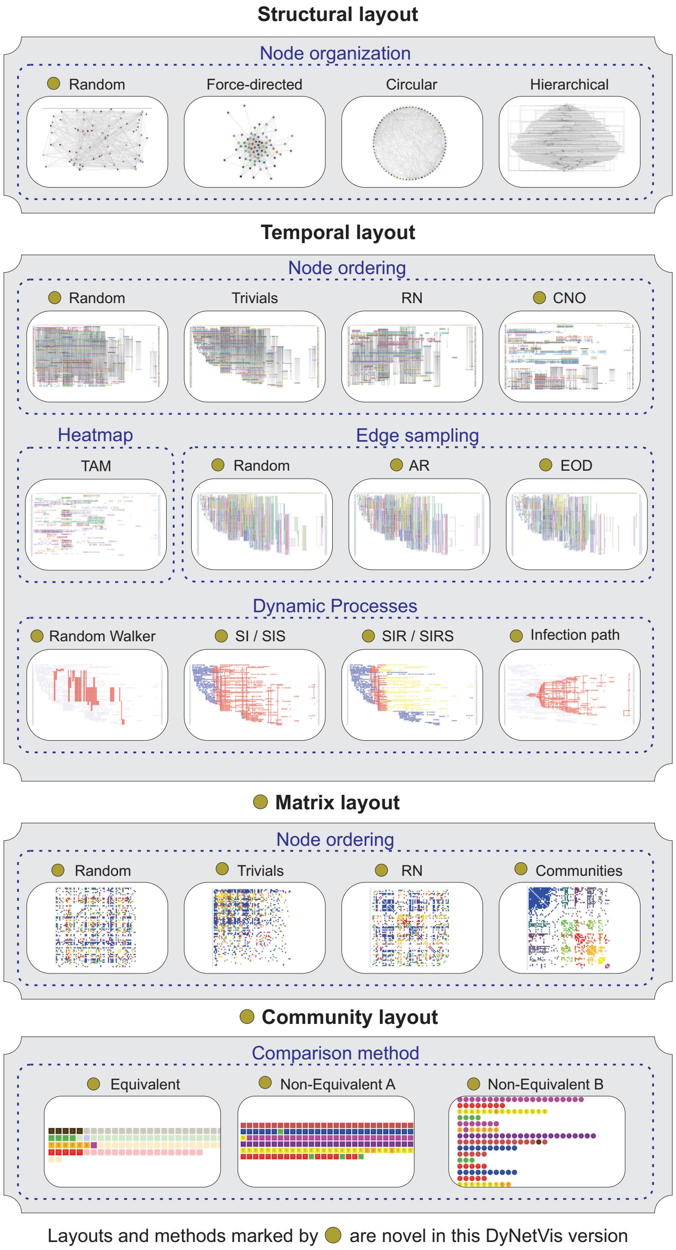

Fig. 2. DyNetVis methods for four different layouts.

between layouts, i.e., nodes and edges selected in a layout are automatically selected in another. These tools comprise different ways to analyze network data through complementary perspectives that lead to different insights. It is also possible to perform a quantitative analysis of visual cluttering, for example, the estimation of overlapping edges and number of intersections [7], to support the choice of the most appropriate ordering and sampling algorithms. Table I shows a summary of the functionalities provided by DyNetVis.

IV. Demonstration

We illustrate in this section applications using a real-world network, the Conference network [22], which contains 113 nodes and 8,892 edges distributed in 3 days. Figure 3 shows a screenshot of the DyNetVis temporal layout for this network, highlighting the functionalities and interactive tools.

TABLE I
FUNCTIONALITIES FOR THE FOUR LAYOUTS IN DYNETVIS.

Interaction/Functionality	Struc.	Temp.	Matrix	Comm.
Zoom and Pan	✓	✓	✓	✓
Animation	✓		✓	
Coordination between layouts	✓	✓		
Quantitative analysis		✓		
Export image	✓	✓	✓	✓
Depth selection of nodes/edges	✓			
Select specific nodes/edges	✓	✓		
Change shape/size of nodes/edges	✓	✓		
Change color of nodes/edges	✓	✓	✓	
Maps scalar values to edges/nodes colors	✓	✓	✓	✓
Network community detection	✓	✓	✓	✓

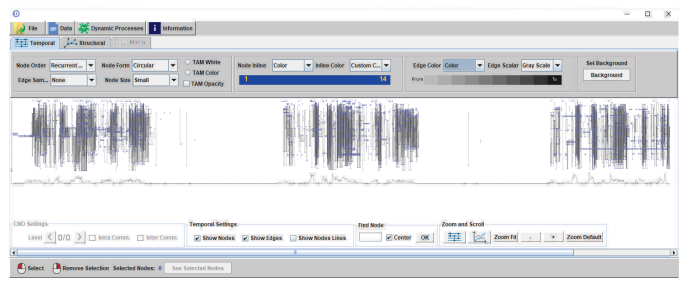

Fig. 3. Screenshot of the temporal layout for the Conference network.

