Exploring Multiple Ontologies with OntoExplore

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Genomics researches have been producing a large amount of information. They require the execution of queries on data that is distributed in several sources. Ontologies are of great help in this scenario, since they help in integrating information and on the annotation process. Thus, the challenge is to put several ontologies together to be queried and to compare concepts in more than one ontology at the same time. This is of great relevance to annotators and, in general, to bioinformaticians.

Visualization mechanisms are fundamental to manipulate and understand ontologies. They are important due to the complexity that ontologies may achieve. Visualization mechanisms should allow editing, holistic understanding, mapping and navigation. There are several visualization techniques, e.g., Hyperbolic, Tree Map, Crop Circle, Self Organizing Maps and 3D Cone Trees [1]. The tools OntoSphere [2] and OntoCover [3] implement some of these techniques. Among the tools supporting visualization for the exploration of ontologies, Protégé [4] is certainly the most popular one. This tool is powered by plugins, installed according to the user's needs. Other tools, such as Jambalaya [5], OntoViz [6] and Growl [7], provide different viewing modes.

Although there is a considerable number of approaches and tools to view ontologies, they lack specific features and capabilities which are essential to bioinformaticians and biologists, such as features to manipulate multiple ontologies. Ontologies in the bioinformatics area are usually very large, and some of the existing tools presented difficulties when dealing with these type of ontologies.

Based on this observation, we propose an approach that has the following features: (i) ability to manipulate several ontologies at the same time; (ii) search and visualization of terms; (iii) retrieval and comparison of terms hierarchy; (iv) comparison of the definition of a term in more than one ontology. These features were implemented on a tool we have developed, called OntoExplore, which aims to solve some of the aforementioned problems and to increase the productivity of biologists and bioinformaticians. OntoExplore allows scientists to work with several ontologies at the same time. The main strengths of the tool are twofold:

Visualization and comparison of terms hierarchies in different ontologies. It is possible to select a term and visualize its hierarchy in two different ontologies (see Figure 1). Thus it is possible to check and study the hierarchy of terms, choosing the best term for annotation.

Search of terms within multiple ontologies. Sometimes the term is found in another ontology with a different name. The goal of this functionality is to find similar terms. This is done by using a synonym dictionary in the mechanism.
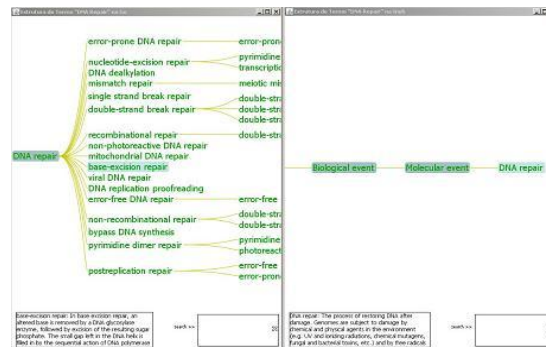
Figure 1. Comparing the same term hierarchy in two ontologies

This mechanism was developed in Java, using the API JENA [8] to parse ontologies in OWL and RDF formats, and the Prefuse Visualization Toolkit [9] to implement interactive data visualization mechanisms. In this first prototype, OntoExplore was tested with 4 ontologies in the bioinformatics area (Gene Ontology, Brenda, Inoh e Pathway).

With OntoExplore the bioinformaticians are allowed to search and explore the hierarchy of terms in several biological ontologies more effectively, using dynamic view trees, ontology subsets and information retrieval, thus providing computational support to the process of annotation using biomedical ontologies. Future enhancements, modifications and investigations are needed to improve our mechanism, such as to provide a larger set of metrics to compare term hierarchies in distinct ontologies. OntoExplore is expected to be soon integrated to the ProtozoaDB annotation platform[10] and it is also to be experimented as an extension of an ontology alignment tool based on FOAM framework[11].

References

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