BUILDING NETWORK VISUALIZATION TOOLS TO FACILITATE METACOGNITION IN COMPLEX ANALYSIS

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Submitted: June 6, 2010

Abstract

If whole communities of domain analysts are to be able to use interactive network visualization tools productively and efficiently, tool design needs to adequately support the metacognition implicit in complex visual analytic tasks. Metacognition for such exploratory network-mediated tasks applies across disciplines. This essay presents metacognitive demands inherent in complex tasks aimed at uncovering relevant relationships for hypothesizing purposes and proposes network visualization tool designs that can support these metacognitive demands.

To make widespread exploratory analysis available and optimally useful, network visualization tools need to be tailored for the actual practices of a large community of domain experts. Unfortunately, in visual analytics generally and in network analytics specifically, a black box surrounds much of the support that domain experts require if they are to engage in the higher order sensemaking that advances discovery-driven analysis with ease of use and value. Because of this insufficient understanding, network designers and developers are often hamstrung in attempts to transform prototypes and proofs of concept into useful tools for whole communities of practice. This essay aims to enhance this understanding by looking specifically at the under-researched area of metacognition in complex analysis and the support it requires from network visualization tool designs.

In this essay, I explain the metacognitive processes that come into play in one class of network analytics based on studies I have conducted with one community of practice: biomedical specialists. I also propose network visualization designs that can better support these metacognitive demands. I argue that in creating interactive network visualizations for usefulness and usability, developers and designers need to understand models of users’ cognition from the start of development and they then need to build in “packages” of features that will afford fluent (cumulative) inquiry and give users multiple means cuing important points in their inquiry.

Background

At our NIH-funded center for bioinformatics we study the support biomedical specialists need for interacting usefully with interactive visualization tools such as Cytoscape and its plug-ins at cytosc ape.org [1]. Biomedical specialists frequently use high dimensional network visualization tools for hypothesizing purposes. With network visualizations of molecular interactions and functional relationships/pathways, for example, they strive to uncover previously unknown insights about functional molecular-level relationships that may influence particular disease processes and phenotype behaviors.

In previous research on these scientists, I have uncovered biomedical specialists’ common patterns of network-mediated analysis and have modeled the higher order cognition they employ when exploring relevant relationships to explain disease mechanisms [2]. Findings for this class of exploratory biomedical analysis suggest that interactive network visualizations must support a flow of inquiry in which tasks throughout the flow comprise multi-modal reasoning, specifically integrated processes of classification, comparison, validation and metacognition.

Usefulness and usability for interactive network visualizations depend on adequate support for this higher order reasoning. Yet usefulness and usability are fairly nascent areas of study in the interactive network visualizations included in bioinformatics tools. To be useful, they need to support domain experts in ways that match their actual problem-solving purposes, practices, ways of thinking and knowing. To be usable they need to be easy and efficient to operate, navigate, access, and understand. Toward these ends, some areas of necessary support for complex analysis amid uncertainty remain a black box, as shown in Fig. 1 [3]:

- Recursively searching information amid uncertainty to find groupings and justifications and reasons relevant to an analysis problem
- Interpreting, inferring, contextualizing, and evaluating salient relationships to turn them into plausible and credible evidence and “stories”
- Managing evolving ideas, emergent insights, and intentions for future paths to pursue and prior paths worth revisiting.

These latter aspects of the workflow are metacognitive tasks, the focus of this essay.

What is Metacognition?

Metacognition allocates individuals’ cognitive functions as they work. Biomedical specialists, for example, allocate cognition partly by purposefully directing visual attention in their workspace. Metacognitively, they visually attend to the workspace aspects necessary for managing and monitoring progress, outcomes, meanings, intentions, false starts, and judgments. Concurrently they selectively attend analytically to reading, drawing inferences from, and variously manipulating different molecules (nodes), molecular interactions (edges), attributes and values (color and other perceptual coding), contexts (biological meaning and events triggered by the information display combined with prior knowledge), structural relations (graph
Fig. 2. Metacognition in a complex workspace for exploratory analysis.

Fig. 3. Highlighting to direct visual attention.

Theorictic values), and details (dynamically linked tabular data). Networks clearly need to support this concurrent metacognition and analysis. As Fig. 2 shows, without adequate support workspaces can be unintelligible.

In biomedical inquiries with networks of molecular interactions, scientists metacognitively set visual cues to mark salient relationships, e.g. by preattentive or gestalt cuing. They set up data into intelligible displays to facilitate a repeated cycling through the same information [4]. They also use this approach as a means for immersing themselves in the data and forming a mental model of its relationships, another strategy for managing progress. Additionally, they leave markers in their workspaces to trigger prior intentions or fruitful tangents to return to, e.g. bookmarked views with meaningful titles or user-defined groupings of items [5]. They keep layouts and other arrangements consistent as they transition to new tasks so that they do not lose track too quickly of the tasks from which they are switching [6].

Implications for Tool Design

As we have found in our national bioinformatics center, having user models that capture metacognitive activities as they interweave with analysts’ other modes of reasoning is vital for guiding the development of networks toward usefulness and usability. User models at the start of development can help avoid the mismatches that undermine usefulness [7]. My studies of biomedical specialists’ use of interactive network visualization tools highlight two design issues relevant to supporting metacognition.

First, certain features often ignored in core interactivity need to be included in network designs. To support metacognition, for example, users need to be able to encode or change color coding in no more than 3 steps. They need to be able to override default coding, interact with legends and have legends update as filtering occurs, and be sure that codings carry over for a number of moves without defaulting to initial settings (see Fig. 3 for color coding that draws attention to salient information). Biomedical specialists need as well to be able to exclude or hide filtered-out items. Second, to anticipate analysts’ applied expertise, network visualization tools need to provide history and bookmarking capabilities, undo and redo, a variety of pre-defined layouts and arrangements, and user-defined arrangements. Similarly, networks should let users recall prior moves and rerun them as needed. Saving and annotating are critical to metacognition, as well.

Exact behaviors of these suggested features often are specific to domains. User studies preceding requirements engineering and development will help define such behaviors. By including these suggested features, network visualization tools will come closer to matching and satisfying the exploratory needs of whole communities of analysts and realize their promise for advancing disciplinary knowledge.

Acknowledgements

This work was funded by NIH Grant #8 U54-DA-021519 and P30DK081943 George M. O’Brien Kidney Research Core Center at the University of Michigan, Applied Systems Biology Core. I thank Felix Eichinger and Ben Keller for their collaborations.

References

* This paper was presented as a contributed talk at Arts | Humanities | Complex Networks – a Leonardo satellite symposium at NetSci2010. See <http://artshumanities.netsci2010.net>