Figure 4 presents patterns that can be found while exploring three different layouts. Figure 4(a) shows part of the temporal layout from Fig. 3. One can assess the network evolution over time, identify different levels of activity (e.g., burst/absence of edges) and highly active groups of nodes, frequently interacting between themselves. Such groups may indicate, for example, groups of individuals from the same university who communicate with each other. Figure 4(b) shows the aggregated network using the force-directed node organization in the structural layout. When adopting this method, the highest degree nodes are positioned in the center of the layout. Finally, in matrix layouts (Figure 4(c)), one can compare community sizes and focus the analysis on specific communities.

Figure 5 shows part of the Conference network highlighting the SIR infection path of an epidemics simulated with two infection probabilities. The patient zero is located in the center of the layout and each new infected node is located around it, recursively. This organization emphasizes the transmission tree (who infected whom and the time of infection). It also allows the identification of groups with the same state (susceptible, infected, or recovered) due to the node colors. When the infection probability is high (Fig. 5(a)), most nodes are quickly infected (red), becoming recovered (yellow) after some time. When the probability is reduced (Fig. 5(b)), several nodes are not infected and thus remain susceptible (blue) during the observation period.

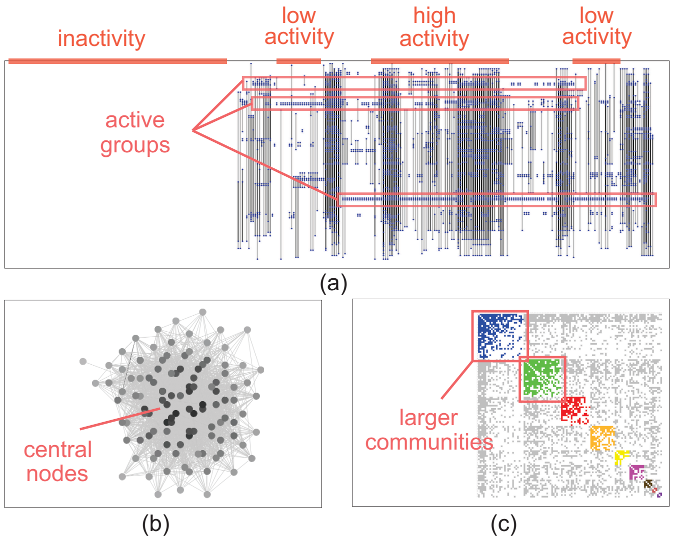

Fig. 4. Conference network. (a) temporal. (b) structural. (c) matrix.

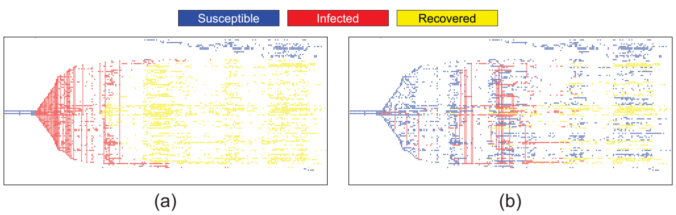

Fig. 5. SIR model over the Conference network analyzed using the infection path ordering: (a) high and (b) low infection probabilities.

V. Conclusion

A number of visualization techniques for temporal networks are available. However, finding appropriate software that includes methods for various tasks is a challenging problem. This paper introduces an extended version of *Dynamic Network Visualization (DyNetVis)*, a freely available and open-source interactive software that provides four layouts and state-of-the-art visualization techniques for temporal network analysis. DyNetVis also implements dynamic processes, including four well-established models for the study of epidemics. As future work, we intend to perform user evaluations to validate the software usability.

Acknowledgment

This research was supported by Conselho Nacional de Desenvolvimento Científico e Tecnológico - CNPq (grant number 456855/2014-9) and Coordenação de Aperfeicoamento de Pessoal de Nível Superior (CAPES PrInt - Grant number 88881.311513/2018-01).

