

Visualization and editing of biomedical ontology alignments in AgreementMakerLight

Catarina Martins¹, Daniel Faria², Catia Pesquita¹

¹LaSIGE, Departamento de Informática, Faculdade de Ciências, Universidade de Lisboa

²Instituto Gulbenkian de Ciência

ABSTRACT

Biomedical ontologies pose interesting challenges to the visualization of ontology alignments due to their size and complexity.

AgreementMakerLight (AML) is a lightweight ontology alignment system that is particularly suited to the alignment of biomedical ontologies.

Here, we present the updates and evolution of the AML graphical user interface, with a focus on alignment visualization and alignment editing.

1 INTRODUCTION

Several biomedical ontologies have overlapping or related domains, and matching them would greatly increase their interoperability. Ontology matching techniques produce an alignment between two ontologies by establishing correspondences between their elements. Each correspondence is called a mapping and an alignment corresponds to the set of all mappings.

Biomedical ontologies pose challenges in ontology alignment and alignment visualization due to their usually large size, and complexity which can lead to several computational and visualization issues.

AgreementMakerLight(AML) is a lightweight ontology matching system that is particularly well-suited to matching biomedical ontologies, since it can handle large ontologies with complex terminology (Faria *et al.*, 2013a). AML has achieved top performances in the biomedical ontologies tasks in OAEI 2013 (Faria *et al.*, 2013b) and 2014 (Faria *et al.*, 2014), an international competition for ontology alignment systems. It includes several matching techniques supported by a graphical user interface (Pesquita *et al.* (2014)).

Other ontology matching systems provide user interfaces and visualization and editing features (e.g.: COMA 3.0 (Massmann *et al.*, 2011), AgreementMaker (Cruz *et al.*, 2009), RepOSE (Ivanova and Lambrix, 2012)). However, they struggle to handle large ontologies with multiple inheritance (which is a common case in the biomedical domain).

We present the latest advancements in the graphical user interface for AML, focusing on the novel user alignment editing capabilities and element inspection views. Editing is accompanied by a mapping graph-based visualization that supports users in decision making.

AML is open-source and freely available (as runnable Jar and Eclipse Project) at <https://github.com/AgreementMakerLight/AML-Project>. For more information, please check: <http://aml.fc.ul.pt>.

2 AGREEMENTMAKERLIGHT GUI

The graphical user interface of AML comprises three main areas: the Resource Panel where information about the ontologies and the alignment is displayed, like the number of classes, properties and

mappings; a Mapping Viewer dedicated to the graph representation of each mapping and its neighbors (Figure 1) and the Alignment Reviewer that lists all the mappings involved in the alignment with information about each one (Figure 2).

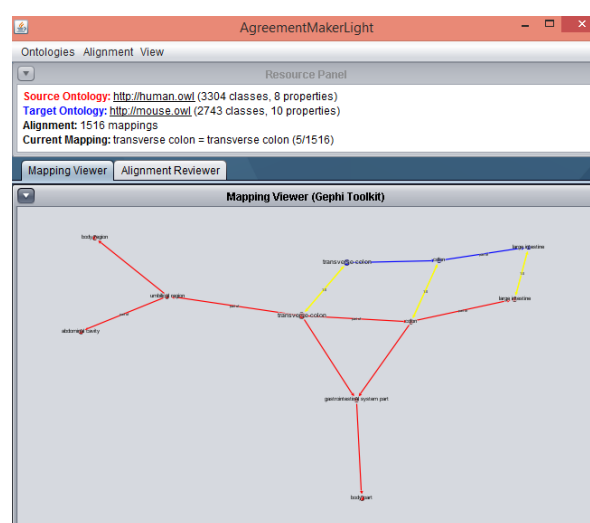


Fig. 1. Visualization of a mapping between two different ontologies in the Mapping Viewer tab.

3 COMPUTING OR LOADING AN ALIGNMENT

The user can load the ontologies in either OWL or RDFs, then he has the option to load a precomputed alignment or to match the ontologies he desires to analyze. In GUI-mode, AML provides two matchers: an automatic matcher and a custom matcher where the user can decide which techniques will be involved in the alignment. The user also has the possibility to repair an alignment (Santos *et al.*, 2013) or to evaluate an alignment against a reference standard. All of these features grant the user the opportunity to save the produced alignment in RDF or in a tab-separated text file.

