

BioOntoVis: An Ontology Visualization Tool

Nassira Achich², Alsayed Algergawy¹, Bassem Bouaziz² and Birgitta König-Ries¹

¹ Institute for Computer Science, Friedrich Schiller University, Jena, Germany

² Higher Institute of Computer Science and Multimedia, University of Sfax, Tunisia
`firstname.lastname@uni-jena.de`

Abstract. As the main way for knowledge representation for the purpose of machine understanding, ontologies are widely used in different application domains. This requires more and more domain specific information to be inserted into ontologies, making them harder to be easily understood by a human and there is a growing need to develop ontology visualization tools. However, most of existing tools focus on either a specific user requirement or ontology-specific features. To this end, in this demo, we introduce a new generic and user-friendly ontology visualization tool, called *BioOntoVis*, for visualizing and editing ontologies. We present the general architecture of the tool focusing on the web-based user interface and different ontology visualization schemes. Through the demonstration of *BioOntoVis*, we introduce the tool's capabilities and highlight its effectiveness and usability.

Keywords: Semantic Web; Ontology visualization; Ontology editing

1 Introduction

Ontologies are the basic components of the Semantic Web, where underlying data are well structured for the purpose of full machine understanding. An ontology consists of a set of concepts (classes), a set of attributes (data type properties), relationships (object properties), and constraints to abstractly represent a specific domain. An important aspect is how to facilitate the process of design, management, and exploration of complex structures. This results in a growing need for ontology visualization tools that simplify the user involvement in different ontology-related management processes [3].

Furthermore, and as a main way of knowledge representation, ontologies have been becoming more and more widely used in different application domains. Therefore, there exist a large number of ontologies, some of them containing hundreds of thousands of concepts or more. For example, **BioPortal**³ contains 737 ontologies with 9,604,539 classes (with an average 13,157 classes per ontology). The arising number of developed ontologies as well as the number of concepts each ontology has make ontology visualization a difficult task. Even though, a

³ <http://bioportal.bioontology.org/> (access on October 25, 2018)

number of ontology visualization approaches have been developed [2,3,4,5], most of the existing ontology visualization tools either cannot cope with visualizing big ontologies or with providing multiple views depending on ontology features and based on user requirements.

To this end, in this paper, we introduce a new ontology visualization tool, called *BioOntoVis*⁴, which is based on a combination of visualization techniques to reflect the mentioned challenges. The proposed tool follows three main steps, including: (i) reading and parsing the input ontology, (ii) a set of processing aspects to make the ontology suitable for visualization, and (iii) finally, the suitable visual representation is selected to visualize the ontology. The proposed *BioOntoVis* tool supports node-link and tree, zoomable, and 3D information landscape [3]. Furthermore, the tool also provides the possibility to edit the visualized ontology by adding/removing one or more ontology entities checking the consistency of the modified ontology.

2 *BioOntoVis*: The tool overview

To deal with visualizing ontologies meeting different application domains as well as variant user requirements, we present a new ontology visualization tool, *BioOntoVis*, introducing a high-level architecture for a generic pipeline for ontology visualization. The pipeline has three main steps: *parsing*, *processing*, and *visual representation*.

Parsing. An *ontology* \mathcal{O} can be represented as a set of entities, such that an entity is either a concept (class), a relation, or an instance (individual). The set of concepts and the set of relations are disjoint, where there is a concept hierarchy between the set of concepts, and there is also a relation hierarchy among relations. Before visualizing an ontology, a parsing step is needed to extract the ontology entities and transform them into a JSON format to be graphically represented. We select working with the OWL API ⁵ to deal with ontologies with different formats. The appropriate parser is automatically selected at runtime when an ontology is loaded.

Processing. This step focuses on the cognitive features included in the visualization tool aiming to strengthen the user's support. It includes both *basic* and *advanced* functionalities. The basic functionalities include: i) **colors**: we define a color scheme for a better distinction between several ontology entities. For example in the fisheye view, we choose a dark-blue scheme for super-classes, light-blue for sub-classes, orange for the properties and a pink scheme for individuals. This color scheme is clearly very helpful in identifying the ontology elements variations, ii) **shapes**: *BioOntoVis* provides various views with various node shapes. This option gives several choices to the user to visualize ontologies. In the network view as an example, we used a rectangle shape, however in the fisheye view we used a circle shape, iii) **zooming**: we use two different zooming types:

⁴ This work was originally motivated by the need to visualize ontologies from the bio domain, hence the name.

⁵ <http://owlcs.github.io/owlapi/>

geometric and *semantics*. The geometric zoom allows the user to explore certain ontology entities in detail when she zooms-in analyzing the global structure of the ontology once she zooms-out. The semantics zoom offers the possibility to see details of a specific entity by zooming, and iv) **details**; an ontology contains a large amount of information and description (metadata), including entity name, label, types, and relations' types, ect. To this end, *BioOntoVis* supports illustrating these information. It contains a circular attractive menu, shows general details about the ontology, such as the metadata, the ontology format and the number of concepts, properties and individuals.