References

[1] M. Newman, *Networks: An Introduction*. New York, NY, USA: Oxford University Press, Inc., 2010.
[2] R. Albert and A.-L. Barabási, "Statistical mechanics of complex networks," *Rev. Mod. Phys.*, vol. 74, pp. 47–97, Jan 2002. [Online]. Available: https://link.aps.org/doi/10.1103/RevModPhys.74.47
[3] P. Holme and J. Saramäki, "Temporal networks," *Physics Reports*, vol. 519, no. 3, p. 97–125, Oct 2012.
[4] M. Dehmer, F. Emmert-Streib, S. Pickl, and A. Holzinger, *Big Data of Complex Networks*. Chapman and Hall CRC, 08 2016.
[5] C. D. G. Linhares, J. R. Ponciano, F. S. F. Pereira, L. E. C. Rocha, J. G. S. Paiva, and B. A. N. Travençolo, "Visual analysis for evaluation of community detection algorithms," *Multimedia Tools and Applications*, 2020. [Online]. Available: https://doi.org/10.1007/s11042-020-08700-4
[6] S.-O. Tergan and T. Keller, *Knowledge and Information Visualization: Searching for Synergies (Lecture Notes in Computer Science)*. Berlin, Heidelberg: Springer-Verlag, 2005.
[7] C. D. G. Linhares, J. R. Ponciano, F. S. F. Pereira, L. E. C. Rocha, J. G. S. Paiva, and B. A. N. Travençolo, "A scalable node ordering strategy based on community structure for enhanced temporal network visualization," *Computers & Graphics*, vol. 84, pp. 185–198, nov 2019.
[8] C. D. G. Linhares, J. R. Ponciano, J. G. S. Paiva, B. A. N. Travençolo, and L. E. C. Rocha, "Visualisation of structure and processes on temporal networks," in *Computational Social Sciences*, P. Holme and J. Saramäki, Eds. Cham: Springer International Publishing, 2019, pp. 83–105.
[9] S. van den Elzen, D. Holten, J. Blaas, and J. J. van Wijk, "Reordering massive sequence views: Enabling temporal and structural analysis of dynamic networks," in *Visualization Symposium (PacificVis), 2013 IEEE Pacific*. IEEE, 2013, pp. 33–40.
[10] F. Beck, M. Burch, S. Diehl, and D. Weiskopf, "A taxonomy and survey of dynamic graph visualization," *Computer Graphics Forum*, vol. 36, no. 1, pp. 133–159, 2017.
[11] C. D. G. Linhares, B. A. N. Travençolo, J. G. S. Paiva, and L. E. C. Rocha, "Dynetvis: A system for visualization of dynamic networks," in *Proceedings of the Symposium on Applied Computing*, ser. SAC '17. New York, NY, USA: ACM, 2017, pp. 187–194.
[12] M. Bastian, S. Heymann, and M. Jacomy, "Gephi: An open source software for exploring and manipulating networks," 2009. [Online]. Available: http://www.aaai.org/ocs/index.php/ICWSM/09/paper/view/154
[13] P. Shannon, A. Markiel, O. Ozier, N. S. Baliga, J. T. Wang, D. Ramage, N. Amin, B. Schwikowski, and T. Ideker, "Cytoscape: a software environment for integrated models of biomolecular interaction networks," *Genome Research*, vol. 13, no. 11, pp. 2498–2504, Nov. 2003.
[14] M. Li, J. Yang, F.-X. Wu, Y. Pan, and J. Wang, "DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization," *Bioinformatics*, vol. 34, no. 9, pp. 1597–1599, 12 2017.
[15] T. Göhnert, S. Ziebarth, H. Detjen, T. Hecking, and H. U. Hoppe, "3D DynNetVis: A 3D Visualization Technique for Dynamic Networks," in *Proceedings of the 2015 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining 2015*, ser. ASONAM '15. NY, USA: Association for Computing Machinery, 2015, p. 737–740.
[16] P. Valdivia, P. Buono, C. Plaisant, N. Dufournaud, and J. Fekete, "Analyzing dynamic hypergraphs with parallel aggregated ordered hypergraph visualization," *IEEE Transactions on Visualization and Computer Graphics*, pp. 1–1, 2019.
[17] V. Batagelj and A. Mrvar, "Pajek-program for large network analysis," *Connect*, vol. 21, pp. 47–57, 01 1998.
[18] C. D. G. Linhares, J. R. Ponciano, B. A. N. Travençolo, J. G. S. Paiva, and L. E. C. Rocha, "Análise temporal de uma rede de contato hospitalar utilizando técnicas de visualização de informação." XVII Workshop de Informática Médica, 2017.
[19] J. R. Ponciano, C. D. G. Linhares, S. L. Melo, L. V. Lima, and B. A. N. Travençolo, "Visual analysis of contact patterns in school environments," *Informatics in Education*, vol. 19, no. 3, pp. 455–472, 2020.
[20] "Algorithms for drawing graphs: an annotated bibliography," *Computational Geometry*, vol. 4, no. 5, pp. 235 – 282, 1994.
[21] Y. Zhao, Y. She, W. Chen, Y. Lu, J. Xia, W. Chen, J. Liu, and F. Zhou, "Eod edge sampling for visualizing dynamic network via massive sequence view," *IEEE Access*, vol. 6, pp. 53 006–53 018, 2018.
[22] L. Isella, J. Stehlé, A. Barrat, C. Cattuto, J. Pinton, and W. Van den Broeck, "What's in a crowd? analysis of face-to-face behavioral networks," *Journal of Theoretical Biology*, vol. 271, no. 1, pp. 166–180, 2011.