Interactive visualization for understanding and analyzing biomedical research collaboration networks – a pilot study

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Abstract

A number of social network analysis (SNA) studies have shed light on the characteristics of research collaboration networks (RCNs). In the Clinical Translational Science Award (CTSA) community, SNA provides us a set of effective tools to assess research collaborations and the impact of CTSA. Although quantitative network metrics are valuable, the understanding of these descriptive network statistics is hard to realize by non-experts. Therefore, we aim to create an analytical platform to help network researchers and administration apprehend the network dynamics of research collaborations through interactive visualization. In this study, we present our pilot study in analyzing the biomedical RCNs using visual analytical methods at the University of Arkansas for Medical Sciences – a CTSA institution.

Introduction

The nature of clinical translational science requires inter-disciplinary collaborations. One of the key objectives of the Clinical Translational Science Award (CTSA) is to promote cross-disciplinary collaborations that can accelerate the translation and application of biomedical research discoveries into clinical settings. To better understand, facilitate, and direct clinical translational research efforts, it is essential to analytically assess the quality and efficiency of existing research collaborations in a CTSA institution.

Social network analysis (SNA) methods have been regarded as an effective tool to assess inter- and intra-institution research collaboration networks (RCNs) in the CTSA community[1]. Visualization of a RCN is often beneficial to a layperson to understand its topology and dynamics. However, due to the limitation of available tools, researchers in RCN studies often choose to only present static visualizations of the networks, which limits the dissemination of their analyses to non-experts.

In this paper, we present experiences in exploring various network visualization techniques to create an easy-to-use and informative interactive analytical system for studying biomedical RCNs, specifically, analyzing network dynamics and characteristics of the biomedical RCN at the University of Arkansas for Medical Sciences (UAMS) – a CTSA institution. This study serves as the first step towards building a comprehensive visual analytical framework for network science.

Figure 1: The graphic interface of our research collaboration network visual analytics system.

Biomedical Research Collaboration Networks

The biomedical research collaboration networks we study are unique in that those RCNs are formed based on collaborative research grants rather than publication co-authorships[2,3,4]. Moreover, distinct from existing network analysis studies on scientific collaborations, we abstract RCNs to reflect the degree of collaboration. We formalize a biomedical RCN as an *undirected weighted* graph, i.e., $G = (V, E)$, where each investigator is represented by a vertex or node ($v_i \in V$), and the collaborative relationship between two investigators (v_i and v_j) is evident by an edge or link between the two nodes

($e_{ij} \in E$). The weight (w_{ij}) of an edge (e_{ij}) is the *number of research grants* the two investigators have collaborated on during the time period of interest.

An Interactive Visual Analytical System for Research Collaboration Networks

An important goal of our study is to provide analytical tools that can help nontechnical biomedical researchers and administration for understanding the nature and evolution of collaboration. As interactive visualization is much more direct, informative, and appropriate than other forms of data representation for a person to apprehend data and derive accurate observations and useful insights, we started to build a web-based visual analytics system for research collaboration network using a number of cutting-edge Web technologies. Figure 1 illustrates the main interface of our research collaboration network visual analytics (RCN-VA) system. The RCN-VA system is open-source and can be accessed at `http://bianjiang.github.io/rcna/`.

As shown in Figure 1, each circle (node) represents an investigator in the collaboration network, and a curved line connecting two nodes indicates the collaborative relationship between the two investigators. Nodes are colored to distinguish CTSA (green) supported investigators from non-CTSA (gray) supported investigators. The strength of collaboration between two investigators is represented by the thickness of line. To realize vivid, accurate, interactive representation, networks in the RCN-VA system are rendered using a physically-based forced-direct graph layout[5]. The forced-direct graph layout in `d3` implements the position Verlet integration to determine moving trajectories of nodes in the network. The physically-based model not only considers repulsive charge forces that spread nodes evenly on the canvas, but also takes into account the gravity forces that keep nodes centered in the visible area and avoid expulsion of isolated components. One immediate benefit of using a forced-direct graph layout for rendering networks is the clustering effect that manifests. A cluster of nodes that are highly connected will naturally be grouped together because of the gravity forces.

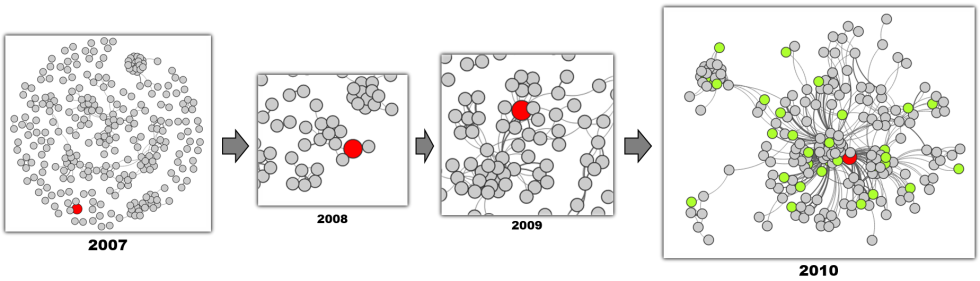

Figure 2: Temporal evolution of an investigator in the research collaboration network at UAMS.

Chronological analysis of network dynamics. The ability to track nodes of interest enables us to study the temporal evolution of individual investigators. For example, as shown in Figure 2, we can track a particular investigator (marked as the red node) in Geriatrics from 2007 to 2010 and observe her collaborative relationships within the network. In 2007, the investigator only collaborated within an isolated small group (four investigators). In 2008, both the size of the group and the number of internal connections increased; however, the group was still disconnected from other parts of the network and the particular investigator still had very few collaborations. In 2009, in preparation of the CTSA program, the group eventually made connections to the largest subgraph of the network. We can easily see in the 2009 graph of Figure 2 that this investigator became a bridge connecting different small clusters. In 2010, the first year after the CTSA, the investigator was drawn towards the center of the network, and her "influence" in the network increased drastically.

Conclusion

In this study, we presented our experiences in exploring various interactive network visualization techniques to facilitate in understanding the network nature and evolution of research collaborations.

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