

# BioMixer: A Web-based Collaborative Ontology Visualization Tool

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## ABSTRACT

Ontology development often requires the participation of various collaborators. Web-based ontology editors, such as WebProtégé, have been developed to provide users with collaborative support such as comments and discussions. There is a large body of work concerning ontology visualization techniques; however, less research attention has been placed on providing the necessary support for collaborative ontology visualization. To explore this research gap, the web-based collaborative ontology visualization tool BioMixer is presented in this paper. In order to assist the collaborative visualization process, BioMixer provides users with sharable workspaces and embeddable visualizations that can be seamlessly inserted into external websites.

## 1 INTRODUCTION

Visualizations can provide essential cognitive support when trying to make sense of the semantics embedded in ontologies. Improving cognitive support for ontology understanding is particularly important in the domain of biomedical ontologies, as such ontologies are typically large and rely on collaborative development (Noy et al., 2008). Despite a large amount of research effort in developing ontology visualization techniques (Katifori & Halatsis, 2007), there has been relatively little attention placed on providing **collaborative** visualization support.

Real world applications of collaborative visualization include social data analysis websites (such as Many Eyes<sup>1</sup> (Viégas et al., 2007)), scientific research projects (such as National Fusion Collaboratory (Schissel et al., 2004)) and environmental planning (Brewer et al., 2000). However, in the field of ontology visualization, collaborative visualization has not received much attention. Although collaborative support is provided in ontology editors such as WebProtégé<sup>2</sup> (Tudorache et al., 2008), however, existing ontology visualization tools lack collaborative visualization support (Sivakumar & Arivoli, 2011; Katifori & Halatsis, 2007; Katifori et al., 2006).

In an attempt to address the need for collaborative ontology visualization, this paper presents the BioMixer<sup>3</sup> tool that allows users to share visualization workspaces and to embed visualizations in websites. The vision for BioMixer is that collaborative ontology visualization will improve ontology

authoring activities and foster collaboration across groups. The remainder of this paper is organized as follows. A brief overview on related work is presented in Section 2. The design, implementation and key features of BioMixer are presented in Section 3. Finally, Section 4 outlines BioMixer’s future research directions.

## 2 RELATED WORK

Building tools for collaborative visualization is identified as one of the key challenges in visual analytics (Thomas & Cook, 2005) and design considerations for such tools have been recommended (Heer & Agrawala, 2007). Collaborative visualization can be described as “the intersection of two major research fields: traditional visualization and computer supported cooperative working” (Isenberg et al., 2011). In computer supported cooperative working (CSCW), one of the most widely cited classifications to describe collaborative aspects is Applegate’s place-time matrix (Applegate, 1991). Applegate states that cooperative work can take place in the same or different place at the same or different time. In the context of CSCW, synchronous collaboration will typically occur at different places at the same time, e.g. video conferencing. Asynchronous collaboration will typically take place at different places at different times, e.g. editing ontologies using WebProtégé. The current BioMixer release can be categorized as an asynchronous collaboration tool for ontology visualization, however, support for synchronous collaboration is planned for a future release.

Expanding on the place-time matrix, Brodlie et al. (Brodlie et al., 2004) further distinguish distributed visualization from collaborative visualization and distributed collaborative visualization. *Distributed visualization* involves collaboration at the system level, whereas *collaborative visualization* refers to collaboration at the human level. *Distributed collaborative visualization* combines distributed visualization and collaborative visualization by allowing collaboration at both the system and the human level. Other definitions for collaborative visualization have also been proposed in the literature (Raje et al., 1998; Johnson, 1998; Li et al., 2006, Wattenberg, 2005). This paper adopts the definition of collaborative visualization proposed by Isenberg et al., which is “the shared use of computer-supported, (interactive) visual representations of data by more than one person with the common goal of contribution to joint information processing activities” (Isenberg et al., 2011).

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<sup>1</sup> <http://www-958.ibm.com/software/data/cognos/manyeyes/>

<sup>2</sup> <http://webprotege.stanford.edu/>

<sup>3</sup> BioMixer is open source and is freely available at <http://github.com/thechiselgroup/biomixer>

The current release can be found at <http://bio-mixer.appspot.com/>

The benefits of using collaborative visualization have been studied in social data analysis websites such as Many Eyes (Viégas et al., 2007). The goal of Many Eyes is two-fold. First, the creation and publication of visualizations can reach out to a larger audience, not just experts. Second, the social potential of web-based visualizations enables discussions among the wider audience. The advantages of collaborative visualization in social data analysis may also hold true for the domain of ontology visualization. As with collaborative support, visualizations will not only serve as a tool for sense-making, but also as a channel to stimulate discussions between users.