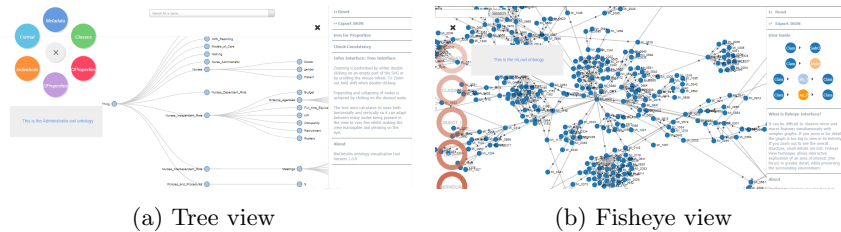


Fig. 1: Different visualization views

Advanced functionalities the proposed tool supports include: i) **search**: finding an ontology entity by visually scanning the ontology graph is a very difficult process, especially in the context of big ontologies. Therefore, the current implementation of the tool contains a search window to quickly find particular entities or other elements by their names/labels. In the tree interface, once a user types in the window, a list containing the set of relevant entities appears to facilitate the search process. We then visualize the searched entity with a different color. ii) **editing operators**: ontologies possess a very complex structure and editing its entities is a hard task. This is due to the fact that each edit process has to check the correctness and consistency of the modified ontology. Therefore, most of existing ontology visualization tools lack the advanced functionalities that are important for the user to interact more with the displayed ontology. For example, ontology modularization partitions an ontology into a set of partitions (modules) [1]. To validate the modularization result, an ontology visualization tool with editing capabilities is required. It should be noted that any edit operation can violate the semantic and structure definitions of ontology entities, thus changing the status of the ontology from consistency into inconsistency. Therefore, the tool asks the user to check before these changes will be applied.

Visual representation. To cover a wide range of ontologies, *BioOntoVis* provides three views of visual representations, which are: *tree*, *network*, and *fish-eye* view. As shown in Fig. 1a, the tree view representation is a hierarchical node-link view, in which the ontology is represented as a set of interconnected nodes in different levels. In this view, the user can extend or compress the tree, by displaying or hiding children nodes allowing the user to control the depth

of the tree. In the network view, the nodes have rectangle shapes and are connected to each other through edges. In this view, colors have their meanings to facilitate distinguishing between ontology entities. Moreover, a detailed box appears once a node is selected to give detailed information about the entity, and its relationships. In large ontology visualization, links between concepts would be drawn crossing and overlapping each others, which cause a very messy and potentially unusable view of the ontology graph. Therefore, we implemented the fisheye view in the tool to deal with this problem. This view demonstrates the selected node surrounded by the ones that are related to it, hiding all the others, as shown in Fig. 1b.

3 Demonstration Scenarios

In this demonstration, we will start by presenting the different features of *BioOntoVis* such as various capabilities of the tool to visualize different ontologies using different views, such as tree, network, or fisheye based on the characteristics of the ontology, as shown in Figs. 1a and 1b. The demonstration will consist of two main parts. First, we would like the user to appreciate the importance of the visualization phase. Second, we present different operations that can be employed on the displayed ontology. To this end, the *BioOntoVis* tool is provided with a nice web interface⁶, where the user can upload her ontology and then select which visualization view to show the ontology. Through this web interface, the user can get some metadata about the ontology, such as format, the number of concepts, the number of properties, etc. Later, the user can adjust the view to fit her needs.

4 Acknowledgments

A part of this research was supported by DAAD funding through the BioDialog project. A. Algergawy' work is partly funded by DFG in the scope of CRC 1067 AquaDiva.

References

1. A. Algergawy, S. Babalou, F. Klan, and B. König-Ries. OAPT: A tool for ontology analysis and partitioning. In *EDBT*, pages 644–647, 2016.
2. Z. Dragisic, V. Ivanova, P. Lambrix, D. Faria, E. Jiménez-Ruiz, and C. Pesquita. User validation in ontology alignment. In *15th ISWC 2016*, pages 200–217, 2016.
3. A. Katifori, C. Halatsis, G. Lepouras, C. Vassilakis, and E. G. Giannopoulou. Ontology visualization methods - a survey. *ACM Comput. Surv.*, 39(4):10, 2007.
4. S. Lohmann, S. Negru, F. Haag, and T. Ertl. Visualizing ontologies with VOWL. *Semantic Web*, 7(4):399–419, 2016.
5. S. Negru and S. Lohmann. A visual notation for the integrated representation of OWL ontologies. In *WEBIST*, pages 308–315, 2013.

⁶ A beta version of the tool: <http://bioontovis.uni-jena.de:8080/BioOntoVis-V1.0-1>