4 EDITING AN ALIGNMENT

The new update allows the user to alter an existing alignment (either loaded or computed by AML) in the Alignment Reviewer tab. To remove an existing mapping, the user can select it from the list of mappings (Figure 2). To add a new mapping, the user can select the appropriate option and then use a label based search for the classes or properties to map (Figure 3). Both types of changes are recorded when the alignment is saved.

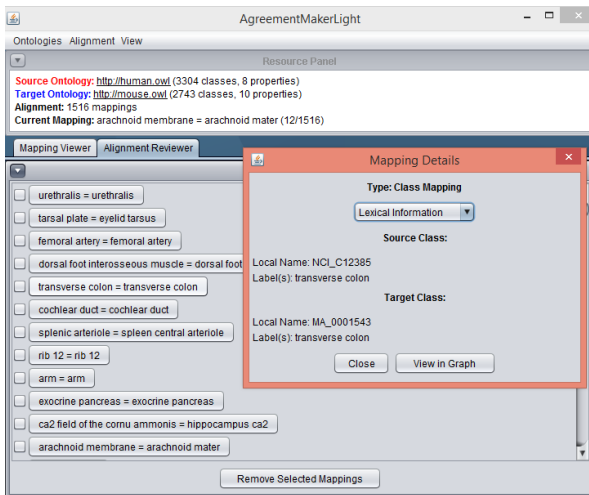


Fig. 2. List of mappings between two different ontologies in the Alignment Reviewer tab.

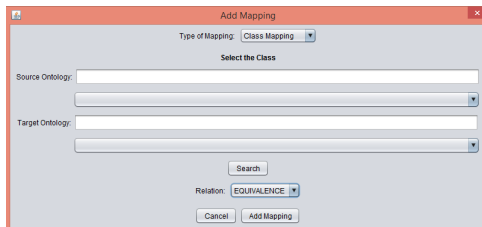


Fig. 3. Add Mapping window in AML.

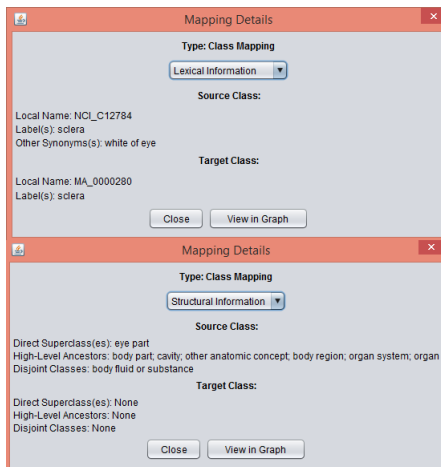


Fig. 4. Class inspection views.

These tasks can be supported by the inspection of each mapping which is accessible from the Alignment Reviewer tab (see Figure 4). The inspection view for classes provides lexical information, which includes local name and synonyms, and structural information, which includes direct superclasses, high-level ancestors and

disjoint axioms. The inspection view for properties includes label, domain, range and property type.

5 VISUALIZING A MAPPING

The alignment can be navigated using three different strategies:

- the next/previous mapping option;
- select a mapping from the list of mappings in the Alignment Reviewer tab or in the appropriate sub-menu;
- searching a certain mapping containing a certain term of interest, which is supported by an auto-complete function.

Once a mapping is selected, it can be visualized in the Mapping Viewer tab which includes a graph-based representation of the mapping and its neighborhood. The neighborhood of a mapping includes the classes that are at a predefined distance from the mapped classes, and any mappings between them (see Figure 1).

6 CONCLUSION

User involvement in ontology matching is greatly influenced by the availability of suitable user interfaces and adequate visualization approaches. The recent updates to AgreementMakerLight's user interface have made it possible for users to edit a loaded or computed alignment, while being supported by element inspection capabilities and graph-based visualization of mappings in their context. In future work, we plan to include the visualization of conflicting mappings caused by logical incoherence (Martins et al., 2015). This will allow user to tailor an alignment to their specific purposes since ensuring absolute coherence can decrease the usefulness of an alignment in some cases, due to the loss of meaningful mappings through the repair process (Pesquita et al., 2013).

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