This trend of collaborative support is already embraced by existing ontology editors. For instance, WebProtégé (Tudorache et al., 2008) aims to support the collaborative ontology development process by providing an online environment for users to edit, discuss and annotate ontologies. visCOntE (Vonrueden & Hampel, 2005) provides support for searching, creating and editing ontologies among collaborators. COVE (Allemang et al., 2004) emphasizes the evolution of ontologies and provides collaborative editing support for ontologies in the space shuttle domain.

Despite the uptake of collaborative support in ontology development tools, little research attention has focused on providing collaborative support for ontology visualization. An extensive review of existing ontology visualization approaches is presented in (Katifori & Halatsis, 2007). A key observation from this review is that most existing ontology visualization tools have focused on providing users with sophisticated views; however, few have explored enabling collaboration among the users. Although a web-based visualization service, FlexViz, has successfully demonstrated the application of online visualizations in the BioPortal ontology library (Noy et al., 2009), so far it has not leveraged the social potential of the web. In order to bring the benefits of the social web to biomedical ontology visualization, BioMixer has been designed with collaborative visualization in mind from the beginning.

### 3 BIOMIXER DESIGN, FEATURES & IMPLEMENTATION

Inspired by previous design recommendations (Heer & Agrawala, 2007) and tool requirements (Isenberg et al., 2011) for collaborative visualization, a list of design considerations for collaborative ontology visualization has been derived and is discussed next. Collaborative ontology visualization tools need to (but not limited to):

- support social interactions around the data, so that a group of collaborators working on the same visualizations can provide commentary and discuss relevant implications on common ground;
- engage a wider audience and provide support for users to share and publish their findings, so that infor-

mation is appropriately distributed for group decision making;

- support long-term use by people with distinct backgrounds and different goals, so that personal visualization preferences and styles can be fully elaborated; and
- enhance decision making by providing collaborative support from the beginning of the design process, so that collaborative features are included in the design process of a visualization tool to prevent these features being developed just as an afterthought.

In order to address the needs identified above, BioMixer is being designed to support visualizations in collaborative settings. In particular, BioMixer:

- supports *social interaction* around the visualization. A user can send an existing visualization workspace to his/her collaborators via email, as well as initiate discussions by adding notes to the visualizations.
- engages a wider audience by providing a *web-based interface*. A user can easily access BioMixer using a web browser and does not need to download or install any software.
- supports the *publication of visualizations* by providing interactive visualization embeds that can be easily inserted into external websites.
- supports users with diverse backgrounds and preferences by presenting *multiple coordinated views*, which aim to engage the audience from different viewpoints.

Figure 1 illustrates an example of using BioMixer for collaborative ontology visualization, exemplifying the features listed above. In this example, the user searches for *tissue* and is given a list of ontologies that contain this term in the *Search* view (see top left window in Fig. 1)<sup>4</sup>. The user then selects the Cell Line Ontology, the RadLex Ontology, the BioTop Ontology and the Gene Regulation Ontology in the search results and subsequently creates *Selection 1* in the view frame. By selecting the *Graph* button under *Views*, an empty graph view is created in the workspace. The user can then drag *Selection 1* and drop this selection onto the graph view. He/she can also add comments by adding a *Note* view (see bottom right view in Fig. 1). To explore the nodes shown in the graph view, the user can select a node and choose to visualize its associated concepts or mappings. In Fig. 1, four ontologies (color coded) are visualized in the circle layout, the *is-a* relations are visualized by solid directional lines and the mappings are visualized by grey dashed lines. Visualizing different types of mappings (e.g. exact, close, related, broad and narrow mappings) are not supported in the current graph view, but will be included in a future release. This visualization can also be displayed using other layouts as shown in Fig. 1 (the panel to the right includes

<sup>4</sup> Searching for ontologies by name is not supported in the current release of BioMixer, but is to be included in a future release.

tree, spring, grid layout, etc.). For example, the spring layout may be appropriate when presenting an overview of several ontologies and how the mappings relate them to one another (an example is shown in Fig. 2), however the tree layout may be more suitable for visualizing the hierarchical relationships among the nodes (an example is shown in Fig. 3). As pointed out in (Motta et al., 2011; Katifori & Halatsis, 2007) and demonstrated by Wang & Parsia (Wang & Parsia, 2006), each type of visualization is associated with its own strengths and weaknesses. Thus, BioMixer

supports a variety of layouts in an effort to better assist the user with his/her understanding of the ontology(ies) at hand through the use of flexible visualization layouts. It is recognized that the graph view can quickly become unusable as the number of nodes increases in a visualization. This scalability issue may be overcome by using other types of visualizations, e.g. nodes can be visualized on the axes and mappings can be visualized in the cells of a matrix layout. Additional types of visualization such as the matrix layout are currently being developed for BioMixer.

**Fig. 1.** An Example of Collaborative Ontology Visualization in BioMixer. The user is presented with four tabs: *Workspace*, *BioPortal Concept Search*, *Views* and *Help*. There are four buttons under *Workspace*, including (from left to right) *Create New workspace*, *Load existing workspace*, *Save* and *Share* a workspace. The current release contains four views (circle 2), including *Graph*, *Text*, *Timeline* and *Note*. A variety of visualization layouts (circle 3) are supported in the *Graph* View. The user can send an existing workspace to collaborators by using the *Share* feature (circle 1 & 6) and add comments to visualizations by using the *Note* view (bottom-right). The user can also obtain an iFrame to embed a single visualization in external websites (see Fig. 4). Details of nodes (circle 5) are displayed on demand (i.e. when a user hovers over a node) in BioMixer. In addition, coordination (circle 4) is achieved by highlighting the node/selection under the mouse cursor across multiple views. Note that the user is free to visualize any selection (i.e. any combination of nodes) by dragging and dropping it into the new view.

In BioMixer, the user can further explore any subset of the current visualization by selecting the nodes he/she is interested in viewing. In the example shown in Fig. 1, the user selects the nodes connected by mapping which subsequently creates *Selection 2*. By selecting the *show mapping nodes* checkbox in *Nodes*, this second selection can be dragged and dropped onto the *Timeline* view, which will then show the creation dates of these mappings (e.g. May

17<sup>th</sup>, 2010 in Fig. 1). If the user is only interested in an overview of all the terms used in the ontology irrespective of the relationships between them, a tag cloud can be generated in the *Text* view.

BioMixer also visualizes mappings between multiple ontologies. This differs from existing tools, such as *Optima* (Kolli & Doshi, 2008), *AlViz* (Lanzenberger & Sampson, 2006) and *CogZ* (Falconer & Storey, 2009), where map-

pings are often visualized between only one pair of ontologies. In contrast, mappings in BioMixer are visualized between two or more ontologies at a time (as shown in Fig. 1, and Fig. 2). This feature presents the user with a much broader view on the relationships among a number of ontologies in one visualization. It supports the user in the process of exploring existing mappings and determining the similarities among the given ontologies more efficiently.

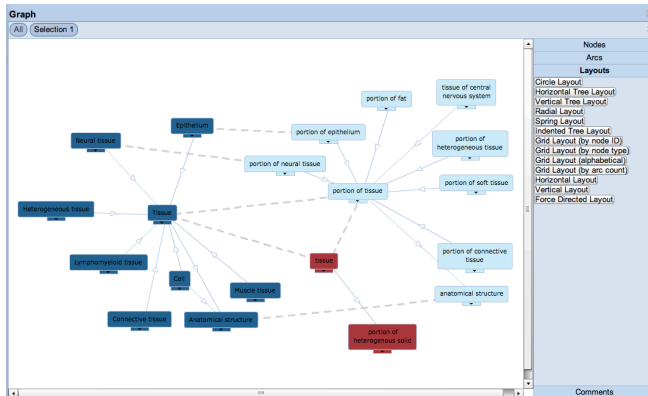


Fig. 2. An Example of Spring Layout. An overview of three ontologies are visualized.

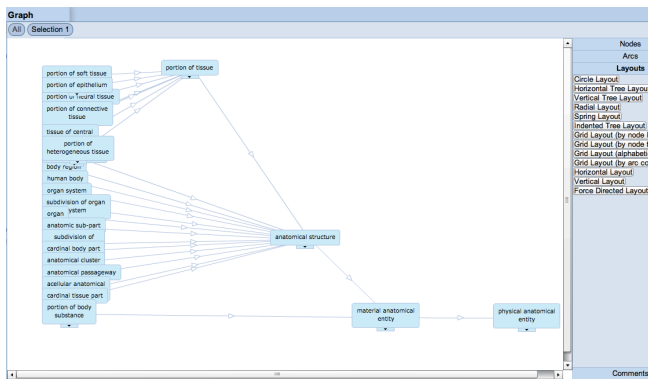


Fig. 3. An Example of Tree Layout. Hierarchical relationships among ontological nodes are visualized.

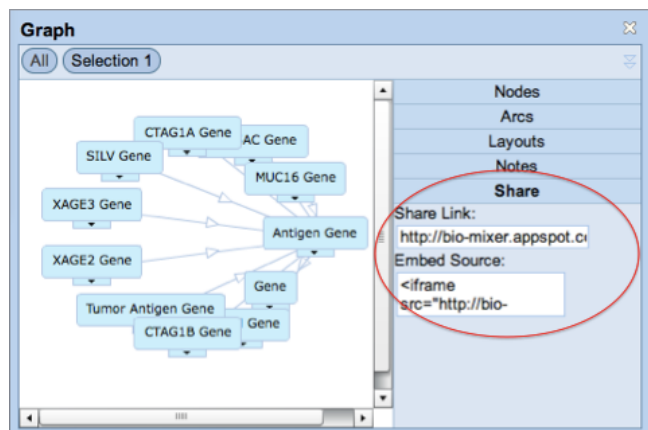


Fig. 4. Collaborative Support in BioMixer. Users can share or embed visualizations by using URL and iFrame.

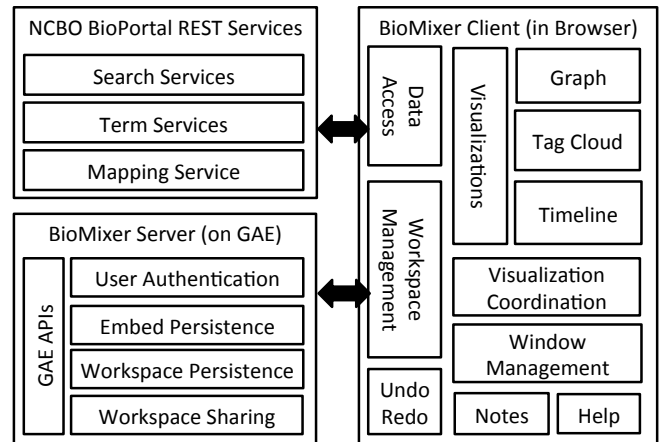


Fig. 5. BioMixer Architecture. There are three main components in BioMixer including the *BioMixer Client*, the *BioMixer Server* and the *NCBO BioPortal REST Services*. The double arrows illustrate the communications between these components.

To share the workspace shown in Fig. 1 with a collaborator, the user can click the *Share* button and enter the collaborator’s email address. An email containing the URL of the workspace will be sent to the collaborator, who can then load this workspace into his/her browser by simply opening the URL. To publish visualizations online, inline frames are provided to the user, which enable the insertion of visualizations in external websites (currently, users must sign in to use this feature). This feature allows the user to quickly update visualizations on external websites when required. Figure 4 demonstrates these *Share* and *Embed* features.

BioMixer is a client-server web application. It is built on top of the Google Web Toolkit<sup>5</sup> (GWT) and the Google App Engine<sup>6</sup> (GAE) technologies, and integrates visualization components written in Flash, Java and JavaScript. Figure 5 presents the BioMixer architecture. The three key components are the BioMixer Client, the BioMixer Server and the BioPortal REST Services<sup>7</sup> provided by the National Center for Biomedical Ontology<sup>8</sup> (NCBO). The *BioMixer client* is an ontology visualization environment that runs in the user’s browser. It is written in Java and compiled to JavaScript using the GWT. The client currently supports graph, text, timeline and note views; however, additional types of visualization can be easily integrated given the extensible architecture of BioMixer. The client also provides visualization coordination such as synchronized highlighting (brushing), filtering and selections across multiple views. In addition, it supports basic features such as window management and undo/redo. The client accesses the data stored in BioPortal through the NCBO *BioPortal REST services*. To enable workspace sharing and persistence, the BioMixer client uses services offered by the BioMixer server. The *BioMixer*

<sup>5</sup> <http://code.google.com/webtoolkit/>

<sup>6</sup> <http://code.google.com/appengine/>

<sup>7</sup> [http://www.bioontology.org/wiki/index.php/BioPortal\\_REST\\_services](http://www.bioontology.org/wiki/index.php/BioPortal_REST_services)

<sup>8</sup> <http://www.bioontology.org/>

server runs on GAE and provides services that require long-term data storage, email notification and user authentication. More specifically, the BioMixer server is responsible for user authentication, embed persistence, workspace persistence and workspace sharing.

#### 4 FUTURE WORK

BioMixer is an on-going research effort. This paper is among the first attempts at applying collaborative support in the field of ontology visualization. The current implementation of BioMixer focuses on the visualization of ontologies from the biomedical domain. However, the underlying architecture is domain independent and could therefore be applied to visualize ontologies from other domains of interest. Future research in BioMixer includes improving its technical infrastructure as well as conducting rigorous evaluation of its usability through real-world case studies. Moreover, we plan to investigate the impact of synchronous and asynchronous collaborative visualization on collaborative biomedical ontology development. In particular, we will continue interacting with different user groups and improve the visualization and collaboration features in BioMixer based on user feedback.

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